

ttt gct gtg gtg aca atc ctg cag tgc ttc ctg att agc aca ctc ttc Phe Ala Val Val Thr Ile Leu Gln Cys Phe Leu Ile Ser Thr Leu Phe 725 730 735 740	2561
tcc aga gcc aac ctg gca gca gcc tgt ggg ggc atc atc tac ttc acg Ser Arg Ala Asn Leu Ala Ala Ala Cys Gly Gly Ile Ile Tyr Phe Thr 745 750 755	2609
ctg tac ctg ccc tac gtc ctg tgt gtg gca tgg cag gac tac gtg ggc Leu Tyr Leu Pro Tyr Val Leu Cys Val Ala Trp Gln Asp Tyr Val Gly 760 765 770	2657
ttc aca ctc aag atc ttc gct agc ctg ctg tct cct gtg gct ttt ggg Phe Thr Leu Lys Ile Phe Ala Ser Leu Leu Ser Pro Val Ala Phe Gly 775 780 785	2705
ttt ggc tgt gag tac ttt gcc ctt ttt gag gag cag ggc att gga gtg Phe Gly Cys Glu Tyr Phe Ala Leu Phe Glu Glu Gln Gly Ile Gly Val 790 795 800	2753
cag tgg gac aac ctg ttt gag agt cct gtg gag gaa gat ggc ttc aat Gln Trp Asp Asn Leu Phe Glu Ser Pro Val Glu Glu Asp Gly Phe Asn 805 810 815 820	2801
ctc acc act tcg gtc tcc atg atg ctg ttt gac acc ttc ctc tat ggg Leu Thr Thr Ser Val Ser Met Met Leu Phe Asp Thr Phe Leu Tyr Gly 825 830 835	2849
gtg atg acc tgg tac att gag gct gtc ttt cca ggc cag tac gga att Val Met Thr Trp Tyr Ile Glu Ala Val Phe Pro Gly Gln Tyr Gly Ile 840 845 850	2897
ccc agg ccc tgg tat ttt cct tgc acc aag tcc tac tgg ttt ggc gag Pro Arg Pro Trp Tyr Phe Pro Cys Thr Lys Ser Tyr Trp Phe Gly Glu 855 860 865	2945
gaa agt gat gag aag agc cac cct ggt tcc aac cag aag aga ata tca Glu Ser Asp Glu Lys Ser His Pro Gly Ser Asn Gln Lys Arg Ile Ser 870 875 880	2993
gaa atc tgc atg gag gag gaa ccc acc cac ttg aag ctg ggc gtg tcc Glu Ile Cys Met Glu Glu Glu Pro Thr His Leu Lys Leu Gly Val Ser 885 890 895 900	3041
att cag aac ctg gta aaa gtc tac cga gat ggg atg aag gtg gct gtc Ile Gln Asn Leu Val Lys Val Tyr Arg Asp Gly Met Lys Val Ala Val 905 910 915	3089
gat ggc ctg gca ctg aat ttt tat gag ggc cag atc acc tcc ttc ctg Asp Gly Leu Ala Leu Asn Phe Tyr Glu Gly Gln Ile Thr Ser Phe Leu 920 925 930	3137
ggc cac aat gga gcg ggg aag acg acc acc atg tca atc ctg acc ggg Gly His Asn Gly Ala Gly Lys Thr Thr Thr Met Ser Ile Leu Thr Gly 935 940 945	3185
ttg ttc ccc ccg acc tcg ggc acc gcc tac atc ctg gga aaa gac att Leu Phe Pro Pro Thr Ser Gly Thr Ala Tyr Ile Leu Gly Lys Asp Ile 950 955 960	3233
cgc tct gag atg agc acc atc cgg cag aac ctg ggg gtc tgt ccc cag Arg Ser Glu Met Ser Thr Ile Arg Gln Asn Leu Gly Val Cys Pro Gln 965 970 975 980	3281

cat aac gtg ctg ttt gac atg ctg act gtc gaa gaa cac atc tgg ttc	3329
His Asn Val Leu Phe Asp Met Leu Thr Val Glu Glu His Ile Trp Phe	
985 990 995	
tat gcc cgc ttg aaa ggg ctc tct gag aag cac gtg aag gcg gag atg	3377
Tyr Ala Arg Leu Lys Gly Leu Ser Glu Lys His Val Lys Ala Glu Met	
1000 1005 1010	
gag cag atg gcc ctg gat gtt ggt ttg cca tca agc aag ctg aaa agc	3425
Glu Gln Met Ala Leu Asp Val Gly Leu Pro Ser Ser Lys Leu Lys Ser	
1015 1020 1025	
aaa aca agc cag ctg tca ggt gga atg cag aga aag cta tct gtg gcc	3473
Lys Thr Ser Gln Leu Ser Gly Gly Met Gln Arg Lys Leu Ser Val Ala	
1030 1035 1040	
ttg gcc ttt gtc ggg gga tct aag gtt gtc att ctg gat gaa ccc aca	3521
Leu Ala Phe Val Gly Gly Ser Lys Val Val Ile Leu Asp Glu Pro Thr	
1045 1050 1055 1060	
gct ggt gtg gac cct tac tcc cgc agg gga ata tgg gag ctg ctg ctg	3569
Ala Gly Val Asp Pro Tyr Ser Arg Arg Gly Ile Trp Glu Leu Leu Leu	
1065 1070 1075	
aaa tac cga caa ggc cgc acc att att ctc tct aca cac cac atg gat	3617
Lys Tyr Arg Gln Gly Arg Thr Ile Ile Leu Ser Thr His His Met Asp	
1080 1085 1090	
gaa gcg gac gtc ctg ggg gac agg att gcc atc atc tcc cat ggg aag	3665
Glu Ala Asp Val Leu Gly Asp Arg Ile Ala Ile Ile Ser His Gly Lys	
1095 1100 1105	
ctg tgc tgt gtg ggc tcc tcc ctg ttt ctg aag aac cag ctg gga aca	3713
Leu Cys Cys Val Gly Ser Ser Leu Phe Leu Lys Asn Gln Leu Gly Thr	
1110 1115 1120	
ggc tac tac ctg acc ttg gtc aag aaa gat gtg gaa tcc tcc ctc agt	3761
Gly Tyr Tyr Leu Thr Leu Val Lys Lys Asp Val Glu Ser Ser Leu Ser	
1125 1130 1135 1140	
tcc tgc aga aac agt agt agc act gtg tca tac ctg aaa aag gag gac	3809
Ser Cys Arg Asn Ser Ser Ser Thr Val Ser Tyr Leu Lys Lys Glu Asp	
1145 1150 1155	
agt gtt tct cag agc agt tct gat gct ggc ctg ggc agc gac cat gag	3857
Ser Val Ser Gln Ser Ser Ser Asp Ala Gly Leu Gly Ser Asp His Glu	
1160 1165 1170	
agt gac acg ctg acc atc gat gtc tct gct atc tcc aac ctc atc agg	3905
Ser Asp Thr Leu Thr Ile Asp Val Ser Ala Ile Ser Asn Leu Ile Arg	
1175 1180 1185	
aag cat gtg tct gaa gcc cgg ctg gtg gaa gac ata ggg cat gag ctg	3953
Lys His Val Ser Glu Ala Arg Leu Val Glu Asp Ile Gly His Glu Leu	
1190 1195 1200	
acc tat gtg ctg cca tat gaa gct gct aag gag gga gcc ttt gtg gaa	4001
Thr Tyr Val Leu Pro Tyr Glu Ala Ala Lys Glu Gly Ala Phe Val Glu	
1205 1210 1215 1220	
ctc ttt cat gag att gat gac cgg ctc tca gac ctg ggc att tct agt	4049
Leu Phe His Glu Ile Asp Asp Arg Leu Ser Asp Leu Gly Ile Ser Ser	
1225 1230 1235	



225	230	235	
ggc tac ttg gtg aat tgg gat gtt cag aga caa gtt tgg gat tac ctt Gly Tyr Leu Val Asn Trp Asp Val Gln Arg Gln Val Trp Asp Tyr Leu 240 245 250			1250
ttt gga aaa gaa atg tat cag gtt gat ttt tta gat act aat att att Phe Gly Lys Glu Met Tyr Gln Val Asp Phe Leu Asp Thr Asn Ile Ile 255 260 265 270			1298
atc act gaa cca tac ttt aac ttc act tca att caa gaa tca atg aat Ile Thr Glu Pro Tyr Phe Asn Phe Thr Ser Ile Gln Glu Ser Met Asn 275 280 285			1346
gaa att cta ttt gaa gaa tac cag ttt caa gca gta tta aga gta aat Glu Ile Leu Phe Glu Glu Tyr Gln Phe Gln Ala Val Leu Arg Val Asn 290 295 300			1394
gct ggg gct ctc agt gca cat agg tat ttc cga gat aat cct tcc gaa Ala Gly Ala Leu Ser Ala His Arg Tyr Phe Arg Asp Asn Pro Ser Glu 305 310 315			1442
tta tgc tgt atc att gtt gat agt gga tat tcc ttt aca cat ata gtt Leu Cys Cys Ile Ile Val Asp Ser Gly Tyr Ser Phe Thr His Ile Val 320 325 330			1490
cct tat tgt aga agt aaa aag aaa aaa gaa gca att att cgg ata aat Pro Tyr Cys Arg Ser Lys Lys Lys Lys Glu Ala Ile Ile Arg Ile Asn 335 340 345 350			1538
gtg gga gga aaa ctc tta acc aat cat cta aag gag atc ata tct tac Val Gly Gly Lys Leu Leu Thr Asn His Leu Lys Glu Ile Ile Ser Tyr 355 360 365			1586
agg cag cta cat gtt atg gat gaa aca cat gtg att aat caa gtg aaa Arg Gln Leu His Val Met Asp Glu Thr His Val Ile Asn Gln Val Lys 370 375 380			1634
gaa gat gta tgc tat gtg tct cag gat ttt tat aga gac atg gat att Glu Asp Val Cys Tyr Val Ser Gln Asp Phe Tyr Arg Asp Met Asp Ile 385 390 395			1682
gca aag ttg aaa gga gaa gaa aat aca gta atg ata gac tat gtc ttg Ala Lys Leu Lys Gly Glu Glu Asn Thr Val Met Ile Asp Tyr Val Leu 400 405 410			1730
cct gac ttc agt aca att aaa aag ggc ttt tgt aag cca agg gaa gag Pro Asp Phe Ser Thr Ile Lys Lys Gly Phe Cys Lys Pro Arg Glu Glu 415 420 425 430			1778
atg gtg ttg agt gga aaa tac aaa tct ggg gaa caa att ctt cgt ttg Met Val Leu Ser Gly Lys Tyr Lys Ser Gly Glu Gln Ile Leu Arg Leu 435 440 445			1826
gcc aat gag aga ttt gct gtt ccg gaa ata ctc ttt aat cct tct gat Ala Asn Glu Arg Phe Ala Val Pro Glu Ile Leu Phe Asn Pro Ser Asp 450 455 460			1874
ata ggc att caa gaa atg gga att cca gaa gct att gtc tat tca att Ile Gly Ile Gln Glu Met Gly Ile Pro Glu Ala Ile Val Tyr Ser Ile 465 470 475			1922
caa aat cta cct gaa gaa atg cag ccg cat ttt ttt aag aac att gtc Gln Asn Leu Pro Glu Glu Met Gln Pro His Phe Phe Lys Asn Ile Val 480 485 490			1970

480	485	490	
ttg aca gga gga aat tcc ctt ttc cca gga ttt agg gat cgg gtt tac			2018
Leu Thr Gly Gly Asn Ser Leu Phe Pro Gly Phe Arg Asp Arg Val Tyr			
495	500	505	510
tca gaa gtt cga tgt ctt act cca aca gat tat gat gtt tct gtt gtg			2066
Ser Glu Val Arg Cys Leu Thr Pro Thr Asp Tyr Asp Val Ser Val Val			
	515	520	525
ctg cct gaa aac cct att act tat gcc tgg gaa ggt gga aaa ttg ata			2114
Leu Pro Glu Asn Pro Ile Thr Tyr Ala Trp Glu Gly Gly Lys Leu Ile			
	530	535	540
tca gag aat gat gat ttt gaa gat atg gtg gta aca aga gaa gat tac			2162
Ser Glu Asn Asp Asp Phe Glu Asp Met Val Val Thr Arg Glu Asp Tyr			
	545	550	555
gaa gaa aat gga cat agc gtc tgt gaa gag aaa ttt gat att taagcaa			2211
Glu Glu Asn Gly His Ser Val Cys Glu Glu Lys Phe Asp Ile			
	560	565	570
catttttgaa tgaaagttgt gaccataagg tttaatttca aagttccttt taaaagaggt			2271
taaggaactg tgttaccttt tgtcctaaga aaaaggcttg aatttatgta aatactttga			2331
tcgattgcta attttcaaag gcttcttagg taggttacta cagtaaactg taactcagtc			2391
cacattttca tttaggagct agactaccat aacaatgctt atgctgtttc caagggtagg			2451
ttatttttca ttaaaagaag aatgaatgca ttttaagttt aattcttcat agctgaaagc			2511
acaaatttaa cggcttcact ggacagtttt ccttagaagg tagttttgtg tgactgtgac			2571
taaactattt tatttttaaaa tgtcattctt atttatacat tctaaagttg gaaagactga			2631
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Met Ser Arg Pro Ala Pro Gly Arg Arg Ala Ala Pro Thr Ala Thr	
1 5 10 15	
gcc gcc gcc gcc atg aac att ttc cgg ctg act ggg gac ctg tcc cac	157
Ala Ala Ala Ala Met Asn Ile Phe Arg Leu Thr Gly Asp Leu Ser His	
20 25 30	
ctg gcg gcc atc gtc atc ctg ctg ctg aag atc tgg aag acg cgc tcc	205

Leu	Ala	Ala	Ile	Val	Ile	Leu	Leu	Leu	Lys	Ile	Trp	Lys	Thr	Arg	Ser		
			35					40					45				
tgc	gcc	ggt	att	tct	ggg	aaa	agc	cag	ctt	ctg	ttt	gca	ctg	gtc	ttc		253
Cys	Ala	Gly	Ile	Ser	Gly	Lys	Ser	Gln	Leu	Leu	Phe	Ala	Leu	Val	Phe		
		50					55					60					
aca	act	cgt	tac	ctg	gat	ctt	ttt	act	tca	ttt	att	tca	ttg	tat	aac		301
Thr	Thr	Arg	Tyr	Leu	Asp	Leu	Phe	Thr	Ser	Phe	Ile	Ser	Leu	Tyr	Asn		
		65				70					75						
aca	tct	atg	aag	gtt	atc	tac	ctt	gcc	tgc	tcc	tat	gcc	aca	gtg	tac		349
Thr	Ser	Met	Lys	Val	Ile	Tyr	Leu	Ala	Cys	Ser	Tyr	Ala	Thr	Val	Tyr		
		80			85				90						95		
ctg	atc	tac	ctg	aaa	ttt	aag	gca	acc	tac	gat	gga	aat	cat	gat	acc		397
Leu	Ile	Tyr	Leu	Lys	Phe	Lys	Ala	Thr	Tyr	Asp	Gly	Asn	His	Asp	Thr		
				100				105					110				
ttc	cga	gtg	gag	ttt	ctg	gtg	gtc	cct	gtg	gga	ggc	ctc	tca	ttt	tta		445
Phe	Arg	Val	Glu	Phe	Leu	Val	Val	Pro	Val	Gly	Gly	Leu	Ser	Phe	Leu		
			115					120					125				
gtt	aat	cac	gat	ttc	tct	cct	ctt	gag	atc	ctc	tgg	acc	ttc	tcc	atc		493
Val	Asn	His	Asp	Phe	Ser	Pro	Leu	Glu	Ile	Leu	Trp	Thr	Phe	Ser	Ile		
		130					135					140					
tac	ctg	gag	tcc	gtg	gct	atc	ctt	ccg	cag	ctg	ttt	atg	atc	agc	aag		541
Tyr	Leu	Glu	Ser	Val	Ala	Ile	Leu	Pro	Gln	Leu	Phe	Met	Ile	Ser	Lys		
		145				150					155						
act	ggg	gag	gcc	gag	acc	atc	acc	acc	cac	tac	ctg	ttc	ttc	ctg	ggc		589
Thr	Gly	Glu	Ala	Glu	Thr	Ile	Thr	Thr	His	Tyr	Leu	Phe	Phe	Leu	Gly		
		160			165					170					175		
ctc	tat	cgt	gct	ttg	tat	ctt	gtc	aac	tgg	atc	tgg	cgc	ttc	tac	ttt		637
Leu	Tyr	Arg	Ala	Leu	Tyr	Leu	Val	Asn	Trp	Ile	Trp	Arg	Phe	Tyr	Phe		
				180				185					190				
gag	ggc	ttc	ttt	gac	ctc	att	gct	gtg	gtg	gcc	ggc	gta	gtc	cag	acc		685
Glu	Gly	Phe	Phe	Asp	Leu	Ile	Ala	Val	Val	Ala	Gly	Val	Val	Gln	Thr		
			195				200					205					
atc	cta	tac	tgt	gac	ttc	ttc	tac	ttg	tac	att	aca	aaa	gta	ctc	aag		733
Ile	Leu	Tyr	Cys	Asp	Phe	Phe	Tyr	Leu	Tyr	Ile	Thr	Lys	Val	Leu	Lys		
		210					215					220					
gga	aag	aag	ctc	agt	ttg	cca	gca	taa	gttgc	caaagaccat	caccagcatc						785
Gly	Lys	Lys	Leu	Ser	Leu	Pro	Ala	*									
		225				230											
tgtccttcag	ggtgctcgga	cagaattctt	accacagcaa	aggcataaga	tgcttgatac												845
ggaaaatcag	aaacttaact	cttttgttgc	agatagtcac	cagtggctct	gtaaaaacgc												905
agaggaaaag	agccagaagg	tttctgttta	atgcatcttg	ccttatcttt	ttttattact												965
gtgtacaaag	atttttttac	acaaagaaac	ttaatgctgt	attaataaat	tcagtgtgta												1025
gcttcaattg	ggatagttcc	aaaagtgaag	attttgtgag	gaataagtgc	aaattttttt												1085
tttattttaa	aaaattcttt	gaaactctta	agtctttgtg	tctgcaatga	aattgtactc												1145
cttgacagtt	gatagattat	gtattcttcc	atccctcaaa	cttgcatccc	actatattta												1205

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 Met Glu Leu Val Gln Val Leu Lys Arg  
 1 5  
 ggg ctg cag cag atc acc ggc cac ggc ggt ctc cga ggc tat cta cgg 161  
 Gly Leu Gln Gln Ile Thr Gly His Gly Gly Leu Arg Gly Tyr Leu Arg  
 10 15 20 25  
 gtt ttt ttc agg aca aat gat gcg aag gtt ggt aca tta gtg ggg gaa 209  
 Val Phe Phe Arg Thr Asn Asp Ala Lys Val Gly Thr Leu Val Gly Glu  
 30 35 40  
 gac aaa tat gga aac aaa tac tat gaa gac aac aag caa ttt ttt ggc 257  
 Asp Lys Tyr Gly Asn Lys Tyr Tyr Glu Asp Asn Lys Gln Phe Phe Gly  
 45 50 55  
 cgt cac cga tgg gtt gta tat act act gaa atg aat ggc aaa aac aca 305  
 Arg His Arg Trp Val Val Tyr Thr Thr Glu Met Asn Gly Lys Asn Thr  
 60 65 70  
 ttc tgg gat gtg gat gga agc atg gtg cct cct gaa tgg cat cgt tgg 353  
 Phe Trp Asp Val Asp Gly Ser Met Val Pro Pro Glu Trp His Arg Trp  
 75 80 85  
 ctt cac agt atg act gat gat cct cca aca aca aaa cca ctt act gct 401  
 Leu His Ser Met Thr Asp Asp Pro Pro Thr Thr Lys Pro Leu Thr Ala  
 90 95 100 105  
 cgt aaa ttc att tgg acg aac cat aaa ttc aac gtg act ggc acc cca 449  
 Arg Lys Phe Ile Trp Thr Asn His Lys Phe Asn Val Thr Gly Thr Pro  
 110 115 120  
 gaa caa tat gta cct tat tct acc act aga aag aag att cag gag tgg 497  
 Glu Gln Tyr Val Pro Tyr Ser Thr Thr Arg Lys Lys Ile Gln Glu Trp  
 125 130 135  
 atc cca cct tca aca cct tac aag taaagacaat gaagaacagt tgaaacatgc 551  
 Ile Pro Pro Ser Thr Pro Tyr Lys  
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 aaaatatgga gcttttcatg taattactct tttactgttt accattcact ataattcaca 611  
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 agttccggag tccagctggc taaaactcat cccagaggat a atg gca acc cat 173  
 Met Ala Thr His  
 1  
 gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg gtg ggc 221  
 Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met Val Gly  
 5 10 15 20  
 aca gtg gct gtc act gtc atg cct cag tgg aga gtg tcg gcc ttc att 269  
 Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val Ser Ala Phe Ile  
 25 30 35  
 gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg tgg atg 317  
 Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu Trp Met  
 40 45 50  
 aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc tat gat 365  
 Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile Tyr Asp  
 55 60 65  
 tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga ctg atg 413  
 Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly Leu Met  
 70 75 80  
 tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc atc ctt 461  
 Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala Ile Leu  
 85 90 95 100  
 ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg aag gct 509  
 Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala  
 105 110 115  
 cac att ctg ctg acg gct gga atc atc ttc atc atc acg ggc atg gtg 557  
 His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val  
 120 125 130  
 gtg ctc atc cct gtg agc tgg gtt gcc aat gcc atc atc aga gat ttc 605  
 Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe  
 135 140 145  
 tat aac tca ata gtg aat gtt gcc caa aaa cgt gag ctt gga gaa gct 653  
 Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala  
 150 155 160

ctc tac tta gga tgg acc acg gca ctg gtg ctg att gtt gga gga gct 701  
Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala  
165 170 175 180

ctg ttc tgc tgc gtt ttt tgt tgc aac gaa aag agc agt agc tac aga 749  
Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr Arg  
185 190 195

tac tcg ata cct tcc cat cgc aca acc caa aaa agt tat cac acc gga 797  
Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His Thr Gly  
200 205 210

aag aag tca ccg agc gtc tac tcc aga agt cag tat gtg tag ttgtgta 846  
Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val \*  
215 220 225

tgtttttttta actttactat aaagccatgc aaatgacaaa aatctatatt actttctcaa 906

aatggacccc aaagaaactt tgatttactg ttcttaactg cctaattctta attacaggaa 966

ctgtgcatca gctatttatg attctataag ctatttcagc agaatgagat attaaatcca 1026

atgctttgat tgnctagaa agtatagtaa tttgttttct aagggtggttc aagcatctac 1086

tcttttnatc atttacttca aaatgacatt gctaaagact gcattatttn actactgtaa 1146

tttctccacg gccatagcat tatgtacata ggtgagtgtg ccatttatta tcctcaccat 1206

tggnnggcat gctttattat gggttttaat ttnaaaattg gaatgccccg gtcccattnc 1266

cacctggnat taantagggc ctccaacctt attgcctttt nnagggggaa atcatggggt 1326

aggggggtgn aaggagggt tncctgttna tntggnntaa aanccagggt tgggggttaa 1386

tggcccccn tttttnattg gcggtttaan atngaggntt nnatccggga ttgttanggg 1446

anttgattgn gttcctggtn tegtggtttt nggccttggg ggttgggncc cnacctcnt 1506

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669



acc atg ctg act gtc ata gag cag cca gta cct cca aca cca gct acc	640
Thr Met Leu Thr Val Ile Glu Gln Pro Val Pro Pro Thr Pro Ala Thr	
95 100 105	
cct gag gac cct gcc ccg ctc tgg ggt ccc cct cct gcc cag ggc agc	688
Pro Glu Asp Pro Ala Pro Leu Trp Gly Pro Pro Pro Ala Gln Gly Ser	
110 115 120	
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Gly Pro Thr Gly Pro Lys Gly Asp Ala Gly Ser Arg Gly Pro Met Gly	
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Met Arg Gly Pro Pro Gly Asp Pro Leu Leu Ser Asn Thr Phe Thr Glu	
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Thr Asn Asn His Trp Pro Gln Gly Pro Thr Gly Pro Pro Gly Pro Pro	
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Gly Pro Met Gly Pro Pro Gly Pro Pro Gly Pro Thr Gly Val Pro Gly	
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Ser Pro Gly His Ile Gly Pro Pro Gly Pro Thr Gly Pro Lys Gly Ile	
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Ser Gly His Pro Gly Glu Lys Gly Glu Arg Gly Leu Arg Gly Glu Pro	
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Gly Pro Gln Gly Ser Ala Gly Gln Arg Gly Glu Pro Gly Pro Lys Gly	
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Asp Pro Gly Glu Lys Ser His Trp Gly Glu Gly Leu His Gln Leu Arg	
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Glu Ala Leu Lys Ile Leu Ala Glu Arg Val Leu Ile Leu Glu Thr Met	
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Ile Gly Leu Tyr Glu Pro Glu Leu Gly Ser Gly Ala Gly Pro Ala Gly	
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Thr Gly Thr Pro Ser Leu Leu Arg Gly Lys Arg Gly Gly His Ala Thr	
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Asn Tyr Arg Ile Val Ala Pro Arg Ser Arg Asp Glu Arg Gly	
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cccagaaaat gataga      atg aga atg aag tat gga gga caa gaa ttt tgg 169
                        Met Arg Met Lys Tyr Gly Gly Gln Glu Phe Trp
                        1          5          10
gca gat ttg aat gcc atg aac gtg tat gaa aca act gaa ttt gac caa 217
Ala Asp Leu Asn Ala Met Asn Val Tyr Glu Thr Thr Glu Phe Asp Gln
                        15          20          25
cta cga agg ctg tcc aca cca ccc tct agc aat gtc aac tct att tac 265
Leu Arg Arg Leu Ser Thr Pro Pro Ser Ser Asn Val Asn Ser Ile Tyr
                        30          35          40
cac aca gtc tgg aaa ttc ttc tgt agg gac cac ttt gga tgg aga gag 313
His Thr Val Trp Lys Phe Phe Cys Arg Asp His Phe Gly Trp Arg Glu
                        45          50          55
tat ccc gag tct gtc att cga ttg att gaa gaa gcc aac tct cgg ggt 361
Tyr Pro Glu Ser Val Ile Arg Leu Ile Glu Glu Ala Asn Ser Arg Gly
                        60          65          70          75

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aat tca ttc ttc agg aga gag ata aaa agg aga ccc ctc ttc cgc tcc	457
Asn Ser Phe Phe Arg Arg Glu Ile Lys Arg Arg Pro Leu Phe Arg Ser	
95 100 105	
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Cys Phe Ile Leu Leu Pro Tyr Leu Gln Thr Leu Gly Gly Val Pro Thr	
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caa gct cct cca cct ctt gaa gca act tca tca tca caa att atc tgc	553
Gln Ala Pro Pro Pro Leu Glu Ala Thr Ser Ser Ser Gln Ile Ile Cys	
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Pro Asp Gly Val Thr Ser Ala Asn Phe Tyr Pro Glu Thr Trp Val Tyr	
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Met His Pro Ser Gln Asp Phe Ile Gln Val Pro Val Ser Ala Glu Asp	
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Lys Ser Tyr Arg Ile Ile Tyr Asn Leu Phe His Lys Thr Val Pro Glu	
175 180 185	
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Phe Lys Tyr Arg Ile Leu Gln Ile Leu Arg Val Gln Asn Gln Phe Leu	
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Trp Glu Lys Tyr Lys Arg Lys Lys Glu Tyr Met Asn Arg Lys Met Phe	
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Cys Gly Lys His Ala Thr Met Phe Gly Gln Gly Ser Tyr Phe Ala Lys	
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Tyr Glu Glu Val Ser Asn Thr Val Ser Ile	
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Thr Asp Asp His Asp Arg Glu Phe Ser Val Ala Asp Leu Ser Val Gln  
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70 75 80

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	140
	145

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Phe Pro Val Arg Asp Glu Lys Arg Gly Lys Arg Pro Ser Pro Leu Ala	
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 Gly Met Arg Ser Tyr Tyr Tyr Gly Lys Phe Met Pro Val Gly Leu Ile  
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Met Thr Ser Asp \*

115

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Val Asn Leu Lys Val Ile Leu Leu Gly His Trp Leu Leu Thr Thr Trp  
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Gly Cys Ile Val Phe Ser Gly Ser Tyr Ala Trp Ala Asn Phe Thr Ile  
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Leu Ala Leu Gly Val Trp Ala Val Ala Gln Arg Asp Ser Ile Asp Ala  
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Ile Ser Met Phe Leu Gly Gly Leu Leu Ala Thr Ile Phe Leu Asp Ile  
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Val His Ile Ser Ile Phe Tyr Pro Arg Val Ser Leu Thr Asp Thr Gly  
70 75 80 85

cgc ttt ggc gtg ggc atg gcc atc ctc agc ttg ctg ctc aag ccg ctc 461  
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90

95

100

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Leu Val His Thr Gly Phe Leu Gly Ser Ser Gln Asp Arg Ser Ala Tyr
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cag acg att gac tca gca gag gcg ccc gca gat ccc ttt gca gtc cca      605
Gln Thr Ile Asp Ser Ala Glu Ala Pro Ala Asp Pro Phe Ala Val Pro
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gag ggc agg agt caa gat gcc cga ggg tac tga agccagcc acgctgcgcc      656
Glu Gly Arg Ser Gln Asp Ala Arg Gly Tyr *
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Phe Met Cys Ser Met Pro Arg Ser Leu Trp Leu Gly Cys Ser Ser Leu
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Asn	Lys	Pro	Pro	Asp	Gly	Asn	Ala	Pro	Pro	Asn	Ser	Phe	Tyr	Arg	Ala	
	255				260					265					270	
ctt	tat	cct	aaa	att	ata	caa	gac	att	gag	aca	ata	gaa	tct	aat	tgg	984
Leu	Tyr	Pro	Lys	Ile	Ile	Gln	Asp	Ile	Glu	Thr	Ile	Glu	Ser	Asn	Trp	
				275				280						285		
aga	tgt	gga	aga	cat	agt	tta	cag	aga	att	cac	tgc	cga	agt	gaa	aca	1032

Arg	Cys	Gly	Arg	His	Ser	Leu	Gln	Arg	Ile	His	Cys	Arg	Ser	Glu	Thr	
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Ser	Lys	Gly	Val	Tyr	Cys	Leu	Gln	Tyr	Asp	Asp	Gln	Lys	Ile	Val	Ser	
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ggc	ctt	cga	gac	aac	aca	atc	aag	atc	tgg	gat	aaa	aac	aca	ttg	gaa	1128
Gly	Leu	Arg	Asp	Asn	Thr	Ile	Lys	Ile	Trp	Asp	Lys	Asn	Thr	Leu	Glu	
		320					325					330				
tgc	aag	cga	att	ctc	aca	ggc	cat	aca	ggg	tca	gtc	ctc	tgt	ctc	cag	1176
Cys	Lys	Arg	Ile	Leu	Thr	Gly	His	Thr	Gly	Ser	Val	Leu	Cys	Leu	Gln	
335					340					345					350	
tat	gat	gag	aga	gtg	atc	ata	aca	gga	tca	tgc	gat	tcc	acg	gtc	aga	1224
Tyr	Asp	Glu	Arg	Val	Ile	Ile	Thr	Gly	Ser	Ser	Asp	Ser	Thr	Val	Arg	
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gtg	tgg	gat	gta	aat	aca	ggg	gaa	atg	cta	aac	acg	ttg	att	cac	cat	1272
Val	Trp	Asp	Val	Asn	Thr	Gly	Glu	Met	Leu	Asn	Thr	Leu	Ile	His	His	
			370					375					380			
tgt	gaa	gca	gtt	ctg	cac	ttg	cgt	ttc	aat	aat	ggc	atg	atg	gtg	acc	1320
Cys	Glu	Ala	Val	Leu	His	Leu	Arg	Phe	Asn	Asn	Gly	Met	Met	Val	Thr	
		385					390					395				
tgc	tcc	aaa	gat	cgt	tcc	att	gct	gta	tgg	gat	atg	gcc	tcc	cca	act	1368
Cys	Ser	Lys	Asp	Arg	Ser	Ile	Ala	Val	Trp	Asp	Met	Ala	Ser	Pro	Thr	
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gac	att	acc	ctc	cgg	agg	gtg	ctg	gtc	gga	cac	cga	gct	gct	gtc	aat	1416
Asp	Ile	Thr	Leu	Arg	Arg	Val	Leu	Val	Gly	His	Arg	Ala	Ala	Val	Asn	
415					420					425					430	
gtt	gta	gac	ttt	gat	gac	aag	tac	att	gtt	tct	gca	tct	ggg	gat	aga	1464
Val	Val	Asp	Phe	Asp	Asp	Lys	Tyr	Ile	Val	Ser	Ala	Ser	Gly	Asp	Arg	
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act	ata	aag	gta	tgg	aac	aca	agt	act	tgt	gaa	ttt	gta	agg	acc	tta	1512
Thr	Ile	Lys	Val	Trp	Asn	Thr	Ser	Thr	Cys	Glu	Phe	Val	Arg	Thr	Leu	
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Asn	Gly	His	Lys	Arg	Gly	Ile	Ala	Cys	Leu	Gln	Tyr	Arg	Asp	Arg	Leu	
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gta	gtg	agt	ggc	tca	tct	gac	aac	act	atc	aga	tta	tgg	gac	ata	gaa	1608
Val	Val	Ser	Gly	Ser	Ser	Asp	Asn	Thr	Ile	Arg	Leu	Trp	Asp	Ile	Glu	
		480					485					490				
tgt	ggg	gca	tgt	tta	cga	gtg	tta	gaa	ggc	cat	gag	gaa	ttg	gtg	cgt	1656
Cys	Gly	Ala	Cys	Leu	Arg	Val	Leu	Glu	Gly	His	Glu	Glu	Leu	Val	Arg	
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tgt	att	cga	ttt	gat	aac	aag	agg	ata	gtc	agt	ggg	gcc	tat	gat	gga	1704
Cys	Ile	Arg	Phe	Asp	Asn	Lys	Arg	Ile	Val	Ser	Gly	Ala	Tyr	Asp	Gly	
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aaa	att	aaa	gtg	tgg	gat	ctt	gtg	gct	gct	ttg	gac	ccc	cgt	gct	cct	1752
Lys	Ile	Lys	Val	Trp	Asp	Leu	Val	Ala	Ala	Leu	Asp	Pro	Arg	Ala	Pro	
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Ala Gly Thr Leu Cys Leu Arg Thr Leu Val Glu His Ser Gly Arg Val	
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Phe Arg Leu Gln Phe Asp Glu Phe Gln Ile Val Ser Ser Ser His Asp	
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Asp Thr Ile Leu Ile Trp Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala	
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Glu Pro Pro Arg Ser Pro Ser Arg Thr Tyr Thr Tyr Ile Ser Arg *	
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gcgatt atg gac ccg gcc gag gcg gtg ctg caa gag aag gca ctc aag	168
Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys	
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Ala Asp Ser Met Pro Ser Leu Arg Cys Leu Tyr Asn Pro Gly Thr Gly	
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Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met Lys Thr Glu Asn	
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Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr Ser Ser Met Ile Val	
80 85 90	
ccc aag caa cgg aaa ctc tca gca agc tat gaa aag gaa aag gaa ctg	456
Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys Glu Lys Glu Leu	
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Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp Gln Val Glu Phe	
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Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln His Gly His Ile	
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Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe Ile Thr Ala Leu	
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cca gct cgg gga ttg gat cat att gct gag aac att ctg tca tac ctg	648
Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile Leu Ser Tyr Leu	
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Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys Lys Glu Trp Tyr	
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cga gtg acc tct gat ggc atg ctg tgg aag aag ctt atc gag aga atg	744
Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu Ile Glu Arg Met	
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Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu Arg Arg Gly Trp	
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Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Gly Asn Ala Pro Pro	
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Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser Leu Gln Arg Ile	
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His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys Leu Gln Tyr Asp	
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gat cag aaa ata gta agc ggc ctt cga gac aac aca atc aag atc tgg	1032
Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr Ile Lys Ile Trp	
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Asp Lys Asn Thr Leu Glu Cys Lys Arg Ile Leu Thr Gly His Thr Gly	
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Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile Ile Thr Gly Ser	
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 Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys  
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 Phe Met Met Glu Phe Arg Ser Trp Cys Pro Gly Trp Asn Thr Met Ala  
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 Pro Arg Ser Leu Trp Leu Gly Cys Ser Ser Leu Ala Asp Ser Met Pro  
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 Lys Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys  
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 115 120 125  
 atg aag act gag aat tgt gtg gcc aaa aca aaa ctt gcc aat ggc act 552  
 Met Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr  
 130 135 140



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Ser Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu	
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Lys Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser	
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Asp Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr	
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Gln His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp	
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ttc ata act gct ctg cca gct cgg gga ttg gat cat att gct gag aac	792
Phe Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn	
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att ctg tca tac ctg gat gcc aaa tca cta tgt gct gct gaa ctt gtg	840
Ile Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val	
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Cys Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys	
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Leu Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala	
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Glu Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp	
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Gly Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile	
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Ile Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His	
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Ser Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr	
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Cys Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn	
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 Leu Ser Arg Asn Gly Pro Ala Leu Gln Glu Ala Tyr Val Arg Val Val  
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 acc gag aag tcc ccg acc gac tgg gct ctc ttt acc tat gaa ggc aac 391  
 Thr Glu Lys Ser Pro Thr Asp Trp Ala Leu Phe Thr Tyr Glu Gly Asn  
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 agc aat gac atc cgc gtg gct ggc aca ggg gag ggt ggc ctg gag gag 439  
 Ser Asn Asp Ile Arg Val Ala Gly Thr Gly Glu Gly Gly Leu Glu Glu  
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 atg gtg gag gag ctc aac agc ggg aag gtg atg tac gcc ttc tgc aga 487  
 Met Val Glu Glu Leu Asn Ser Gly Lys Val Met Tyr Ala Phe Cys Arg  
 55 60 65  
 gtg aag gac ccc aac tct gga ctg ccc aaa ttt gtc ctc atc aac tgg 535  
 Val Lys Asp Pro Asn Ser Gly Leu Pro Lys Phe Val Leu Ile Asn Trp  
 70 75 80  
 aca ggc gag ggc gtg aac gat gtg cgg aag gga gcc tgt gcc agc cac 583  
 Thr Gly Glu Gly Val Asn Asp Val Arg Lys Gly Ala Cys Ala Ser His  
 85 90 95 100  
 gtc agc acc atg gcc agc ttc ctg aag ggg gcc cat gtg acc atc aac 631  
 Val Ser Thr Met Ala Ser Phe Leu Lys Gly Ala His Val Thr Ile Asn  
 105 110 115  
 gca cgg gcc gag gag gat gtg gag cct gag tgc atc atg gag aag gtg 679  
 Ala Arg Ala Glu Glu Asp Val Glu Pro Glu Cys Ile Met Glu Lys Val

	120		125		130	
gcc aag gct tca ggt gcc aac tac agc ttt cac aag gag agt ggc cgc						727
Ala Lys Ala Ser Gly Ala Asn Tyr Ser Phe His Lys Glu Ser Gly Arg						
	135		140		145	
ttc cag gac gtg gga ccc cag gcc cca gtg ggc tct gtg tac cag aag						775
Phe Gln Asp Val Gly Pro Gln Ala Pro Val Gly Ser Val Tyr Gln Lys						
	150		155		160	
acc aat gcc gtg tct gag att aaa agg gtt ggt aaa gac agc ttc tgg						823
Thr Asn Ala Val Ser Glu Ile Lys Arg Val Gly Lys Asp Ser Phe Trp						
	165		170		175	180
gcc aaa gca gag aag gag gag gag aac cgt cgg ctg gag gaa aag cgg						871
Ala Lys Ala Glu Lys Glu Glu Glu Asn Arg Arg Leu Glu Glu Lys Arg						
		185		190		195
cgg gcc gag gag gca cag cgg cag ctg gag cag gag cgc cgg gag cgt						919
Arg Ala Glu Glu Ala Gln Arg Gln Leu Glu Gln Glu Arg Arg Glu Arg						
	200		205		210	
gag ctg cgt gag gct gca cgc cgg gag cag cgc tat cag gag cag ggt						967
Glu Leu Arg Glu Ala Ala Arg Arg Glu Gln Arg Tyr Gln Glu Gln Gly						
	215		220		225	
ggc gag gcc agc ccc cag agg acg tgg gag cag cag caa gaa gtg gtt						1015
Gly Glu Ala Ser Pro Gln Arg Thr Trp Glu Gln Gln Gln Glu Val Val						
	230		235		240	
tca agg aac cga aat gag cag gag tct gcc gtg cac ccg agg gag att						1063
Ser Arg Asn Arg Asn Glu Gln Glu Ser Ala Val His Pro Arg Glu Ile						
	245		250		255	260
ttc aag cag aag gag agg gcc atg tcc acc acc tcc atc tcc agt cct						1111
Phe Lys Gln Lys Glu Arg Ala Met Ser Thr Thr Ser Ile Ser Ser Pro						
	265		270		275	
cag cct ggc aag ctg agg agc ccc ttc ctg cag aag cag ctc acc caa						1159
Gln Pro Gly Lys Leu Arg Ser Pro Phe Leu Gln Lys Gln Leu Thr Gln						
	280		285		290	
cca gag acc cac ttt ggc aga gag cca gct gct gcc atc tca agg ccc						1207
Pro Glu Thr His Phe Gly Arg Glu Pro Ala Ala Ala Ile Ser Arg Pro						
	295		300		305	
agg gca gat ctc cct gct gag gag ccg gcg ccc agc act cct cca tgt						1255
Arg Ala Asp Leu Pro Ala Glu Glu Pro Ala Pro Ser Thr Pro Pro Cys						
	310		315		320	
ctg gtg cag gca gaa gag gag gct gtg tat gag gaa cct cca gag cag						1303
Leu Val Gln Ala Glu Glu Glu Ala Val Tyr Glu Glu Pro Pro Glu Gln						
	325		330		335	340
gag acc ttc tac gag cag ccc cca ctg gtg cag cag caa ggt gct ggc						1351
Glu Thr Phe Tyr Glu Gln Pro Pro Leu Val Gln Gln Gln Gly Ala Gly						
	345		350		355	
tct gag cac att gac cac cac att cag ggc cag ggg ctc agt ggg caa						1399
Ser Glu His Ile Asp His His Ile Gln Gly Gln Gly Leu Ser Gly Gln						
	360		365		370	
ggg ctc tgt gcc cgt gcc ctg tac gac tac cag gca gcc gac gac aca						1447
Gly Leu Cys Ala Arg Ala Leu Tyr Asp Tyr Gln Ala Ala Asp Asp Thr						

375	380	385	
gag atc tcc ttt gac ccc gag aac ctc atc acg ggc atc gag gtg atc			1495
Glu Ile Ser Phe Asp Pro Glu Asn Leu Ile Thr Gly Ile Glu Val Ile			
390	395	400	
gac gaa ggc tgg tgg cgt ggc tat ggg ccg gat ggc cat ttt ggc atg			1543
Asp Glu Gly Trp Trp Arg Gly Tyr Gly Pro Asp Gly His Phe Gly Met			
405	410	415	420
ttc cct gcc aac tac gtg gag ctc att gag tga ggctgagg gcacatcttg			1594
Phe Pro Ala Asn Tyr Val Glu Leu Ile Glu *			
425	430		
cccttcccct ctcagacatg gcttccttat tgctggaaga ggaggcctgg gagttgacat			1654
tcagcactct tccaggaata ggacccccag tgaggatgag gcctcagggc tccctccggc			1714
ttggcagact cagcctgtca ccccaaatgc agcaatggcc tggtgattcc cacacatcct			1774
tcctgcatcc cccgaccctc ccagacagct tggtctcttg ccctgacagg atactgagcc			1834
aagccctgcc tgtggccaag ccctgagtgg ccactgccaa gctgcgggga agggctcctga			1894
gcaggggcat ctgggaggct ctggctgect tctgcattta tttgcctttt ttctttttct			1954
cttgcttcta aggggtggtg gccaccactg tttagaatga cccttgggaa cagtgaacgt			2014
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gcaggggaatt tgtcttggtg gagcctgctc tgtgctcccc actccatttc tctgtccctc			2134
tgccctgggct atgggaagtg gggatgcaga tggccaagct cccaccctgg gtattcaaaa			2194
acggcagaca caacatgttc ctccacgcgg ctccactgat gcctgcaggg ccagtggtgt			2254
gcctcaactg attctgactt caggaaaagt aacacagagt ggccttggcc tgttgtcttc			2314
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aaaa			2378

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caccaaacc aaaaaaagag atctctcgag gatccgaatt cgcgccgcg tctaccgcta	120
ggaagaggcc gcgtggggcg aaggcggcgc ttggctggtg gggcccgcg cggtatttct	180
ccgggcggcg agagcggatc tatcttggga tccc	
atg gct ttc ttt act ggg	232
Met Ala Phe Phe Thr Gly	
1 5	

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ctc tgg ggc ccc ttc acc tgt gta agc aga gtg ctg agc cat cac tgt      280
Leu Trp Gly Pro Phe Thr Cys Val Ser Arg Val Leu Ser His His Cys
          10                      15                      20

ttc agc acc act ggg agt ctg agt gcg att cag aag atg acg cgg gta      328
Phe Ser Thr Thr Gly Ser Leu Ser Ala Ile Gln Lys Met Thr Arg Val
          25                      30                      35

cga gtg gtg gac aac agt gcc ctg ggg aac agc cca tac cat cgg gct      376
Arg Val Val Asp Asn Ser Ala Leu Gly Asn Ser Pro Tyr His Arg Ala
          40                      45                      50

cct cgc tgc atc cat gtc tat aag aag aat gga gtg ggc aag gtg ggc      424
Pro Arg Cys Ile His Val Tyr Lys Lys Asn Gly Val Gly Lys Val Gly
          55                      60                      65                      70

gac cag ata cta ctg gcc atc aag gga cag aag aaa aag gcg ctc att      472
Asp Gln Ile Leu Leu Ala Ile Lys Gly Gln Lys Lys Lys Ala Leu Ile
          75                      80                      85

gtg ggg cac tgc atg cct ggc ccc cga atg acc ccc aga ttt gac tcc      520
Val Gly His Cys Met Pro Gly Pro Arg Met Thr Pro Arg Phe Asp Ser
          90                      95                      100

aac aac gtg gtc ctc att gag gac aac ggg aac cct gtg ggg aca cga      568
Asn Asn Val Val Leu Ile Glu Asp Asn Gly Asn Pro Val Gly Thr Arg
          105                      110                      115

att aag aca ccc atc ccc acc agc ctg cgc aag cgg gaa ggc gag tat      616
Ile Lys Thr Pro Ile Pro Thr Ser Leu Arg Lys Arg Glu Gly Glu Tyr
          120                      125                      130

tcc aag gtg ctg gcc att gct cag aac ttt gtg tga gttg agcccaggcc      666
Ser Lys Val Leu Ala Ile Ala Gln Asn Phe Val *
          135                      140                      145

tctggttgca ggactcgtga atggagcagt tctgagaacc acccttttgc taaggagct      726

tgaggagccac atggctgctc ccttcacact gggtaacagt gtagtatacct gtgagagaat      786

aaatgtattc atttatgtgt ttttccagag ctttctggga tgtgggaaaa taaattacac      846

tgaagcagtt gaaaggtggc ttacccgagt ctggccacac ggggtagcat tctttacatg      906

gagcagcctt ggtgccaggg tctgagccct tgcttttctg gtttggaccc tataagttca      966

tccaggactg tcaggccctg gaaaactgag gtacacacca aatgcccaatt tataaatgta    1026

ccgtggctct aacca                                                    1041

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<400> 265



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gcc agc ccc acc tca ggc ccc cag gag tgt gca aag ggc tcc acg gtg	96
Ala Ser Pro Thr Ser Gly Pro Gln Glu Cys Ala Lys Gly Ser Thr Val	
20 25 30	
tgg tgt cag gat ctg cag aca gct gcc agg tgc ggg gct gtg ggg tac	144
Trp Cys Gln Asp Leu Gln Thr Ala Ala Arg Cys Gly Ala Val Gly Tyr	
35 40 45	
tgc caa ggg gcc gta tgg aac aaa ccc acc gcg aag tct ctg ccc tgc	192
Cys Gln Gly Ala Val Trp Asn Lys Pro Thr Ala Lys Ser Leu Pro Cys	
50 55 60	
gac gta tgc cag gac ata gca gcc gcc gct ggc aat ggg ctg aac cct	240
Asp Val Cys Gln Asp Ile Ala Ala Ala Ala Gly Asn Gly Leu Asn Pro	
65 70 75 80	
gac gcc acg gag tct gac atc ctg gct ttg gtg atg aag acc tgt gag	288
Asp Ala Thr Glu Ser Asp Ile Leu Ala Leu Val Met Lys Thr Cys Glu	
85 90 95	
tgg ctc ccc agc cag gag tct tca gcc gga tgc aag tgg atg gtg gat	336
Trp Leu Pro Ser Gln Glu Ser Ser Ala Gly Cys Lys Trp Met Val Asp	
100 105 110	
gcc cac agt tgc gcc atc ctg agc atg ctc cgt ggg gcc ccg gac agt	384
Ala His Ser Ser Ala Ile Leu Ser Met Leu Arg Gly Ala Pro Asp Ser	
115 120 125	
gcc ccg gca cag gtg tgc aca gcg ctc agc ctc tgt gag ccg ctg cag	432
Ala Pro Ala Gln Val Cys Thr Ala Leu Ser Leu Cys Glu Pro Leu Gln	
130 135 140	
agg cac ctg gcc acc ctg agg cca ctc tcc aaa gag gac acc ttt gag	480
Arg His Leu Ala Thr Leu Arg Pro Leu Ser Lys Glu Asp Thr Phe Glu	
145 150 155 160	
gct gtg gct ccg ttc atg gcc aat ggg ccc ctt acc ttc cac ccc cgc	528
Ala Val Ala Pro Phe Met Ala Asn Gly Pro Leu Thr Phe His Pro Arg	
165 170 175	
cag gcg cct gaa gga gct ctg tgc caa gac tgt gta cgg cag gtc tcc	576
Gln Ala Pro Glu Gly Ala Leu Cys Gln Asp Cys Val Arg Gln Val Ser	
180 185 190	
cga ctc cag gag gct gtc cgg tcc aac ttg acc ttg gcc gac ttg aac	624
Arg Leu Gln Glu Ala Val Arg Ser Asn Leu Thr Leu Ala Asp Leu Asn	
195 200 205	
atc cag gag cag tgt gag tcc ttg ggg cct ggc ctg gcc gtc ctc tgc	672
Ile Gln Glu Gln Cys Glu Ser Leu Gly Pro Gly Leu Ala Val Leu Cys	
210 215 220	
aag aac tac ctc ttc cag ttt ttt gtc cct gct gac caa gca ctg agg	720
Lys Asn Tyr Leu Phe Gln Phe Phe Val Pro Ala Asp Gln Ala Leu Arg	
225 230 235 240	
ctt ctc ccc ccg cag gag ctc tgc agg aag ggg gga ttc tgt gag gag	768
Leu Leu Pro Pro Gln Glu Leu Cys Arg Lys Gly Gly Phe Cys Glu Glu	
245 250 255	

cta ggg gca cct gcc cgt ttg act caa gta gtg gcc atg gac ggg gtc Leu Gly Ala Pro Ala Arg Leu Thr Gln Val Val Ala Met Asp Gly Val	816
260 265 270	
ccc tcc ctg gag ctg ggg ttg cca agg aaa cag agc gag atg cag atg Pro Ser Leu Glu Leu Gly Leu Pro Arg Lys Gln Ser Glu Met Gln Met	864
275 280 285	
aag gcc ggt gtg acc tgt gag gtg tgc atg aac gtg gtg cag aag ctg Lys Ala Gly Val Thr Cys Glu Val Cys Met Asn Val Val Gln Lys Leu	912
290 295 300	
gac cac tgg ctc atg tcc aac agc tct gag ctc atg atc acc cat gcc Asp His Trp Leu Met Ser Asn Ser Ser Glu Leu Met Ile Thr His Ala	960
305 310 315 320	
ctg gag cgc gtg tgc tcg gta atg cct gcc tct atc acg aag gag tgc Leu Glu Arg Val Cys Ser Val Met Pro Ala Ser Ile Thr Lys Glu Cys	1008
325 330 335	
atc atc ttg gtg gac acc tac agc ccc tcc ttg gtg cag ctt gtg gcc Ile Ile Leu Val Asp Thr Tyr Ser Pro Ser Leu Val Gln Leu Val Ala	1056
340 345 350	
aaa atc acc cca gag aag gtg tgc aag ttc atc cgt ctg tgt ggc aac Lys Ile Thr Pro Glu Lys Val Cys Lys Phe Ile Arg Leu Cys Gly Asn	1104
355 360 365	
cgg agg cgg gcc cgg gca gtc cat gat gcc tat gcc atc gtg ccg tcc Arg Arg Arg Ala Arg Ala Val His Asp Ala Tyr Ala Ile Val Pro Ser	1152
370 375 380	
cca gag tgg gac gcg gag aac cag ggc agc ttc tgc aat ggg tgc aag Pro Glu Trp Asp Ala Glu Asn Gln Gly Ser Phe Cys Asn Gly Cys Lys	1200
385 390 395 400	
agg ctg ctc acg gtg tcc tcc cac aac ctg gag agc aag agc acc aag Arg Leu Leu Thr Val Ser Ser His Asn Leu Glu Ser Lys Ser Thr Lys	1248
405 410 415	
cga gac atc ctg gtg gcc ttc aag ggt ggc tgc agc atc ctg ccg ctg Arg Asp Ile Leu Val Ala Phe Lys Gly Gly Cys Ser Ile Leu Pro Leu	1296
420 425 430	
ccc tat atg atc cag tgc aag cac ttc gtc acc cag tac gag ccc gtg Pro Tyr Met Ile Gln Cys Lys His Phe Val Thr Gln Tyr Glu Pro Val	1344
435 440 445	
ctc att gag agt ctc aag gac atg atg gac ccc gtg gct gtg tgc aag Leu Ile Glu Ser Leu Lys Asp Met Met Asp Pro Val Ala Val Cys Lys	1392
450 455 460	
aag gtg ggg gcc tgc cac ggc ccc agg acc cca ctg ctg ggc acc gac Lys Val Gly Ala Cys His Gly Pro Arg Thr Pro Leu Leu Gly Thr Asp	1440
465 470 475 480	
cag tgt gcc ctg ggc cca agc ttc tgg tgc agg agc cag gag gcc gcc Gln Cys Ala Leu Gly Pro Ser Phe Trp Cys Arg Ser Gln Glu Ala Ala	1488
485 490 495	
aag ctg tgc aac gct gtg caa cac tgc cag aag cat gta tgg aaa gag Lys Leu Cys Asn Ala Val Gln His Cys Gln Lys His Val Trp Lys Glu	1536
500 505 510	

atg cac ctc cac gct ggg gaa cac gcg tga c cgtggctgcc agagacccag 1587  
 Met His Leu His Ala Gly Glu His Ala \*

515

520

agcctgctag cgaggcccat gaggtgggtg ccttcccat cccatttca caaatgaaaa 1647  
 actgaagctc tgaggaggga ggctgggaag gagcagagct gaagttcaaa accaagtatt 1707  
 cctgatcccg aaagcctctc tcttaacaac ggtgccgcac agctttgccc ttgaaagcat 1767  
 ctctactgga ccggaacaca ctcatgtgcc ccgctccctg accagccaa gcctgccctt 1827  
 tcactctcaa ggctgagatg ttgccggggg tcccatgaga gcctgcccatt gggctcaggt 1887  
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 c 1948

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<220>  
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gcc agc ccc acc tca ggc ccc cag gag tgt gca aag ggc tcc acg gtg 96  
 Ala Ser Pro Thr Ser Gly Pro Gln Glu Cys Ala Lys Gly Ser Thr Val  
 20 25 30

tgg tgt cag gat ctg cag aca gct gcc agg tgc ggg gct gtg ggg tac 144  
 Trp Cys Gln Asp Leu Gln Thr Ala Ala Arg Cys Gly Ala Val Gly Tyr  
 35 40 45

tgc caa ggg gcc gta tgg aac aaa ccc acc gcg aag tct ctg ccc tgc 192  
 Cys Gln Gly Ala Val Trp Asn Lys Pro Thr Ala Lys Ser Leu Pro Cys  
 50 55 60

gac gta tgc cag gac ata gca gcc gcc gct ggc aat ggg ctg aac cct 240  
 Asp Val Cys Gln Asp Ile Ala Ala Ala Ala Gly Asn Gly Leu Asn Pro  
 65 70 75 80

gac gcc acg gag tct gac atc ctg gct ttg gtg atg aag acc tgt gag 288  
 Asp Ala Thr Glu Ser Asp Ile Leu Ala Leu Val Met Lys Thr Cys Glu  
 85 90 95

tgg ctc ccc agc cag gag tct tca gcc gga tgc aag tgg atg gtg gat 336  
 Trp Leu Pro Ser Gln Glu Ser Ser Ala Gly Cys Lys Trp Met Val Asp  
 100 105 110

gcc cac agt tcg gcc atc ctg agc atg ctc cgt ggg gcc ccg gac agt 384  
 Ala His Ser Ser Ala Ile Leu Ser Met Leu Arg Gly Ala Pro Asp Ser  
 115 120 125

gcc ccg gca cag gtg tgc aca gcg ctc agc ctc tgt gag ccg ctg cag 432

Ala	Pro	Ala	Gln	Val	Cys	Thr	Ala	Leu	Ser	Leu	Cys	Glu	Pro	Leu	Gln		
130						135					140						
agg	cac	ctg	gcc	acc	ctg	agg	cca	ctc	tcc	aaa	gag	gac	acc	ttt	gag	480	
Arg	His	Leu	Ala	Thr	Leu	Arg	Pro	Leu	Ser	Lys	Glu	Asp	Thr	Phe	Glu		
145					150					155					160		
gct	gtg	gct	ccg	ttc	atg	gcc	aat	ggg	ccc	ctt	acc	ttc	cac	ccc	cgc	528	
Ala	Val	Ala	Pro	Phe	Met	Ala	Asn	Gly	Pro	Leu	Thr	Phe	His	Pro	Arg		
				165				170						175			
cag	gcg	cct	gaa	gga	gct	ctg	tgc	caa	gac	tgt	gta	cgg	cag	ctt	gtg	576	
Gln	Ala	Pro	Glu	Gly	Ala	Leu	Cys	Gln	Asp	Cys	Val	Arg	Gln	Leu	Val		
			180					185						190			
gcc	aaa	atc	acc	cca	gag	aag	gtg	tgc	aag	ttc	atc	cgt	ctg	tgt	ggc	624	
Ala	Lys	Ile	Thr	Pro	Glu	Lys	Val	Cys	Lys	Phe	Ile	Arg	Leu	Cys	Gly		
		195					200					205					
aac	cgg	agg	cgg	gcc	cgg	gca	gtc	cat	gat	gcc	tat	gcc	atc	gtg	ccg	672	
Asn	Arg	Arg	Arg	Ala	Arg	Ala	Val	His	Asp	Ala	Tyr	Ala	Ile	Val	Pro		
		210				215					220						
tcc	cca	gag	tgg	gac	gcg	gag	aac	cag	ggc	agc	ttc	tgc	aat	ggg	tgc	720	
Ser	Pro	Glu	Trp	Asp	Ala	Glu	Asn	Gln	Gly	Ser	Phe	Cys	Asn	Gly	Cys		
225					230					235					240		
aag	agg	ctg	ctc	acg	gtg	tcc	tcc	cac	aac	ctg	gag	agc	aag	agc	acc	768	
Lys	Arg	Leu	Leu	Thr	Val	Ser	Ser	His	Asn	Leu	Glu	Ser	Lys	Ser	Thr		
				245					250					255			
aag	cga	gac	atc	ctg	gtg	gcc	ttc	aag	ggt	ggc	tgc	agc	atc	ctg	ccg	816	
Lys	Arg	Asp	Ile	Leu	Val	Ala	Phe	Lys	Gly	Gly	Cys	Ser	Ile	Leu	Pro		
			260					265						270			
ctg	ccc	tat	atg	atc	cag	tgc	aag	cac	ttc	gtc	acc	cag	tac	gag	ccc	864	
Leu	Pro	Tyr	Met	Ile	Gln	Cys	Lys	His	Phe	Val	Thr	Gln	Tyr	Glu	Pro		
		275					280					285					
gtg	ctc	att	gag	agt	ctc	aag	gac	atg	atg	gac	ccc	gtg	gct	gtg	tgc	912	
Val	Leu	Ile	Glu	Ser	Leu	Lys	Asp	Met	Met	Asp	Pro	Val	Ala	Val	Cys		
		290				295					300						
aag	aag	gtg	ggg	gcc	tgc	cac	ggc	ccc	agg	acc	cca	ctg	ctg	ggc	acc	960	
Lys	Lys	Val	Gly	Ala	Cys	His	Gly	Pro	Arg	Thr	Pro	Leu	Leu	Gly	Thr		
305					310					315					320		
gac	cag	tgt	gcc	ctg	ggc	cca	agc	ttc	tgg	tgc	agg	agc	cag	gag	gcc	1008	
Asp	Gln	Cys	Ala	Leu	Gly	Pro	Ser	Phe	Trp	Cys	Arg	Ser	Gln	Glu	Ala		
				325					330					335			
gcc	aag	ctg	tgc	aac	gct	gtg	caa	cac	tgc	cag	aag	cat	gta	tgg	aaa	1056	
Ala	Lys	Leu	Cys	Asn	Ala	Val	Gln	His	Cys	Gln	Lys	His	Val	Trp	Lys		
			340					345					350				
gag	atg	cac	ctc	cac	gct	ggg	gaa	cac	gcg	tga	ccgtggct	gccagagacc				1107	
Glu	Met	His	Leu	His	Ala	Gly	Glu	His	Ala	*							
		355					360										
cagagcctgc	tagcgaggcc	catgaggtgg	gtgccttccc	catccccatt	tcacaaatga											1167	
aaaactgaag	ctctgaggag	ggaggctggg	aaggagcaga	gctgaagtgc	aaaaccaagt											1227	
attcctgatc	ccgaaagcct	ctctcttaac	aacggtgccg	cacagctttg	cccttgaaag											1287	

catctctact ggaccggaac acactcatgt gccccgctcc ctgacccagc caagcctgcc 1347  
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 ccgc 1471

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<400> 267

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aca gct ggt tat aag acc ctt ctc aag tgc ctc tca ggt aaa ttc tgc 96  
 Thr Ala Gly Tyr Lys Thr Leu Leu Lys Cys Leu Ser Gly Lys Phe Cys  
 20 25 30

cgc cgg gag ctg att ggc atc atg ggc ccc tca ggg gct ggc aag tct 144  
 Arg Arg Glu Leu Ile Gly Ile Met Gly Pro Ser Gly Ala Gly Lys Ser  
 35 40 45

aca ttc atg aac atc ttg gca gga tac agg gag tct gga atg aag ggg 192  
 Thr Phe Met Asn Ile Leu Ala Gly Tyr Arg Glu Ser Gly Met Lys Gly  
 50 55 60

cag atc ctg gtt aat gga agg cca cgg gag ctg agg acc ttc cgc aag 240  
 Gln Ile Leu Val Asn Gly Arg Pro Arg Glu Leu Arg Thr Phe Arg Lys  
 65 70 75 80

atg tcc tgc tac atc atg caa gat gac atg ctg ctg ccg cac ctc acg 288  
 Met Ser Cys Tyr Ile Met Gln Asp Asp Met Leu Leu Pro His Leu Thr  
 85 90 95

gtg ttg gaa gcc atg atg gtc tct gct aac ctg aag ctg agt gag aag 336  
 Val Leu Glu Ala Met Met Val Ser Ala Asn Leu Lys Leu Ser Glu Lys  
 100 105 110

cag gag gtg aag aag gag ctg gtg aca gag atc ctg acg gca ctg ggc 384  
 Gln Glu Val Lys Lys Glu Leu Val Thr Glu Ile Leu Thr Ala Leu Gly  
 115 120 125

ctg atg tgc tgc tcc cac acg agg aca gcc ctg ctc tct ggc ggg cag 432  
 Leu Met Ser Cys Ser His Thr Arg Thr Ala Leu Leu Ser Gly Gly Gln  
 130 135 140

agg aag cgt ctg gcc atc gcc ctg gag ctg gtc aac aac ccg cct gtc 480  
 Arg Lys Arg Leu Ala Ile Ala Leu Glu Leu Val Asn Asn Pro Pro Val  
 145 150 155 160

atg ttc ttt gat gag ccc acc agt ggt ctg gat agc gcc tct tgt ttc 528  
 Met Phe Phe Asp Glu Pro Thr Ser Gly Leu Asp Ser Ala Ser Cys Phe

	165	170	175	
caa gtg gtg tcc ctc atg aag tcc ctg gca cag ggg ggc cgt acc atc				576
Gln Val Val Ser Leu Met Lys Ser Leu Ala Gln Gly Gly Arg Thr Ile				
	180	185	190	
atc tgc acc atc cac cag ccc agt gcc aag ctc ttt gag atg ttt gac				624
Ile Cys Thr Ile His Gln Pro Ser Ala Lys Leu Phe Glu Met Phe Asp				
	195	200	205	
aag tgc atc ttc aaa ggc gtg gtc acc aac ctg atc ccc tat cta aag				672
Lys Cys Ile Phe Lys Gly Val Val Thr Asn Leu Ile Pro Tyr Leu Lys				
	210	215	220	
gga ctc ggc ttg cat tgc ccc acc tac cac aac ccg gct gac ttc atc				720
Gly Leu Gly Leu His Cys Pro Thr Tyr His Asn Pro Ala Asp Phe Ile				
	225	230	235	240
atc gag gtg gcc tct ggc gag tat gga gac ctg aac ccc atg ttg ttc				768
Ile Glu Val Ala Ser Gly Glu Tyr Gly Asp Leu Asn Pro Met Leu Phe				
	245	250	255	
agg gct gtg cag aat ggg ctg tgc gct atg gct gag aag aag agc agc				816
Arg Ala Val Gln Asn Gly Leu Cys Ala Met Ala Glu Lys Lys Ser Ser				
	260	265	270	
cct gag aag aac gag gtc cct gcc cca tgc cct cct tgt cct ccg gaa				864
Pro Glu Lys Asn Glu Val Pro Ala Pro Cys Pro Pro Cys Pro Pro Glu				
	275	280	285	
gtg gat ccc att gaa agc cac acc ttt gcc acc agc acc ctc aca cag				912
Val Asp Pro Ile Glu Ser His Thr Phe Ala Thr Ser Thr Leu Thr Gln				
	290	295	300	
ttc tgc atc ctc ttc aag agg acc ttc ctg tcc atc ctc agg gac acg				960
Phe Cys Ile Leu Phe Lys Arg Thr Phe Leu Ser Ile Leu Arg Asp Thr				
	305	310	315	320
gtg gtg tgt ccg gtg gtc tac tgc agc att gtg tac tgg atg acg ggc				1008
Val Val Cys Pro Val Val Tyr Cys Ser Ile Val Tyr Trp Met Thr Gly				
	325	330	335	
cag ccc gct gag acc agc cgc ttc ctg ctc ttc tca gcc ctg gcc acc				1056
Gln Pro Ala Glu Thr Ser Arg Phe Leu Leu Phe Ser Ala Leu Ala Thr				
	340	345	350	
gcc acc gcc ttg gtg gcc caa tct ttg ggg ctg ctg atc gga gct gct				1104
Ala Thr Ala Leu Val Ala Gln Ser Leu Gly Leu Leu Ile Gly Ala Ala				
	355	360	365	
tcc aac tcc cta cag gtg gcc act ttt gtg ggc cca gtt acc gcc atc				1152
Ser Asn Ser Leu Gln Val Ala Thr Phe Val Gly Pro Val Thr Ala Ile				
	370	375	380	
cct gtc ctc ttg ttc tcc ggc ttc ttt gtc agc ttc aag acc atc ccc				1200
Pro Val Leu Leu Phe Ser Gly Phe Phe Val Ser Phe Lys Thr Ile Pro				
	385	390	395	400
act tac ctg caa tgg agc tcc tat ctc tcc tat gtc agg tat ggc ttt				1248
Thr Tyr Leu Gln Trp Ser Ser Tyr Leu Ser Tyr Val Arg Tyr Gly Phe				
	405	410	415	
gag ggt gtg atc ctg acg atc tat ggc atg gag cga gga gac ctg aca				1296
Glu Gly Val Ile Leu Thr Ile Tyr Gly Met Glu Arg Gly Asp Leu Thr				



420	425	430	
tgt tta gag gaa cgc tgc ccg ttc cgg gag cca cag agc atc ctc cga Cys Leu Glu Glu Arg Cys Pro Phe Arg Glu Pro Gln Ser Ile Leu Arg 435 440 445			1344
gcg ctg gat gtg gag gat gcc aag ctc tac atg gac ttc ctg gtc ttg Ala Leu Asp Val Glu Asp Ala Lys Leu Tyr Met Asp Phe Leu Val Leu 450 455 460			1392
ggc atc ttc ttc cta gcc ctg cgg ctg ctg gcc tac ctt gtg ctg cgt Gly Ile Phe Phe Leu Ala Leu Arg Leu Leu Ala Tyr Leu Val Leu Arg 465 470 475 480			1440
tac cgg gaa tgt ggc ttt tgt tct ctg gac agt tct gct gac ctc atc Tyr Arg Glu Cys Gly Phe Cys Ser Leu Asp Ser Ser Ala Asp Leu Ile 485 490 495			1488
cgc cat gtc tac ttc cac tgc tac cac acc aag ctg aaa cag tgg ggg Arg His Val Tyr Phe His Cys Tyr His Thr Lys Leu Lys Gln Trp Gly 500 505 510			1536
ctg cag gcc ttg caa agc cag gct gac ctt ggc ccc tgc atc ctg gac Leu Gln Ala Leu Gln Ser Gln Ala Asp Leu Gly Pro Cys Ile Leu Asp 515 520 525			1584
ttc cag agc cgg aac gtc atc cct gat atc cct gac cac ttc ctg tgt Phe Gln Ser Arg Asn Val Ile Pro Asp Ile Pro Asp His Phe Leu Cys 530 535 540			1632
ctg tgg gag cac tgt gag ttg ccc ctg gca cag aat tcc ttc gac aat Leu Trp Glu His Cys Glu Leu Pro Leu Ala Gln Asn Ser Phe Asp Asn 545 550 555 560			1680
cct gag tgg ttt tat cgg cat gtg gaa gca cac agt ctg tgc tgt gaa Pro Glu Trp Phe Tyr Arg His Val Glu Ala His Ser Leu Cys Cys Glu 565 570 575			1728
tac gaa gca gtc ggc aag gac aac ccg gtg gtg ctg tgt ggc tgg aaa Tyr Glu Ala Val Gly Lys Asp Asn Pro Val Val Leu Cys Gly Trp Lys 580 585 590			1776
ggc tgt acc tgc acc ttc aag gac cgc agt aaa ctt cga gag cac ctc Gly Cys Thr Cys Thr Phe Lys Asp Arg Ser Lys Leu Arg Glu His Leu 595 600 605			1824
cgc agc cat acc cag gag aaa gtg gta gcc tgc ccc acc tgt ggg ggc Arg Ser His Thr Gln Glu Lys Val Val Ala Cys Pro Thr Cys Gly Gly 610 615 620			1872
atg ttt gcc aac aat acc aag ttc tta gat cac atc cgt cgc cag acc Met Phe Ala Asn Asn Thr Lys Phe Leu Asp His Ile Arg Arg Gln Thr 625 630 635 640			1920
tca ttg gat cag cag cac ttc cag tgt tct cac tgt tcc aag aga ttt Ser Leu Asp Gln Gln His Phe Gln Cys Ser His Cys Ser Lys Arg Phe 645 650 655			1968
gcc aca gag cgg cta ttg cgg gac cac atg cgc aac cat gtg aat cac Ala Thr Glu Arg Leu Leu Arg Asp His Met Arg Asn His Val Asn His 660 665 670			2016
tat aag tgc cct ctg tgt gac atg acc tgc ccg ctg cct tcc tcc ctc Tyr Lys Cys Pro Leu Cys Asp Met Thr Cys Pro Leu Pro Ser Ser Leu 680 685 690			2064

675	680	685	
cgc aac cac atg cgc ttt cgt cac agt gag gac cgg ccc ttt aaa tgt Arg Asn His Met Arg Phe Arg His Ser Glu Asp Arg Pro Phe Lys Cys 690 695 700			2112
gac tgt tgt gac tac agc tgc aag aat ctt att gac ctc cag aag cac Asp Cys Cys Asp Tyr Ser Cys Lys Asn Leu Ile Asp Leu Gln Lys His 705 710 715 720			2160
ctg gat acc cac agc gag gag cca gcc tac agg tgt gat ttt gag aac Leu Asp Thr His Ser Glu Glu Pro Ala Tyr Arg Cys Asp Phe Glu Asn 725 730 735			2208
tgc acc ttc agt gcc cga tcc ctc tgc tct atc aag tcc cat tac cgc Cys Thr Phe Ser Ala Arg Ser Leu Cys Ser Ile Lys Ser His Tyr Arg 740 745 750			2256
aaa gta cat gaa gga gac tct gag cca agg tac aaa tgt cat gtg tgt Lys Val His Glu Gly Asp Ser Glu Pro Arg Tyr Lys Cys His Val Cys 755 760 765			2304
gac aaa tgc ttc aca cgg ggc aac aac ctc acc gtg cac ctt cgc aag Asp Lys Cys Phe Thr Arg Gly Asn Asn Leu Thr Val His Leu Arg Lys 770 775 780			2352
aag cac cag ttc aag tgg ccc tca ggg cat ccc cgt ttt cgg tac aag Lys His Gln Phe Lys Trp Pro Ser Gly His Pro Arg Phe Arg Tyr Lys 785 790 795 800			2400
gaa cat gaa gat ggc tat atg cgg ctg cag ctg gtt cgc tac gag agt Glu His Glu Asp Gly Tyr Met Arg Leu Gln Leu Val Arg Tyr Glu Ser 805 810 815			2448
gta gag ctg aca cag caa ctg ctg cgg caa cca caa gag gga tcg ggc Val Glu Leu Thr Gln Gln Leu Leu Arg Gln Pro Gln Glu Gly Ser Gly 820 825 830			2496
ctg gga acg tcg ctg aac gag agc agc ctg cag ggc att att cta gaa Leu Gly Thr Ser Leu Asn Glu Ser Ser Leu Gln Gly Ile Ile Leu Glu 835 840 845			2544
aca gtg cca ggg gag cca gga cgt aag gaa gag gaa gag gag ggc aag Thr Val Pro Gly Glu Pro Gly Arg Lys Glu Glu Glu Glu Glu Gly Lys 850 855 860			2592
ggt agc gaa ggg aca gcc ctc tca gcc tct cag gac aac ccc agt tct Gly Ser Glu Gly Thr Ala Leu Ser Ala Ser Gln Asp Asn Pro Ser Ser 865 870 875 880			2640
gtc atc cac gtg gtg aat cag acc aat gcc caa ggc cag caa gag att Val Ile His Val Val Asn Gln Thr Asn Ala Gln Gly Gln Gln Glu Ile 885 890 895			2688
gtc tac tat gtg ctg tct gaa gcc cca ggg gag cct ccc cca gtc cct Val Tyr Tyr Val Leu Ser Glu Ala Pro Gly Glu Pro Pro Pro Val Pro 900 905 910			2736
gag cca cct tca ggg ggc atc atg gaa aag ctt caa gga ata gct gag Glu Pro Pro Ser Gly Gly Ile Met Glu Lys Leu Gln Gly Ile Ala Glu 915 920 925			2784
gag cca gag atc cag atg gtt tga aggcgcgaga gccagaccat ttcttcccca Glu Pro Glu Ile Gln Met Val *			2838

930

935

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ggtcctgaag tttgagccag gcaagtggca gtgcccctag tgggcagccg ttgccaatgg 2898
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tacaacccca aggactttca tgattatcct cagggacagg attggaggca ttgagcgtgt 3318
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cgt ggc acc ggc ctg gtg ctg gat gga gac acc agc tac aca tac cat 96
Arg Gly Thr Gly Leu Val Leu Asp Gly Asp Thr Ser Tyr Thr Tyr His
      20             25             30

ctg gtg tgc atg ggc ccc gag gcc agc ggc tgg ggc cag gat gag ccg 144
Leu Val Cys Met Gly Pro Glu Ala Ser Gly Trp Gly Gln Asp Glu Pro
      35             40             45

cag aca tgg ccc act gac cac agg gcc cag cag ggc gtg cag agg cag 192
Gln Thr Trp Pro Thr Asp His Arg Ala Gln Gln Gly Val Gln Arg Gln
      50             55             60

ggg gtg tcc tac agc gtg cat gcc tac act ggc cag ccg tcc cca cgg 240
Gly Val Ser Tyr Ser Val His Ala Tyr Thr Gly Gln Pro Ser Pro Arg
      65             70             75             80

ggg ctc cac tcg gag aac agg gag gat gag ggt tgg cag gtt tac cgc 288
Gly Leu His Ser Glu Asn Arg Glu Asp Glu Gly Trp Gln Val Tyr Arg
      85             90             95

ctg ggc acc agg gat gcc cac cag gga cgt cca aca tgg gca ctc cgc 336
Leu Gly Thr Arg Asp Ala His Gln Gly Arg Pro Thr Trp Ala Leu Arg
      100            105            110

cca gag gac ggg gag gac aag gag atg aag acc tac cgc ctg gat gct 384
Pro Glu Asp Gly Glu Asp Lys Glu Met Lys Thr Tyr Arg Leu Asp Ala
      115            120            125

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ggg gac gct gac ccc agg agg ctg tgt gac ctg gag cgg gag cgc tgg Gly Asp Ala Asp Pro Arg Arg Leu Cys Asp Leu Glu Arg Glu Arg Trp 130 135 140	432
gcc gtc atc cag ggc cag gca gtc agg aag agc agc acc gtg gcc acg Ala Val Ile Gln Gly Gln Ala Val Arg Lys Ser Ser Thr Val Ala Thr 145 150 155 160	480
ctc cag ggc act cct gac cac gga gac ccc agg acc ccc ggc cca cct Leu Gln Gly Thr Pro Asp His Gly Asp Pro Arg Thr Pro Gly Pro Pro 165 170 175	528
cgg tcc acg ccc ctg gag gag aac gtg gtt gac agg gag cag att gac Arg Ser Thr Pro Leu Glu Glu Asn Val Val Asp Arg Glu Gln Ile Asp 180 185 190	576
ttc ctg gca gcg aga cag cag ttc ctg agt ctg gag cag gcg aac aag Phe Leu Ala Ala Arg Gln Gln Phe Leu Ser Leu Glu Gln Ala Asn Lys 195 200 205	624
ggg gcc cct cat agc tcc ccg gcc agg ggg acc ccc gca ggc aca acc Gly Ala Pro His Ser Ser Pro Ala Arg Gly Thr Pro Ala Gly Thr Thr 210 215 220	672
cca ggg gcc agc cag gcc ccc aag gcc ttc aac aag ccc cac ctg gcc Pro Gly Ala Ser Gln Ala Pro Lys Ala Phe Asn Lys Pro His Leu Ala 225 230 235 240	720
aac ggg cac gtg gtt ccc atc aag ccc cag gtg aag ggg gtg gtc agg Asn Gly His Val Val Pro Ile Lys Pro Gln Val Lys Gly Val Val Arg 245 250 255	768
gaa gag aac aag gtg cgt gct gtg ccc acc tgg gcc agt gtc caa gtt Glu Glu Asn Lys Val Arg Ala Val Pro Thr Trp Ala Ser Val Gln Val 260 265 270	816
gtg gat gac cct ggc tcc ttg gcc tca gtg gag tcc ccg ggg acc ccc Val Asp Asp Pro Gly Ser Leu Ala Ser Val Glu Ser Pro Gly Thr Pro 275 280 285	864
aag gag acg ccc atc gag cgg gag atc cgt ctg gct cag gag cgt gag Lys Glu Thr Pro Ile Glu Arg Glu Ile Arg Leu Ala Gln Glu Arg Glu 290 295 300	912
gca gac ctg cga gag cag agg ggg ctt cgg cag gca acc gac cac cag Ala Asp Leu Arg Glu Gln Arg Gly Leu Arg Gln Ala Thr Asp His Gln 305 310 315 320	960
gag ctg gtg gaa atc ccc acc agg ccg ctg ctg acc aag ctg agc ctg Glu Leu Val Glu Ile Pro Thr Arg Pro Leu Leu Thr Lys Leu Ser Leu 325 330 335	1008
atc aca gcc cca cgg cgg gag aga ggg cgc ccg tcc ctc tac gtg cag Ile Thr Ala Pro Arg Arg Glu Arg Gly Arg Pro Ser Leu Tyr Val Gln 340 345 350	1056
cgg gac ata gta cag gag aca cag cgt gag gaa gac cac cgg cgg gag Arg Asp Ile Val Gln Glu Thr Gln Arg Glu Glu Asp His Arg Arg Glu 355 360 365	1104
ggc ctg cac gtg ggc cgg gcg tcc aca ccc gac tgg gtc tcg gag ggt Gly Leu His Val Gly Arg Ala Ser Thr Pro Asp Trp Val Ser Glu Gly 370 375 380	1152

ccc cag ccc gga ctc cgg aga gcc ctc agc tca gat tcc atc ctc agc	1200
Pro Gln Pro Gly Leu Arg Arg Ala Leu Ser Ser Asp Ser Ile Leu Ser	
385 390 395 400	
ccg gcc cca gat gcc cgt gcg gcc gac cca gct cca gaa gtg agg aag	1248
Pro Ala Pro Asp Ala Arg Ala Ala Asp Pro Ala Pro Glu Val Arg Lys	
405 410 415	
gtg aac cgc atc cca cct gat gcc tac cag ccg tac ctg agc ccc ggg	1296
Val Asn Arg Ile Pro Pro Asp Ala Tyr Gln Pro Tyr Leu Ser Pro Gly	
420 425 430	
acc ccc cag cta gaa ttc tca gcc ttc gga gca ttc ggc aag ccc agc	1344
Thr Pro Gln Leu Glu Phe Ser Ala Phe Gly Ala Phe Gly Lys Pro Ser	
435 440 445	
agt ctc tcc aca gcg gag gcc aag gct gcg act tca cca aag gcc acg	1392
Ser Leu Ser Thr Ala Glu Ala Lys Ala Ala Thr Ser Pro Lys Ala Thr	
450 455 460	
atg tcc ccg agg cat ctc tca gaa tcc tct gga aaa ccc ctg agc aca	1440
Met Ser Pro Arg His Leu Ser Glu Ser Ser Gly Lys Pro Leu Ser Thr	
465 470 475 480	
aag caa gag gca tcg aag ccc cct cgg gga tgc ccg caa gcc aac agg	1488
Lys Gln Glu Ala Ser Lys Pro Pro Arg Gly Cys Pro Gln Ala Asn Arg	
485 490 495	
ggg gtc gtg cgg tgg gag tac ttc cgc ctg cgt cct ctg cgg ttc agg	1536
Gly Val Val Arg Trp Glu Tyr Phe Arg Leu Arg Pro Leu Arg Phe Arg	
500 505 510	
gcc cca gac gag ccc cag cag gcc caa gtc ccc cat gtc tgg ggc tgg	1584
Ala Pro Asp Glu Pro Gln Gln Ala Gln Val Pro His Val Trp Gly Trp	
515 520 525	
gag gtg gct ggg gcc cct gca ctg agg ctg cag aag tcc cag tca tct	1632
Glu Val Ala Gly Ala Pro Ala Leu Arg Leu Gln Lys Ser Gln Ser Ser	
530 535 540	
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Asp Leu Leu Glu Arg Glu Arg Glu Ser Val Leu Arg Arg Glu Gln Glu	
545 550 555 560	
gtg gca gag gag cgg aga aat gct ctc ttc cca gag gtc ttc tcc cca	1728
Val Ala Glu Glu Arg Arg Asn Ala Leu Phe Pro Glu Val Phe Ser Pro	
565 570 575	
acg cca gat gag aac tct gac cag aac tcc agg agc tcc tcc cag gca	1776
Thr Pro Asp Glu Asn Ser Asp Gln Asn Ser Arg Ser Ser Ser Gln Ala	
580 585 590	
tcc ggc atc acg ggc agt tac tcg gtg tct gag tct ccc ttc ttc agc	1824
Ser Gly Ile Thr Gly Ser Tyr Ser Val Ser Glu Ser Pro Phe Phe Ser	
595 600 605	
ccc atc cac cta cac tca aac gtg gcg tgg aca gtg gaa gat cca gtg	1872
Pro Ile His Leu His Ser Asn Val Ala Trp Thr Val Glu Asp Pro Val	
610 615 620	
gac agt gct cct ccc ggg cag aga aag aag gag caa tgg tac gct ggc	1920
Asp Ser Ala Pro Pro Gly Gln Arg Lys Lys Glu Gln Trp Tyr Ala Gly	
625 630 635 640	

atc aac ccc tcg gac ggt atc aac tca gag gtc ctg gaa gcc ata cgg 1968  
 Ile Asn Pro Ser Asp Gly Ile Asn Ser Glu Val Leu Glu Ala Ile Arg  
 645 650 655  
 gtg acc cgt cac aag aac gcc atg gca gag cgc tgg gaa tcc cgc atc 2016  
 Val Thr Arg His Lys Asn Ala Met Ala Glu Arg Trp Glu Ser Arg Ile  
 660 665 670  
 tac gcc agt gag gag gat gac tga gcctcgggat ggggcgccca cccctgccc 2070  
 Tyr Ala Ser Glu Glu Asp Asp \*  
 675 680  
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 aagctgagag gggagacctg cccctttcca accctgggaa accatccagt ctgagggagg 2550  
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 Met  
 1  
 tcg aag cga gga cgt ggt ggg tcc tct ggt gcg aaa ttc cgg att tcc 164  
 Ser Lys Arg Gly Arg Gly Gly Ser Ser Gly Ala Lys Phe Arg Ile Ser  
 5 10 15  
 ttg ggt ctt ccg gta gga gct gta atc aat tgt gct gac aac aca gga 212  
 Leu Gly Leu Pro Val Gly Ala Val Ile Asn Cys Ala Asp Asn Thr Gly  
 20 25 30



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gcc aaa aac ctg tat atc atc tcc gtg aag ggg atc aag gga cgg ctg      260
Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly Arg Leu
      35                      40                      45

aac aga ctt ccc gct gct ggt gtg ggt gac atg gtg atg gcc aca gtc      308
Asn Arg Leu Pro Ala Ala Gly Val Gly Asp Met Val Met Ala Thr Val
      50                      55                      60                      65

aag aaa ggc aaa cca gag ctc aga aaa aag gta cat cca gca gtg gtc      356
Lys Lys Gly Lys Pro Glu Leu Arg Lys Lys Val His Pro Ala Val Val
                        70                      75                      80

att cga caa cga aag tca tac cgt aga aaa gat ggc gtg ttt ctt tat      404
Ile Arg Gln Arg Lys Ser Tyr Arg Arg Lys Asp Gly Val Phe Leu Tyr
                        85                      90                      95

ttt gaa gat aat gca gga gtc ata gtg aac aat aaa ggc gag atg aaa      452
Phe Glu Asp Asn Ala Gly Val Ile Val Asn Asn Lys Gly Glu Met Lys
      100                      105                      110

ggt tct gcc att aca gga cca gta gca aag gag tgt gca gac ttg tgg      500
Gly Ser Ala Ile Thr Gly Pro Val Ala Lys Glu Cys Ala Asp Leu Trp
      115                      120                      125

ccc cgg att gca tcc aat gct ggc agc att gca tga ttct cccagtatat      550
Pro Arg Ile Ala Ser Asn Ala Gly Ser Ile Ala *
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accccaggtc tgtctcccat gtcattcacc tcgttgctgt gttttctcag accccagagt      180
cagaaggagt gagaaccctg acccctaatc ccactgcac cagccaatag gagcccagcc      240
acc  atg gcg gag ctg cag gag gtg cag atc aca gag gag aag cca ctg      288
      Met Ala Glu Leu Gln Glu Val Gln Ile Thr Glu Glu Lys Pro Leu
          1                      5                      10                      15

ttg cca gga cag acg cct gag gcg gcc aag gag gct gag tta gct gcc      336
Leu Pro Gly Gln Thr Pro Glu Ala Ala Lys Glu Ala Glu Leu Ala Ala
          20                      25                      30

cga atc ctc ctg gac cag gga cag act cac tct gtg gag aca cca tac      384
Arg Ile Leu Leu Asp Gln Gly Gln Thr His Ser Val Glu Thr Pro Tyr
          35                      40                      45

ggc tct gtc act ttc act gtc tat ggc acc ccc aaa ccc aaa cgc cca      432

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Gly	Ser	Val	Thr	Phe	Thr	Val	Tyr	Gly	Thr	Pro	Lys	Pro	Lys	Arg	Pro	
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gcg	atc	ctt	acc	tac	cac	gat	gtg	gga	ctc	aac	tat	aaa	tct	tgc	ttc	480
Ala	Ile	Leu	Thr	Tyr	His	Asp	Val	Gly	Leu	Asn	Tyr	Lys	Ser	Cys	Phe	
	65					70				75						
cag	cca	ctg	ttt	cag	ttc	gag	gac	atg	cag	gaa	atc	att	cag	aac	ttt	528
Gln	Pro	Leu	Phe	Gln	Phe	Glu	Asp	Met	Gln	Glu	Ile	Ile	Gln	Asn	Phe	
	80				85				90						95	
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Val	Arg	Val	His	Val	Asp	Ala	Pro	Gly	Met	Glu	Glu	Gly	Ala	Pro	Val	
				100				105					110			
ttc	cct	ttg	gga	tat	cag	tac	cca	tct	ctg	gac	cag	ctt	gca	gac	atg	624
Phe	Pro	Leu	Gly	Tyr	Gln	Tyr	Pro	Ser	Leu	Asp	Gln	Leu	Ala	Asp	Met	
			115					120					125			
atc	cct	tgc	gtc	ctg	cag	tac	cta	aat	ttc	tct	aca	ata	att	gga	gtt	672
Ile	Pro	Cys	Val	Leu	Gln	Tyr	Leu	Asn	Phe	Ser	Thr	Ile	Ile	Gly	Val	
		130					135					140				
ggt	gtt	gga	gct	gga	gcc	tac	atc	ctg	gcg	aga	tat	gct	ctt	aac	cac	720
Gly	Val	Gly	Ala	Gly	Ala	Tyr	Ile	Leu	Ala	Arg	Tyr	Ala	Leu	Asn	His	
	145					150					155					
ccg	gac	act	gtt	gaa	ggt	ctt	gtc	ctc	atc	aac	att	gat	ccc	aat	gcc	768
Pro	Asp	Thr	Val	Glu	Gly	Leu	Val	Leu	Ile	Asn	Ile	Asp	Pro	Asn	Ala	
	160				165					170					175	
aag	ggt	tgg	atg	gat	tgg	gca	gcc	cac	aag	cta	aca	ggc	ctc	acc	tcc	816
Lys	Gly	Trp	Met	Asp	Trp	Ala	Ala	His	Lys	Leu	Thr	Gly	Leu	Thr	Ser	
				180					185					190		
tgc	agt	ccg	gag	atg	atc	ctt	gga	cat	ctt	ttc	agc	cag	gaa	gag	ctc	864
Cys	Ser	Pro	Glu	Met	Ile	Leu	Gly	His	Leu	Phe	Ser	Gln	Glu	Glu	Leu	
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tct	gga	aat	tct	gag	ttg	ata	caa	aag	tac	aga	aat	atc	att	aca	cat	912
Ser	Gly	Asn	Ser	Glu	Leu	Ile	Gln	Lys	Tyr	Arg	Asn	Ile	Ile	Thr	His	
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gca	ccc	aac	ctg	gat	aac	att	gaa	ttg	tac	tgg	aac	agc	tac	aac	aac	960
Ala	Pro	Asn	Leu	Asp	Asn	Ile	Glu	Leu	Tyr	Trp	Asn	Ser	Tyr	Asn	Asn	
	225					230					235					
cgc	cga	gac	ctg	aac	ttt	gag	cgt	gga	ggt	gat	atc	acc	ctc	agg	tgt	1008
Arg	Arg	Asp	Leu	Asn	Phe	Glu	Arg	Gly	Gly	Asp	Ile	Thr	Leu	Arg	Cys	
	240				245					250					255	
cct	gtg	atg	ctg	gtg	gta	gga	gac	caa	gca	cct	cat	gaa	gat	gca	gtg	1056
Pro	Val	Met	Leu	Val	Val	Gly	Asp	Gln	Ala	Pro	His	Glu	Asp	Ala	Val	
				260				265						270		
gtg	gaa	tgt	aac	tca	aaa	ctg	gac	ccc	acc	cag	acc	tcg	ttc	ctc	aag	1104
Val	Glu	Cys	Asn	Ser	Lys	Leu	Asp	Pro	Thr	Gln	Thr	Ser	Phe	Leu	Lys	
			275					280					285			
atg	gct	gac	tcc	gga	ggt	cag	ccc	cag	ctg	act	cag	cca	ggc	aag	ctg	1152
Met	Ala	Asp	Ser	Gly	Gly	Gln	Pro	Gln	Leu	Thr	Gln	Pro	Gly	Lys	Leu	
		290					295					300				
acc	gag	gcc	ttc	aag	tac	ttc	ctg	caa	ggc	atg	ggc	tac	atg	gcc	tca	1200

Thr	Glu	Ala	Phe	Lys	Tyr	Phe	Leu	Gln	Gly	Met	Gly	Tyr	Met	Ala	Ser	
305						310					315					
tcc	tgc	atg	act	cgg	ctg	tcc	cgg	tct	cgt	aca	gcc	tct	ctg	acc	agt	1248
Ser	Cys	Met	Thr	Arg	Leu	Ser	Arg	Ser	Arg	Thr	Ala	Ser	Leu	Thr	Ser	
320					325				330					335		
gca	gaa	tcc	gtt	gat	ggg	aac	cgg	tcc	cgc	tct	cgc	acc	ctg	tcc	cag	1296
Ala	Glu	Ser	Val	Asp	Gly	Asn	Arg	Ser	Arg	Ser	Arg	Thr	Leu	Ser	Gln	
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agc	aga	gag	tct	gga	act	ctt	tct	tgc	ggg	ccc	ccg	ggg	cac	acc	atg	1344
Ser	Arg	Glu	Ser	Gly	Thr	Leu	Ser	Ser	Gly	Pro	Pro	Gly	His	Thr	Met	
			355				360					365				
gag	gtc	tcc	tgt	tga	atggcccttg	ttgccctaga	gtgggaccca	gccctcacct								1399
Glu	Val	Ser	Cys	*												
			370													
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 <212> DNA  
 <213> Homo sapiens

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 <222> (255) .. (1817)

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721

cct gag cgc tac act ggt tac aag gga cca gat gct tgg aaa ata tgg	1010
Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp Ala Trp Lys Ile Trp	
240 245 250	
aat gtc atc tac gaa gaa aac tgt ttt aag cca cag aca att aaa aga	1058
Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys Pro Gln Thr Ile Lys Arg	
255 260 265	
cct tta aat cct ttg gct tct ggt caa ggg aca agt gaa gag aac act	1106
Pro Leu Asn Pro Leu Ala Ser Gly Gln Gly Thr Ser Glu Glu Asn Thr	
270 275 280	
ttt tac agt tgg cta gaa ggt ctc tgt gta gaa aaa aga gca ttc tac	1154
Phe Tyr Ser Trp Leu Glu Gly Leu Cys Val Glu Lys Arg Ala Phe Tyr	
285 290 295 300	
aga ctt ata tct ggc cta cat gca agc att aat gtg cat ttg agt gca	1202
Arg Leu Ile Ser Gly Leu His Ala Ser Ile Asn Val His Leu Ser Ala	
305 310 315	
aga tat ctt tta caa gag acc tgg tta gaa aag aaa tgg gga cac aac	1250
Arg Tyr Leu Leu Gln Glu Thr Trp Leu Glu Lys Lys Trp Gly His Asn	
320 325 330	
att aca gaa ttt caa cag cga ttt gat gga att ttg act gaa gga gaa	1298
Ile Thr Glu Phe Gln Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu	
335 340 345	
ggt cca aga agg ctt aag aac ttg tat ttt ctc tac tta ata gaa cta	1346
Gly Pro Arg Arg Leu Lys Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu	
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agg gct tta tcc aaa gtg tta cca ttc ttc gag cgc cca gat ttt caa	1394
Arg Ala Leu Ser Lys Val Leu Pro Phe Phe Glu Arg Pro Asp Phe Gln	
365 370 375 380	
ctc ttt act gga aat aaa att cag gat gag gaa aac aaa atg tta ctt	1442
Leu Phe Thr Gly Asn Lys Ile Gln Asp Glu Glu Asn Lys Met Leu Leu	
385 390 395	
ctg gaa ata ctt cat gaa atc aag tca ttt cct ttg cat ttt gat gag	1490
Leu Glu Ile Leu His Glu Ile Lys Ser Phe Pro Leu His Phe Asp Glu	
400 405 410	
aat tca ttt ttt gct ggg gat aaa aaa gaa gca cac aaa cta aag gag	1538
Asn Ser Phe Phe Ala Gly Asp Lys Lys Glu Ala His Lys Leu Lys Glu	
415 420 425	
gac ttt cga ctg cat ttt aga aat att tca aga att atg gat tgt gtt	1586
Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp Cys Val	
430 435 440	
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Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr Gln Gly Leu	
445 450 455 460	
ggc act gct ctg aag atc tta ttt tct gag aaa ttg ata gca aat atg	1682
Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu Ile Ala Asn Met	
465 470 475	
cca gaa agt gga cct agt tat gaa ttc cat cta acc aga caa gaa ata	1730
Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu Thr Arg Gln Glu Ile	
480 485 490	

gta tca tta ttc aac gca ttt gga aga att tct aca agt gtg aaa gaa 1778  
 Val Ser Leu Phe Asn Ala Phe Gly Arg Ile Ser Thr Ser Val Lys Glu  
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tta gaa aac ttc agg aac ttg tta cag aat att cat taa agaaaacaag 1827  
 Leu Glu Asn Phe Arg Asn Leu Leu Gln Asn Ile His \*  
           510                                  515                                  520

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 aatagcaatg acagtcttaa gccaaacatt ttatataaag ttgcttttgt aaaggagaat 1947  
 tatattgttt taagtaaaca cattttttaa aattgtgtta agtctatgta taatactact 2007  
 gtgagtaaaa gtaatacttt aataatgtgg tacaaatttt aaagtttaat attgaataaa 2067  
 aggaggatta tcaaattcat atatgataaa agtgaatgtt ctaagtctct caaactagcg 2127  
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 cctccctgct ccttcgcttt ttctctctcc tctctctccg gccccggctg ccagcacc 178  
 atg tcc gca ggg gga gat ttt ggg aat cca ctg aga aaa ttc aag ttg 226  
 Met Ser Ala Gly Gly Asp Phe Gly Asn Pro Leu Arg Lys Phe Lys Leu  
       1                  5                                  10                                  15

gtg ttc ttg ggg gag cag agc gtc ggg aag acg tct ctg att acg agg 274



Val	Phe	Leu	Gly	Glu	Gln	Ser	Val	Gly	Lys	Thr	Ser	Leu	Ile	Thr	Arg		
			20					25					30				
ttc	atg	tac	gac	agc	ttc	gac	aac	aca	tac	cag	gca	acc	att	ggg	att		322
Phe	Met	Tyr	Asp	Ser	Phe	Asp	Asn	Thr	Tyr	Gln	Ala	Thr	Ile	Gly	Ile		
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gac	ttc	ttg	tca	aaa	acc	atg	tac	ttg	gag	gac	cgc	acg	gtg	cga	ctg		370
Asp	Phe	Leu	Ser	Lys	Thr	Met	Tyr	Leu	Glu	Asp	Arg	Thr	Val	Arg	Leu		
		50				55					60						
cag	ctc	tgg	gac	aca	gct	ggc	cag	gag	agg	ttc	cgc	agc	ctg	atc	ccc		418
Gln	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Arg	Phe	Arg	Ser	Leu	Ile	Pro		
		65			70				75						80		
agc	tac	atc	cgg	gac	tcc	acg	gtg	gct	gtg	gtg	gtg	tac	gac	atc	aca		466
Ser	Tyr	Ile	Arg	Asp	Ser	Thr	Val	Ala	Val	Val	Val	Tyr	Asp	Ile	Thr		
				85				90						95			
aat	ctc	aac	tcc	ttc	caa	cag	acc	tct	aag	tgg	atc	gac	gac	gtc	agg		514
Asn	Leu	Asn	Ser	Phe	Gln	Gln	Thr	Ser	Lys	Trp	Ile	Asp	Asp	Val	Arg		
			100					105					110				
aca	gag	agg	ggc	agt	gat	gtt	atc	atc	atg	ctg	gtg	ggc	aac	aag	acg		562
Thr	Glu	Arg	Gly	Ser	Asp	Val	Ile	Ile	Met	Leu	Val	Gly	Asn	Lys	Thr		
		115				120						125					
gac	ctg	gct	gat	aag	agg	cag	ata	acc	atc	gag	gag	ggg	gag	cag	cgc		610
Asp	Leu	Ala	Asp	Lys	Arg	Gln	Ile	Thr	Ile	Glu	Glu	Gly	Glu	Gln	Arg		
		130				135						140					
gcc	aaa	gaa	ctg	agc	gtc	atg	ttc	att	gag	acc	agt	gcg	aag	act	ggc		658
Ala	Lys	Glu	Leu	Ser	Val	Met	Phe	Ile	Glu	Thr	Ser	Ala	Lys	Thr	Gly		
		145			150				155						160		
tac	aac	gtg	aag	cag	ctt	ttt	cga	cgt	gtg	gcg	tcg	gct	cta	ccc	gga		706
Tyr	Asn	Val	Lys	Gln	Leu	Phe	Arg	Arg	Val	Ala	Ser	Ala	Leu	Pro	Gly		
				165				170						175			
atg	gag	aat	gtc	cag	gag	aaa	agc	aaa	gaa	ggg	atg	att	gac	atc	aag		754
Met	Glu	Asn	Val	Gln	Glu	Lys	Ser	Lys	Glu	Gly	Met	Ile	Asp	Ile	Lys		
			180					185					190				
ctg	gac	aaa	ccc	cag	gag	ccc	ccg	gcc	agc	gag	ggc	ggc	tgc	tcc	tgc		802
Leu	Asp	Lys	Pro	Gln	Glu	Pro	Pro	Ala	Ser	Glu	Gly	Gly	Cys	Ser	Cys		
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tggttagctt	cctaaggggg	gaggaaccg	agttatcaag	atgggaggat	ttttcttttc												922
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attaattagg	gcttcagtct	ggggggccat	ctggcncccc	ttcttctagg	ggcccctact												1342

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actgctgcac	ttt	atg aga gag aag	gag caa gaa agg	gaa gaa cag tta			229
		Met Arg Glu Lys	Glu Gln Glu Arg	Glu Glu Gln Leu			
		1	5	10			
atg gaa gac aag	aaa agg aag	aaa gag gat	aaa aag aaa	aaa gaa gcc			277
Met Glu Asp Lys	Lys Arg Lys	Lys Glu Asp	Lys Lys Lys	Lys Lys Glu Ala			
	15	20	25				
act cag aag gtc	acg gaa caa	aaa acc aaa	gtg ccc gaa	gtg acg aaa			325
Thr Gln Lys Val	Thr Glu Gln	Lys Thr Lys	Val Pro Glu	Val Thr Lys			
	30	35	40				
cca agt tta agc	caa cca acg	gcc gcc agc	cca att ggc	agc tct cca			373
Pro Ser Leu Ser	Gln Pro Thr	Ala Ala Ser	Pro Ile Gly	Ser Ser Pro			
	45	50	55	60			
tcg cca cca gtc	aat ggt ggc	aac aat gcc	aaa agg gtg	gca gtg ccg			421
Ser Pro Pro Val	Asn Gly Gly	Asn Asn Ala	Lys Arg Val	Ala Val Pro			
	65	70	75				
aac gga caa ccg	cca agc gcc	gcc cgc tac	atg cct cgg	gag gtg ccg			469
Asn Gly Gln Pro	Pro Ser Ala	Ala Arg Tyr	Met Pro Arg	Glu Val Pro			
	80	85	90				
ccg cga ttc cgt	tgc cag cag	gac cac aaa	gtg tta cta	aaa cgt ggg			517
Pro Arg Phe Arg	Cys Gln Gln	Asp His Lys	Val Leu Leu	Lys Arg Gly			
	95	100	105				
cag ccc cct cca	ccg tcc tgc	atg ctc ctt	ggg ggt ggg	gca ggg cct			565
Gln Pro Pro Pro	Pro Ser Cys	Met Leu Leu	Gly Gly Gly	Ala Gly Pro			
	110	115	120				
cct ccc tgc aca	gca cct gga	gca aac cca	aac aac gca	caa gtg aca			613
Pro Pro Cys Thr	Ala Pro Gly	Ala Asn Pro	Asn Asn Ala	Gln Val Thr			
	125	130	135	140			
gga gcg ctg ctg	cag agt gag	agt ggg act	gcg cca gac	tca acc ctt			661
Gly Ala Leu Leu	Gln Ser Glu	Ser Gly Thr	Ala Pro Asp	Ser Thr Leu			
	145	150	155				

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Gly Gly Ala Ala Ala Ser Asn Tyr Ala Asn Ser Thr Trp Gly Ser Gly	
160 165 170	
gcc tcc tcc aac aac ggc acc tcc ccc aac cca att cac atc tgg gac	757
Ala Ser Ser Asn Asn Gly Thr Ser Pro Asn Pro Ile His Ile Trp Asp	
175 180 185	
aag gtg att gta gac ggg tct gac atg gaa gag tgg cct tgt att gcc	805
Lys Val Ile Val Asp Gly Ser Asp Met Glu Glu Trp Pro Cys Ile Ala	
190 195 200	
agc aaa gac act gaa tct tct tcc gaa aac acc acc gat aac aac agt	853
Ser Lys Asp Thr Glu Ser Ser Ser Glu Asn Thr Thr Asp Asn Asn Ser	
205 210 215 220	
gcc tcg aac cct ggc tct gag aag agc act ctg cca gga agc acc act	901
Ala Ser Asn Pro Gly Ser Glu Lys Ser Thr Leu Pro Gly Ser Thr Thr	
225 230 235	
agt aac aaa gga aaa ggg agc cag tgc cag tct gca agt tct ggg aac	949
Ser Asn Lys Gly Lys Gly Ser Gln Cys Gln Ser Ala Ser Ser Gly Asn	
240 245 250	
gaa tgt aat ctt ggg gtc tgg aaa tct gac cct aag gct aaa tct gtt	997
Glu Cys Asn Leu Gly Val Trp Lys Ser Asp Pro Lys Ala Lys Ser Val	
255 260 265	
caa tct tcc aac tct act aca gag aac aac aat gga cta gga aat tgg	1045
Gln Ser Ser Asn Ser Thr Thr Glu Asn Asn Asn Gly Leu Gly Asn Trp	
270 275 280	
agg aat gtg agt ggt cag gat aga att gga cct ggc tct ggc ttc agc	1093
Arg Asn Val Ser Gly Gln Asp Arg Ile Gly Pro Gly Ser Gly Phe Ser	
285 290 295 300	
aac ttt aac cca aat agc aac cca tct gcc tgg cca gca ctg gtc caa	1141
Asn Phe Asn Pro Asn Ser Asn Pro Ser Ala Trp Pro Ala Leu Val Gln	
305 310 315	
gaa gga act tct agg aaa ggg gca ttg gaa aca gat aat agt aat tcc	1189
Glu Gly Thr Ser Arg Lys Gly Ala Leu Glu Thr Asp Asn Ser Asn Ser	
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Ser Ala Gln Val Ser Thr Val Gly Gln Thr Ser Arg Glu Gln Gln Ser	
335 340 345	
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Lys Met Glu Asn Ala Gly Val Asn Phe Val Val Ser Gly Arg Glu Gln	
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gct caa att cat aac act gat gga cca aaa aat gga aac act aac tcc	1333
Ala Gln Ile His Asn Thr Asp Gly Pro Lys Asn Gly Asn Thr Asn Ser	
365 370 375 380	
ttg aac tta agt tca cca aac ccc atg gag aat aag gga atg ccc ttt	1381
Leu Asn Leu Ser Ser Pro Asn Pro Met Glu Asn Lys Gly Met Pro Phe	
385 390 395	
gga atg ggc ttg ggg aac acc tcc agg agc act gat gcc cct tca caa	1429
Gly Met Gly Leu Gly Asn Thr Ser Arg Ser Thr Asp Ala Pro Ser Gln	
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ctgcccctgc ctagcagttt cccagctccc aacagcctgg ggaagctttg cacagagtga	2349
cctgagacca ggtacaggaa acctgtagct caatcagtgt ctctttaact gcataagcaa	2409
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aa	2471

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 <211> 955  
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<220>  
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 <222> (109) .. (714)

<400> 275	
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Met Lys Trp	

gtg tgg gcg ctc ttg ctg ttg gcg gcg ctg ggc agc ggc cgc gcg gag Val Trp Ala Leu Leu Leu Leu Ala Ala Leu Gly Ser Gly Arg Ala Glu 5 10 15	165
cgc gac tgc cga gtg agc agc ttc cga gtc aag gag aac ttc gac aag Arg Asp Cys Arg Val Ser Ser Phe Arg Val Lys Glu Asn Phe Asp Lys 20 25 30 35	213
gct cgc ttc tct ggg acc tgg tac gcc atg gcc aag aag gac ccc gag Ala Arg Phe Ser Gly Thr Trp Tyr Ala Met Ala Lys Lys Asp Pro Glu 40 45 50	261
ggc ctc ttt ctg cag gac aac atc gtc gcg gag ttc tcc gtg gac gag Gly Leu Phe Leu Gln Asp Asn Ile Val Ala Glu Phe Ser Val Asp Glu 55 60 65	309
acc ggc cag atg agc gcc aca gcc aag ggc cga gtc cgt ctt ttg aat Thr Gly Gln Met Ser Ala Thr Ala Lys Gly Arg Val Arg Leu Leu Asn 70 75 80	357
aac tgg gac gtg tgc gca gac atg gtg ggc acc ttc aca gac acc gag Asn Trp Asp Val Cys Ala Asp Met Val Gly Thr Phe Thr Asp Thr Glu 85 90 95	405
gac cct gcc aag ttc aag atg aag tac tgg ggc gta gcc tcc ttt ctc Asp Pro Ala Lys Phe Lys Met Lys Tyr Trp Gly Val Ala Ser Phe Leu 100 105 110 115	453
cag aaa gga aat gat gac cac tgg atc gtc gac aca gac tac gac acg Gln Lys Gly Asn Asp Asp His Trp Ile Val Asp Thr Asp Tyr Asp Thr 120 125 130	501
tat gcc gtg cag tac tcc tgc cgc ctc ctg aac ctc gat ggc acc tgt Tyr Ala Val Gln Tyr Ser Cys Arg Leu Leu Asn Leu Asp Gly Thr Cys 135 140 145	549
gct gac agc tac tcc ttc gtg ttt tcc cgg gac ccc aac ggc ctg ccc Ala Asp Ser Tyr Ser Phe Val Phe Ser Arg Asp Pro Asn Gly Leu Pro 150 155 160	597
cca gaa gcg cag aag att gta agg cag cgg cag gag gag ctg tgc ctg Pro Glu Ala Gln Lys Ile Val Arg Gln Arg Gln Glu Glu Leu Cys Leu 165 170 175	645
gcc agg cag tac agg ctg atc gtc cac aac ggt tac tgc gat ggc aga Ala Arg Gln Tyr Arg Leu Ile Val His Asn Gly Tyr Cys Asp Gly Arg 180 185 190 195	693
tca gaa aga aac ctt ttg tag ca atatcaagaa tctagtttca tctgagaact Ser Glu Arg Asn Leu Leu *	746
200	
tctgattagc tctcagtctt cagctctatt tatcttagga gtttaatttg cccttctctc	806
cccatcttcc ctcagttccc ataaaacctt cattacacat aaagatacac gtgggggtca	866
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<220>
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<222> (463)..(1107)
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736

Tyr	Met	Lys	Glu	Lys	Pro	Leu	Thr	Tyr	Glu	His	Gly	Val	Lys	Leu	Ala	
150						155					160					

  

aaa	gcg	atc	gga	gca	cag	tgc	tac	ttg	gaa	tgt	tca	gct	ctg	act	cag	1002
Lys	Ala	Ile	Gly	Ala	Gln	Cys	Tyr	Leu	Glu	Cys	Ser	Ala	Leu	Thr	Gln	
165					170					175					180	

  

aaa	ggt	ctc	aaa	gcg	gtt	ttt	gat	gaa	gca	atc	ctc	acc	att	ttc	cac	1050
Lys	Gly	Leu	Lys	Ala	Val	Phe	Asp	Glu	Ala	Ile	Leu	Thr	Ile	Phe	His	
				185					190					195		

  

ccc	aag	aaa	aag	aag	aaa	cgc	tgt	tct	gag	ggt	cac	agc	tgc	tgt	tca	1098
Pro	Lys	Lys	Lys	Lys	Lys	Arg	Cys	Ser	Glu	Gly	His	Ser	Cys	Cys	Ser	
			200						205					210		

  

att	atc	tga	ggttgtc	tgggacctgc	ctccacccca	tccagggatg	agaatggcag	1154
Ile	Ile	*						
		215						

  

ccaatctctg	tggccaagct	ccagccaaaa	aggagggcac	gaccagaaag	gaactccctt	1214
tgcacggagg	cttgcccat	cacctctga	gccctcccaa	cacagcacac	tagtcagccc	1274
actgccacga	cctccctgcc	agccagaagc	atccgtactg	cacgctgtct	gagaatgctg	1334
ggcctggatt	gcagacagtg	ccgctgctga	tcgcatcaaa	aacaaagtca	aaggccatct	1394
cacattttac	aaatccccag	ctcatgaacg	tgaagctgat	aggaaatcac	cccagggaac	1454
ccgaaaaaga	aacttgattc	ctctattgct	ggccttactt	gatgtctttt	ataaaaacttg	1514
ggactacaat	actaaccttt	ttttctgaat	ctgctgttct	acccatgtgt	ctcacattca	1574
tttgtattat	ttcaagaaat	gtactaattt	ccagttcact	caggccttac	taatccatac	1634
caaattagcc	taaagacaag	gcattttata	ttcattttcta	ttttcagcat	gtttctacca	1694
aagctattag	aaccaacacg	tacctctgaa	tgcccgatta	taagaagaca	tgagaagact	1754
ttaaaagttt	tggaaattta	cagagccatg	atttttgaac	ctaattgaaa	gaaaaccatc	1814
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ctgatttttt	tccatgtatt	gccacgacaa	actaaaaatg	aactgtgttt	aagaatgtag	1934
tatttctgtt	tttcatccaa	gttgattggg	ggaagaatat	ggcaggatcc	atctttttaca	1994
gtatttttga	ttcagtaaag	tggacattcc	tgctcctccc	ttccccatt	gcatgccctc	2054
ttcctccctt	gatttcactt	tctctcatgc	ccggatcctt	ttattctccc	cagttataac	2114
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ggaaagtgcc	ttaaaaaaaa	aa				2196

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 <212> DNA  
 <213> Homo sapiens

<220>

&lt;221&gt; CDS

&lt;222&gt; (95) .. (766)

&lt;400&gt; 277

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tccctaggct atttctgccg ggcgctccgc gaag      atg cag ctc aag ccg atg      112
                                         Met Gln Leu Lys Pro Met
                                         1                               5

gag atc aac ccc gag atg ctg aac aaa gtg ctg tcc cgg ctg ggg gtc      160
Glu Ile Asn Pro Glu Met Leu Asn Lys Val Leu Ser Arg Leu Gly Val
                        10                               15                               20

gcc ggc cag tgg cgc ttc gtg gac gtg ctg ggg ctg gaa gag gag tct      208
Ala Gly Gln Trp Arg Phe Val Asp Val Leu Gly Leu Glu Glu Glu Ser
                        25                               30                               35

ctg ggc tcg gtg cca gcg cct gcc tgc gcg ctg ctg ctg ctg ttt ccc      256
Leu Gly Ser Val Pro Ala Pro Ala Cys Ala Leu Leu Leu Leu Phe Pro
                        40                               45                               50

ctc acg gcc cag cat gag aac ttc agg aaa aag cag att gaa gag ctg      304
Leu Thr Ala Gln His Glu Asn Phe Arg Lys Lys Gln Ile Glu Glu Leu
                        55                               60                               65                               70

aag gga caa gaa gtt agt cct aaa gtg tac ttc atg aag cag acc att      352
Lys Gly Gln Glu Val Ser Pro Lys Val Tyr Phe Met Lys Gln Thr Ile
                        75                               80                               85

ggg aat tcc tgt ggc aca atc gga ctt att cac gca gtg gcc aat aat      400
Gly Asn Ser Cys Gly Thr Ile Gly Leu Ile His Ala Val Ala Asn Asn
                        90                               95                               100

caa gac aaa ctg gga ttt gag gat gga tca gtt ctg aaa cag ttt ctt      448
Gln Asp Lys Leu Gly Phe Glu Asp Gly Ser Val Leu Lys Gln Phe Leu
                        105                               110                               115

tct gaa aca gag aaa atg tcc cct gaa gcc aga gca aaa tgc ttt gaa      496
Ser Glu Thr Glu Lys Met Ser Pro Glu Ala Arg Ala Lys Cys Phe Glu
                        120                               125                               130

aag aat gag gcc ata cag gca gcc cat gat gcc gtg gca cag gaa ggc      544
Lys Asn Glu Ala Ile Gln Ala Ala His Asp Ala Val Ala Gln Glu Gly
                        135                               140                               145                               150

caa tgt cgg gta gat gac aag gtg aat ttc cat ttt att ctg ttt aac      592
Gln Cys Arg Val Asp Asp Lys Val Asn Phe His Phe Ile Leu Phe Asn
                        155                               160                               165

aac gtg gat ggc cac ctc tat gaa ctt gat gga cga atg cct ttt ccg      640
Asn Val Asp Gly His Leu Tyr Glu Leu Asp Gly Arg Met Pro Phe Pro
                        170                               175                               180

gtg aac cat ggc gcc agt tca gag gac acc ctg ctg aag gac gct gcc      688
Val Asn His Gly Ala Ser Ser Glu Asp Thr Leu Leu Lys Asp Ala Ala
                        185                               190                               195

aag gtc tgc aga gaa ttc acc gag cgt gag caa gga gaa gtc cgc ttc      736
Lys Val Cys Arg Glu Phe Thr Glu Arg Glu Gln Gly Glu Val Arg Phe
                        200                               205                               210

tct gcc gtg gct ctc tgc aag gca gcc taa t gctctgtggg agggactttg      787
Ser Ala Val Ala Leu Cys Lys Ala Ala *

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215

220

ctgatttccc ctcttccctt caacatgaaa atatataccc ccccatgcag tctaaaatgc 847  
 ttcagtactt gtgaaacaca gctgttcttc tgttctgcag acacgccttc ccctcagcca 907  
 caccagggca cttaagcaca agcagagtgc acagctgtcc actgggcat tgtgggtgtga 967  
 gcttcagatg gtgaagcatt ctccccagtg tatgtcttgt atccgatatc taacgcttta 1027  
 aatggctact ttggtttctg tctgtaagtt aagaccttgg atgtgggttta attgtttgtc 1087  
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 ccccgaaac cagacgag 1165

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 <212> DNA  
 <213> Homo sapiens

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 <222> (366) .. (1478)

<220>  
 <221> misc\_feature  
 <222> (1) ... (2543)  
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 ccgggcgccc gctggaggtc gccgaggagc cacagggctg actgggtctgc tgcccggggc 120  
 caggagtgcc tgggtgtagca gtgcggagc catcccggcg tctgctgcca tgaccgactc 180  
 tcccctcaga ggagactctt cctcagcggg ggctgcagag acagatgagc ggcggtcctc 240  
 ggccgcggga ccgtgagacg ggttcgtggc cggccattta gggggacgct gcgaccaccg 300  
 cctgcgcccc tccggactgg ttccttgggc cccggaagct cgcggcgggc cctgcgggag 360  
 gcggc atg ctc ccg cgg agg ctg ctg gcc gcc tgg ctg gcg ggg acg 407  
 Met Leu Pro Arg Arg Leu Leu Ala Ala Trp Leu Ala Gly Thr  
 1 5 10  
 cgg ggc ggg ggc ctg ctg gcg ctt ctg gcc aat cag tgc cgc ttc gtc 455  
 Arg Gly Gly Gly Leu Leu Ala Leu Leu Ala Asn Gln Cys Arg Phe Val  
 15 20 25 30  
 acg ggc ctg cgc gtg cgg cgc gcg cag cag atc gcg cag ctc tac ggc 503  
 Thr Gly Leu Arg Val Arg Arg Ala Gln Gln Ile Ala Gln Leu Tyr Gly  
 35 40 45  
 cgc ctc tac tcc gag agc tca cgc cgc gtt ctc ctc ggc cgc ctc tgg 551  
 Arg Leu Tyr Ser Glu Ser Ser Arg Arg Val Leu Leu Gly Arg Leu Trp  
 50 55 60  
 cgc cgg ctg cac ggc cgt cct ggc cat gcc tct gcc ttg atg gcg gcg 599  
 Arg Arg Leu His Gly Arg Pro Gly His Ala Ser Ala Leu Met Ala Ala

65	70	75	
tta gcc ggc gtc ttc gtt tgg gac gag gag agg atc cag gag gag gag Leu Ala Gly Val Phe Val Trp Asp Glu Glu Arg Ile Gln Glu Glu Glu 80 85 90			647
ttg cag aga tct att aat gag atg aag cgg ttg gaa gaa atg tca aat Leu Gln Arg Ser Ile Asn Glu Met Lys Arg Leu Glu Glu Met Ser Asn 95 100 105 110			695
atg ttt cag agc tct gga gtc cag cac cac cct cca gaa cca aaa gcc Met Phe Gln Ser Ser Gly Val Gln His His Pro Pro Glu Pro Lys Ala 115 120 125			743
caa aca gaa ggg aat gaa gat tca gag ggc aaa gag caa cgt tgg gaa Gln Thr Glu Gly Asn Glu Asp Ser Glu Gly Lys Glu Gln Arg Trp Glu 130 135 140			791
atg gtg atg gat aag aaa cac ttt aag ctg tgg cgg cgc cca att aca Met Val Met Asp Lys Lys His Phe Lys Leu Trp Arg Arg Pro Ile Thr 145 150 155			839
ggc acc cac ctt tac cag tac cga gtt ttt gga acc tac aca gat gtg Gly Thr His Leu Tyr Gln Tyr Arg Val Phe Gly Thr Tyr Thr Asp Val 160 165 170			887
aca cct cgg cag ttc ttc aat gtt cag ctg gac aca gag tat aga aaa Thr Pro Arg Gln Phe Phe Asn Val Gln Leu Asp Thr Glu Tyr Arg Lys 175 180 185 190			935
aaa tgg gat gcc ctg gta atc aag ctg gag gtg att gag agg gat gtg Lys Trp Asp Ala Leu Val Ile Lys Leu Glu Val Ile Glu Arg Asp Val 195 200 205			983
gtt agt ggt tcc gag gtt ctt cac tgg gta acc cat ttt cct tat cca Val Ser Gly Ser Glu Val Leu His Trp Val Thr His Phe Pro Tyr Pro 210 215 220			1031
atg tac tca cgg gat tat gtt tat gtt cgg cgg tat agt gtg gat cag Met Tyr Ser Arg Asp Tyr Val Tyr Val Arg Arg Tyr Ser Val Asp Gln 225 230 235			1079
gaa aac aac atg atg gtg ttg gtg tcg cgt gct gtg gag cat ccg agt Glu Asn Asn Met Met Val Leu Val Ser Arg Ala Val Glu His Pro Ser 240 245 250			1127
gtg cca gag tct cca gaa ttc gtc agg gtc aga tca tat gaa tcc caa Val Pro Glu Ser Pro Glu Phe Val Arg Val Arg Ser Tyr Glu Ser Gln 255 260 265 270			1175
atg gtt atc cgt ccc cac aag tca ttt gat gag aat ggc ttt gac tac Met Val Ile Arg Pro His Lys Ser Phe Asp Glu Asn Gly Phe Asp Tyr 275 280 285			1223
tta cta aca tac agt gac aat ccc caa acg gtg ttt cct cgc tac tgt Leu Leu Thr Tyr Ser Asp Asn Pro Gln Thr Val Phe Pro Arg Tyr Cys 290 295 300			1271
gtt agt tgg atg gtt tcc agt ggc atg cca gat ttc ctg gag aag ctg Val Ser Trp Met Val Ser Ser Gly Met Pro Asp Phe Leu Glu Lys Leu 305 310 315			1319
cac atg gcc act ctg aaa gcc aag aat atg gag att aaa gta aag gac His Met Ala Thr Leu Lys Ala Lys Asn Met Glu Ile Lys Val Lys Asp 320 325 330 335 340 345 350			1367

320	325	330	
tac atc tca gct aag cct ctg gaa atg agt agt gaa gcc aag gcc acc			1415
Tyr Ile Ser Ala Lys Pro Leu Glu Met Ser Ser Glu Ala Lys Ala Thr			
335	340	345	350
agc cag tcc tct gag cga aag aac gag ggc agc tgt ggc cct gct cgg			1463
Ser Gln Ser Ser Glu Arg Lys Asn Glu Gly Ser Cys Gly Pro Ala Arg			
	355	360	365
att gag tat gct tga caggctttgg gataagaagg gacaaggtgc ttctagccct			1518
Ile Glu Tyr Ala *			
	370		
gtctcagtcc gttatcactc tgctgtagaa gggggacatg ccacatgtat tagaaggcat			1578
ctgctgtaac ttccagtgcg agataattca ataactgatg tcccatttca ttcagagccc			1638
ttattgctct tatcaaaaca gaagaaggct acatttgtgg gagtgttgtc atattctcag			1698
gccaaactgtt ttgaaattcg gtatctcact gagctaactt ggaacaaacc tctcacctca			1758
ggccagaagg ggatgacctc catttgcttc tctgagtagt ttcctctgct gacattccaa			1818
atcccaccat cgattgtgca gcgctttgga tttccttcag ttctccaggt ccacctggaa			1878
agtatagttg gccagttgag tctctcaaact gaggggctac tgggagtgct cttggtaaca			1938
atcatgatgt gaatgggtgt gaacgatact tggctatgtt aagtgccttg tccgcacctt			1998
gcttttatct ctagagacat gaagttatta ttaatttttt ttttttttaa gtagagatgg			2058
agtttcactc tgtttcccag gctggtcttg aactcctggg ccattgcctgg ccagggacat			2118
gaatttgtag aaagaaattt ccctccctgc ctgcacaata tcaccattg actcacctta			2178
tccaaagcaa gtttcctgtg aatcgggccag ttcttctata ttcattggat cattgcctcc			2238
ttcctaacct tccccattta ccaagaacac tgggagacta atccttttag atagtagctt			2298
tttgatgctc aaaacatcac atttaaattt agtttaaaaa ttttttaact tttgtgtcaa			2358
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gaattcggat cctcgagaga tctctttttt tgggttttgt ggggtatctt catcatcgaa			2478
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tcccc			2543

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 <222> (101)..(1570)

<400> 279  
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agccggtgcc tcagtcacct gcgcccccg tgaccccgac	atg tcc ttc cgc aaa	115
	Met Ser Phe Arg Lys	
	1 5	
gtg gtc cgg cag agc aaa ttc cgg cat gtg ttc ggg cag ccg gtc aag	163	
Val Val Arg Gln Ser Lys Phe Arg His Val Phe Gly Gln Pro Val Lys		
10 15 20		
aac gac cag tgc tat gag gac att cgc gtg tcc cgt gtt acc tgg gac	211	
Asn Asp Gln Cys Tyr Glu Asp Ile Arg Val Ser Arg Val Thr Trp Asp		
25 30 35		
agc acc ttc tgc gcc gtc aac ccc aag ttc ctg gcg gtg att gtg gag	259	
Ser Thr Phe Cys Ala Val Asn Pro Lys Phe Leu Ala Val Ile Val Glu		
40 45 50		
gcc agt gga ggg ggt gcc ttt ctg gtg ctc ccc cta agc aag acg ggc	307	
Ala Ser Gly Gly Gly Ala Phe Leu Val Leu Pro Leu Ser Lys Thr Gly		
55 60 65		
cgc att gac aag gcc tac ccg acg gtg tgt ggg cac acg gga cct gtc	355	
Arg Ile Asp Lys Ala Tyr Pro Thr Val Cys Gly His Thr Gly Pro Val		
70 75 80 85		
ctg gac atc gac tgg tgt cct cac aac gac gaa gtc ata gcc agc ggc	403	
Leu Asp Ile Asp Trp Cys Pro His Asn Asp Glu Val Ile Ala Ser Gly		
90 95 100		
tcg gag gac tgc acg gtc atg gtg tgg cag atc cca gag aac ggg ctg	451	
Ser Glu Asp Cys Thr Val Met Val Trp Gln Ile Pro Glu Asn Gly Leu		
105 110 115		
acc tcc ccg ctg aca gag ccg gtg gtg gta ctg gag ggg cac acc aag	499	
Thr Ser Pro Leu Thr Glu Pro Val Val Leu Glu Gly His Thr Lys		
120 125 130		
cga gtg ggc atc atc gcc tgg cac ccc acg gcc cga aac gtg ctg ctc	547	
Arg Val Gly Ile Ile Ala Trp His Pro Thr Ala Arg Asn Val Leu Leu		
135 140 145		
agt gca ggc tgc gac aac gtg gta ctc atc tgg aat gtg ggc aca gcg	595	
Ser Ala Gly Cys Asp Asn Val Val Leu Ile Trp Asn Val Gly Thr Ala		
150 155 160 165		
gag gag ctg tac cgc ctg gac agc ctg cac cct gac ctc atc tac aat	643	
Glu Glu Leu Tyr Arg Leu Asp Ser Leu His Pro Asp Leu Ile Tyr Asn		
170 175 180		
gtc agc tgg aac cac aat ggc agc ctg ttt tgc tca gca tgc aag gac	691	
Val Ser Trp Asn His Asn Gly Ser Leu Phe Cys Ser Ala Cys Lys Asp		
185 190 195		
aag agc gtg cgc atc atc gac ccc cgt cgg ggc acc ctg gtg gca gag	739	
Lys Ser Val Arg Ile Ile Asp Pro Arg Arg Gly Thr Leu Val Ala Glu		
200 205 210		
cgg gag aag gct cat gag ggg gcc cgg ccc atg cgg gcc atc ttc ctg	787	
Arg Glu Lys Ala His Glu Gly Ala Arg Pro Met Arg Ala Ile Phe Leu		
215 220 225		
gca gat ggc aag gtg ttc acc aca ggc ttc agc cga atg agc gag cgg	835	
Ala Asp Gly Lys Val Phe Thr Thr Gly Phe Ser Arg Met Ser Glu Arg		
230 235 240 245		

cag ctg gcg ctc tgg gac cca gaa aac ctc gag gaa ccc atg gcc ctg Gln Leu Ala Leu Trp Asp Pro Glu Asn Leu Glu Glu Pro Met Ala Leu 250 255 260	883
cag gaa ctg gac tcg agc aac ggg gcc ctg ctg ccc ttc tac gac ccc Gln Glu Leu Asp Ser Ser Asn Gly Ala Leu Leu Pro Phe Tyr Asp Pro 265 270 275	931
gac acc agt gtg gtc tac gtc tgc ggc aag ggt gac tcc agc atc cgg Asp Thr Ser Val Val Tyr Val Cys Gly Lys Gly Asp Ser Ser Ile Arg 280 285 290	979
tac ttt gag atc aca gag gag cct ccc tac atc cac ttc ctg aac acg Tyr Phe Glu Ile Thr Glu Glu Pro Pro Tyr Ile His Phe Leu Asn Thr 295 300 305	1027
ttc acc agc aag gag ccg cag cgg ggt atg ggc agc atg ccc aag cgg Phe Thr Ser Lys Glu Pro Gln Arg Gly Met Gly Ser Met Pro Lys Arg 310 315 320 325	1075
ggc ctg gag gtc agc aag tgc gag atc gcc cgg ttc tac aaa ctg cat Gly Leu Glu Val Ser Lys Cys Glu Ile Ala Arg Phe Tyr Lys Leu His 330 335 340	1123
gag cgc aag tgt gag ccc atc gtc atg act gtg cca aga aag tcg gac Glu Arg Lys Cys Glu Pro Ile Val Met Thr Val Pro Arg Lys Ser Asp 345 350 355	1171
ctc ttc cag gat gat ctg tac ccc gac aca gcc ggg ccc gag gca gcc Leu Phe Gln Asp Asp Leu Tyr Pro Asp Thr Ala Gly Pro Glu Ala Ala 360 365 370	1219
ctg gag gct gag gag tgg gtg agc ggg cgg gat gcc gac ccg atc ctc Leu Glu Ala Glu Glu Trp Val Ser Gly Arg Asp Ala Asp Pro Ile Leu 375 380 385	1267
atc tca ctg cgg gag gcc tac gtg ccc agc aag cag cgg gac ctg aag Ile Ser Leu Arg Glu Ala Tyr Val Pro Ser Lys Gln Arg Asp Leu Lys 390 395 400 405	1315
atc agc cgg cgc aac gtg ttg tct gac agc cgg ccc gcc atg gcc ccg Ile Ser Arg Arg Asn Val Leu Ser Asp Ser Arg Pro Ala Met Ala Pro 410 415 420	1363
ggc tcc tcc cac cta ggg gcc ccc gcc tcc acc acc act gct gct gat Gly Ser Ser His Leu Gly Ala Pro Ala Ser Thr Thr Thr Ala Ala Asp 425 430 435	1411
gcc acc ccc agc ggc agc ctg gcc aga gcc ggg gag gct ggg aag ctg Ala Thr Pro Ser Gly Ser Leu Ala Arg Ala Gly Glu Ala Gly Lys Leu 440 445 450	1459
gag gag gtg atg cag gag ctg cgg gcc ctg agg gcg ctg gtc aag gag Glu Glu Val Met Gln Glu Leu Arg Ala Leu Arg Ala Leu Val Lys Glu 455 460 465	1507
cag ggc gac cgc atc tgc cgc ctg gag gag cag ctg ggc cgc atg gag Gln Gly Asp Arg Ile Cys Arg Leu Glu Glu Gln Leu Gly Arg Met Glu 470 475 480 485	1555
aac ggg gat gcg tag ggccacagcc acacgccacc ttcattctcct ccgccgcccc Asn Gly Asp Ala * 490	1610

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<210> 280
<211> 888
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (104)..(673)

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Met Gly Thr Ala
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gga gcc atg cag ctg tgc tgg gtg atc ctg ggc ttc ctc ctg ttc cga 163
Gly Ala Met Gln Leu Cys Trp Val Ile Leu Gly Phe Leu Leu Phe Arg
5 10 15 20
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Gly His Asn Ser Gln Pro Thr Met Thr Gln Thr Ser Ser Ser Gln Gly
25 30 35
ggc ctt ggc ggt cta agt ctg acc aca gag cca gtt tct tcc aac cca 259
Gly Leu Gly Gly Leu Ser Leu Thr Thr Glu Pro Val Ser Ser Asn Pro
40 45 50
gga tac atc cct tcc tca gag gct aac agg cca agc cat ctg tcc agc 307
Gly Tyr Ile Pro Ser Ser Glu Ala Asn Arg Pro Ser His Leu Ser Ser
55 60 65
act ggt acc cca gac aca ttt caa act gtt ccc ccc aat tca acc acc 355
Thr Gly Thr Pro Asp Thr Phe Gln Thr Val Pro Pro Asn Ser Thr Thr
70 75 80
atg agc ctg agc atg agg gaa gat gcg acc atc ctg ccc agc ccc acg 403
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**PCT/US01/04098**

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					Met Gly Thr Ala		
					1		
gga gcc atg cag ctg tgc tgg gtg atc ctg ggc ttc ctc ctg ttc cga							163
Gly Ala Met Gln Leu Cys Trp Val Ile Leu Gly Phe Leu Leu Phe Arg							
5		10			15		20
ggc cac aac tcc cag ccc aca atg acc cag acc tct agc tct cag gga							211
Gly His Asn Ser Gln Pro Thr Met Thr Gln Thr Ser Ser Ser Gln Gly							
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ggc ctt ggc ggt cta agt ctg acc aca gag cca gtt tct tcc aac cca							259
Gly Leu Gly Gly Leu Ser Leu Thr Thr Glu Pro Val Ser Ser Asn Pro							
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gga tac atc cct tcc tca gag gct aac agg cca agc cat ctg tcc agc							307

Gly	Tyr	Ile	Pro	Ser	Ser	Glu	Ala	Asn	Arg	Pro	Ser	His	Leu	Ser	Ser		
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Thr	Gly	Thr	Pro	Gly	Ala	Gly	Val	Pro	Ser	Ser	Gly	Arg	Asp	Gly	Gly		
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aca	agc	aga	gac	aca	ttt	caa	act	gtt	ccc	ccc	aat	tca	acc	acc	atg		403
Thr	Ser	Arg	Asp	Thr	Phe	Gln	Thr	Val	Pro	Pro	Asn	Ser	Thr	Thr	Met		
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agc	ctg	agc	atg	agg	gaa	gat	gcg	acc	atc	ctg	ccc	agc	ccc	acg	tca		451
Ser	Leu	Ser	Met	Arg	Glu	Asp	Ala	Thr	Ile	Leu	Pro	Ser	Pro	Thr	Ser		
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gag	act	gtg	ctc	act	gtg	gct	gca	ttt	ggt	gtt	atc	agc	ttc	att	gtc		499
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Ile	Leu	Val	Val	Val	Val	Ile	Ile	Leu	Val	Gly	Val	Val	Ser	Leu	Arg		
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Phe	Lys	Cys	Arg	Lys	Ser	Lys	Glu	Ser	Glu	Asp	Pro	Gln	Lys	Pro	Gly		
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Ser	Ser	Gly	Leu	Ser	Glu	Ser	Cys	Ser	Thr	Ala	Asn	Gly	Glu	Lys	Asp		
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Ser	Ile	Thr	Leu	Ile	Ser	Met	Lys	Asn	Ile	Asn	Met	Asn	Asn	Gly	Lys		
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Gln	Ser	Leu	Ser	Ala	Glu	Lys	Val	Leu	*								
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&lt;210&gt; 282

&lt;211&gt; 4424

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1425) .. (4214)

&lt;220&gt;

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 <223> n = a,t,c or g

<400> 282

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Arg Ser Gln Asp Asp Gly Gly Glu Asn Arg Ser Arg Asp His Asp Tyr
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cgg gac atg gac tac cgt tca tat cct cgc gag tat ggc agc cag gag     1580

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Pro	His	Ser	Thr	Met	Asp	Ser	Ile	Leu	Gly	Ala	Leu	Ala	Pro	Tyr	Ala		
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Leu	Asn	Arg	Gly	Phe	Ala	Phe	Ile	Gln	Leu	Ser	Thr	Ile	Glu	Ala	Ala		
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Gln	Leu	Leu	Gln	Ile	Leu	Gln	Ala	Leu	His	Pro	Pro	Leu	Thr	Ile	Asp		
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Gln	Glu	Arg	Gly	Gly	Pro	Glu	Arg	Glu	Glu	Lys	Leu	Thr	Asp	Trp	Gln	
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Lys	Leu	Ala	Cys	Leu	Leu	Cys	Arg	Arg	Gln	Phe	Pro	Ser	Lys	Glu	Ala	
			760					765					770			
ctc	atc	cgg	cac	cag	cag	ctc	tca	ggg	ctc	cac	aag	caa	aac	ctt	gag	3788
Leu	Ile	Arg	His	Gln	Gln	Leu	Ser	Gly	Leu	His	Lys	Gln	Asn	Leu	Glu	
		775					780					785				
att	cac	cgg	cga	gcc	cac	ttg	tca	gaa	aac	gag	cta	gaa	gca	cta	gag	3836
Ile	His	Arg	Arg	Ala	His	Leu	Ser	Glu	Asn	Glu	Leu	Glu	Ala	Leu	Glu	
		790				795					800					
aag	aat	gac	atg	gag	caa	atg	aag	tac	cgg	gac	cgt	gca	gct	gaa	cgc	3884

Lys Asn Asp Met Glu Gln Met Lys Tyr Arg Asp Arg Ala Ala Glu Arg  
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 Arg Glu Lys Tyr Gly Ile Pro Glu Pro Pro Glu Pro Lys Arg Arg Lys  
 825 830 835  
 tac ggc ggc ata tcc aca gcc tct gta gac ttc gag cag cct act cgg 3980  
 Tyr Gly Gly Ile Ser Thr Ala Ser Val Asp Phe Glu Gln Pro Thr Arg  
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 Asp Gly Leu Gly Ser Asp Asn Ile Gly Ser Arg Met Leu Gln Ala Met  
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 Gly Trp Lys Glu Gly Ser Gly Leu Gly Arg Lys Lys Gln Gly Ile Val  
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 Thr Pro Ile Glu Ala Gln Thr Arg Val Arg Gly Ser Gly Leu Gly Ala  
 885 890 895 900  
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 Arg Gly Ser Ser Tyr Gly Val Thr Ser Thr Glu Ser Tyr Lys Glu Thr  
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 Leu His Lys Thr Met Val Thr Arg Phe Asn Glu Ala Gln \*  
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 tttgtaataa aagctgaaaa gtc 4424

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 <222> (18)..(1277)

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 Thr His Ala Ser Ala Pro Ser Phe Leu Asn Thr Gly Leu Gly Pro Thr  
 15 20 25  
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 Ala Leu Gly Val Leu Gly Gly Ala Gly Ala Gly Leu Met Ser Asn Pro  
 30 35 40

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Ser Pro Gln Val Pro Glu Glu Glu Ala Ser Thr Ser Val Cys Arg Pro	
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Lys Ser Ser Met Ala Ser Thr Ser Arg Arg Gln Arg Arg Glu Arg Arg	
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Phe Arg Arg Tyr Leu Ser Ala Gly Arg Leu Val Arg Ala Gln Ala Leu	
80 85 90	
ctc cag cga cac cca ggc ctc gat gta gat gct ggg cag ccc cca cca	338
Leu Gln Arg His Pro Gly Leu Asp Val Asp Ala Gly Gln Pro Pro Pro	
95 100 105	
ctg cac cgg gcc tgt gcc cgc cac gat gcc cct gcc ctg tgc ctg ctg	386
Leu His Arg Ala Cys Ala Arg His Asp Ala Pro Ala Leu Cys Leu Leu	
110 115 120	
ctt cgg ctc ggg gct gac cct gcc cac cag gac cgc cat ggg gac acg	434
Leu Arg Leu Gly Ala Asp Pro Ala His Gln Asp Arg His Gly Asp Thr	
125 130 135	
gca ctg cat gct gct gcc cgc cag ggc cca gat gcc tac acc gat ttc	482
Ala Leu His Ala Ala Ala Arg Gln Gly Pro Asp Ala Tyr Thr Asp Phe	
140 145 150 155	
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Phe Leu Pro Leu Leu Ser Arg Cys Pro Ser Ala Met Gly Ile Lys Asn	
160 165 170	
aag gat ggg gag acc cct ggc caa att ttg ggc tgg gga ccc ccc tgg	578
Lys Asp Gly Glu Thr Pro Gly Gln Ile Leu Gly Trp Gly Pro Pro Trp	
175 180 185	
gat tct gct gaa gag gag gaa gaa gat gat gcc tcc aag gag cgg gaa	626
Asp Ser Ala Glu Glu Glu Glu Glu Asp Asp Ala Ser Lys Glu Arg Glu	
190 195 200	
tgg aga cag aag ctc cag ggt gag ctg gag gac gag tgg cag gaa gtc	674
Trp Arg Gln Lys Leu Gln Gly Glu Leu Glu Asp Glu Trp Gln Glu Val	
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Met Gly Arg Phe Glu Gly Asp Ala Ser His Glu Thr Gln Glu Pro Glu	
220 225 230 235	
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Ser Phe Ser Ala Trp Ser Asp Arg Leu Ala Arg Glu His Ala Gln Lys	
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255 260 265	
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Ala Glu Gly Ser Ser Gln Ser Trp Arg Gln Gln Glu Glu Glu Gln Arg	
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Leu Phe Arg Glu Arg Ala Arg Ala Lys Glu Glu Glu Leu Arg Glu Ser	
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 Ser Leu Trp Arg Phe Gly Asp Val Pro Trp Pro Cys Pro Gly Gly Gly  
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 Asp Pro Glu Ala Met Ala Ala Ala Leu Val Ala Arg Gly Pro Pro Leu  
 350 355 360  
 gag gaa cag ggg gct ctg agg agg tac ttg agg gtc cag cag gtc cgc 1154  
 Glu Glu Gln Gly Ala Leu Arg Arg Tyr Leu Arg Val Gln Gln Val Arg  
 365 370 375  
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 Trp His Pro Asp Arg Phe Leu Gln Arg Phe Arg Ser Gln Ile Glu Thr  
 380 385 390 395  
 tgg gag ctg ggc cgt gtg atg gga gca gtg aca gcc ctt tct cag gcc 1250  
 Trp Glu Leu Gly Arg Val Met Gly Ala Val Thr Ala Leu Ser Gln Ala  
 400 405 410  
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 Leu Asn Arg His Ala Glu Ala Leu Lys  
 415 420  
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 aatacattaa aataaatata aagaaaaaat tctcccagca aatactagat tcaatcccaa 180  
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 acggaaaaaa gggttttggt ttctctctac taacgaggat gatactgttt cacatgcttc 360



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gaataacggt tgatagttgt gataatcttt ttctctctta gggtttggtt ttcaaagct 600
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acttggaact ttaggagcac tgctatcaag aacctgggtt tctgccaaaa cgtctgcttc 720
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<210> 285  
<211> 4064  
<212> DNA  
<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (4062) .. (4073)

&lt;400&gt; 285

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cagaaactcc ggccgttgta ttgatgggtga cttaaagagaa atagaagcct ctatataagg      180
caagagtcca taccagaaga attcgaccaa tatgagatac ctccaaaaaa atcaactcaa      240
tgacctactt tatatgtaag agacccaaaa aagtcagctt ttgtgggaag ttgatatgca      300
gtttattgaa caaacagagt gtacagtaac taaacgaact gtgtatttcc aaaggaatta      360
agaccgcata tctggattca cacctaaaag cacatagaaa attaaaccaa agaagggcaa      420
gttttgtact aaaatcactt gggcccaggt tattctataa gaagattctc actggcattt      480
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<210> 286
<211> 1409
<212> DNA
<213> Homo sapiens

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<222> (1286) .. (1456)

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Tyr Pro Glu Lys Pro Leu Lys Gly Ser Gly Phe Arg Cys Val His Ile	
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160 165 170	
ccc atc acc ttc acc acc gcc tcc ttc gct gcc acc aaa ttt ggc tcc Pro Ile Thr Phe Thr Thr Ala Ser Phe Ala Ala Thr Lys Phe Gly Ser	817
175 180 185	
act aag atg aag aag ggg ggc ggg gca gca agt ggt ggg ggt gta gcc Thr Lys Met Lys Lys Gly Gly Gly Ala Ala Ser Gly Gly Gly Val Ala	865
190 195 200	
agc agt ggg gcg ggt ggc cag cag cca cac cag cag cct cgc atg gcc Ser Ser Gly Ala Gly Gly Gln Gln Pro His Gln Gln Pro Arg Met Ala	913
205 210 215 220	
cgc tca ccc acc aac agc ctg ctg aag cac aag agc ctc tct ctg tct Arg Ser Pro Thr Asn Ser Leu Leu Lys His Lys Ser Leu Ser Leu Ser	961
225 230 235	
atg cat tca ctg aac ttc atc acg gcc aac ccg gcc cct cag tcc cag Met His Ser Leu Asn Phe Ile Thr Ala Asn Pro Ala Pro Gln Ser Gln	1009
240 245 250	
ctc tca ccc aat gcc aag gag ttc gtg tac aac ggt ggt ggc tca ccc Leu Ser Pro Asn Ala Lys Glu Phe Val Tyr Asn Gly Gly Gly Ser Pro	1057
255 260 265	
agc ctc ttc ttt gat gcg gcc gat ggc agg gca gcg gca ccc cag gcc Ser Leu Phe Phe Asp Ala Ala Asp Gly Arg Ala Ala Ala Pro Gln Ala	1105
270 275 280	
cgt ttg gag gca gtg ggg ctg gca cct gca aca gca gca gct ttg aca Arg Leu Glu Ala Val Gly Leu Ala Pro Ala Thr Ala Ala Ala Leu Thr	1153
285 290 295 300	
tgg ccc agg tat ttg gag gtg gtg cca aca gcc tct tcc tgg aga aga Trp Pro Arg Tyr Leu Glu Val Val Pro Thr Ala Ser Ser Trp Arg Arg	1201
305 310 315	
cac ccc ttt gtg gaa ggc ctc agc tac aac ctg aac acc atg cag tat His Pro Phe Val Glu Gly Leu Ser Tyr Asn Leu Asn Thr Met Gln Tyr	1249
320 325 330	



ccc agc cag cag ttc cag ccc gtg gtg ctg gcc aac tga 1288  
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 ctgagcgctc cccagaggtg agctgatccc cagccacagc acacaggacc aggctgcgag 180  
 aacagcatca tcagcatc atg cta tta caa tcc caa acc atg ggg gtt tct 231  
                           Met Leu Leu Gln Ser Gln Thr Met Gly Val Ser  
                           1                          5                          10  
 cac agc ttt aca cca aag ggc atc act atc cct caa aga gag aaa cct 279  
 His Ser Phe Thr Pro Lys Gly Ile Thr Ile Pro Gln Arg Glu Lys Pro  
                           15                          20                          25  
 gga cac atg tac caa aac gaa gat tac ctg cag aac ggg ctg cca aca 327  
 Gly His Met Tyr Gln Asn Glu Asp Tyr Leu Gln Asn Gly Leu Pro Thr  
                           30                          35                          40  
 gaa acc acc gtt ctt ggg act gtc cag atc ctg tgt tgc cta ttg att 375  
 Glu Thr Thr Val Leu Gly Thr Val Gln Ile Leu Cys Cys Leu Leu Ile  
                           45                          50                          55  
 tca agt ctg ggg gcc atc ttg gtt ttt gct ccc tac ccc tcc cac ttc 423  
 Ser Ser Leu Gly Ala Ile Leu Val Phe Ala Pro Tyr Pro Ser His Phe  
                           60                          65                          70                          75  
 aat cca gca att tcc acc act ttg atg tct ggg tac cca ttt tta gga 471  
 Asn Pro Ala Ile Ser Thr Thr Leu Met Ser Gly Tyr Pro Phe Leu Gly  
                           80                          85                          90  
 gct ctg tgt ttt ggc att act gga tcc ctc tca att atc tct gga aaa 519  
 Ala Leu Cys Phe Gly Ile Thr Gly Ser Leu Ser Ile Ile Ser Gly Lys  
                           95                          100                          105  
 caa tca act aag ccc ttt gac ctg agc agc ttg acc tca aat gca gtg 567  
 Gln Ser Thr Lys Pro Phe Asp Leu Ser Ser Leu Thr Ser Asn Ala Val  
                           110                          115                          120  
 agt tct gtt act gca gga gca ggc ctc ttc ctc ctt gct gac agc atg 615  
 Ser Ser Val Thr Ala Gly Ala Gly Leu Phe Leu Leu Ala Asp Ser Met  
                           125                          130                          135  
 gta gcc ctg agg act gcc tct caa cat tgt ggc tca gaa atg gat tat 663  
 Val Ala Leu Arg Thr Ala Ser Gln His Cys Gly Ser Glu Met Asp Tyr  
                           140                          145                          150                          155

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cta tcc tca ttg cct tat tcg gag tac tat tat cca ata tat gaa atc      711
Leu Ser Ser Leu Pro Tyr Ser Glu Tyr Tyr Tyr Pro Ile Tyr Glu Ile
                160                165                170

aaa gat tgt ctc ctg acc agt gtc agt tta aca ggt gtc cta gtg gtg      759
Lys Asp Cys Leu Leu Thr Ser Val Ser Leu Thr Gly Val Leu Val Val
                175                180                185

atg ctc atc ttc act gtg ctg gag ctc tta tta gct gca tac agt tct      807
Met Leu Ile Phe Thr Val Leu Glu Leu Leu Leu Ala Ala Tyr Ser Ser
                190                195                200

gtc ttt tgg tgg aaa cag ctc tac tcc aac aac cct ggg agt tca ttt      855
Val Phe Trp Trp Lys Gln Leu Tyr Ser Asn Asn Pro Gly Ser Ser Phe
                205                210                215

tcc tcg acc cag tca caa gat cat atc caa cag gtc aaa aag agt tct      903
Ser Ser Thr Gln Ser Gln Asp His Ile Gln Gln Val Lys Lys Ser Ser
                220                225                230                235

tca cgg tct tgg ata taa gtaact cttggcctca gaggaaggaa aagcaactca      957
Ser Arg Ser Trp Ile *
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acactcatgg tcaagtgtga ttagactttc ctgaaatctc tgccatttta gatactgtga 1017

aacaaactaa aaaaaaaaaa                                         1036

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<210> 289
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<213> Homo sapiens

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<222> (169)..(456)

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attgggagat ctacagctaa gacgccagga acccctggaa gcctagaa atg gag aac      177
                                   Met Glu Asn
                                   1

ctg aag tct gga gtg tat cct ctc aag gaa gca agt gga tgc cct ggg      225
Leu Lys Ser Gly Val Tyr Pro Leu Lys Glu Ala Ser Gly Cys Pro Gly
                5                10                15

gct gac agg aat ctt ctg gtg tac tct ttt tat gaa aag ggg cca ttg      273
Ala Asp Arg Asn Leu Leu Val Tyr Ser Phe Tyr Glu Lys Gly Pro Leu
                20                25                30                35

aca ttt agg gat gtg gcc ata gaa ttt tct ctg gag gag tgg caa tgc      321
Thr Phe Arg Asp Val Ala Ile Glu Phe Ser Leu Glu Glu Trp Gln Cys
                40                45                50

ctg gac act gct cag cag gat ttg tat aga aaa gtg atg tta gag aac      369
Leu Asp Thr Ala Gln Gln Asp Leu Tyr Arg Lys Val Met Leu Glu Asn

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Tyr Arg Asn Leu Val Phe Leu Gly Glu Asn Asn Phe Asn Thr Lys Ser				
	70	75	80	
ctt ata tac cct aaa gtt ttc att tct ctg ttt tca tag aataattttt				466
Leu Ile Tyr Pro Lys Val Phe Ile Ser Leu Phe Ser *				
	85	90	95	
ggtaatttat gctttgcata agtgagtttc tgatgcctgt tttaaagaaa tcttgaagaa				526
ctgtccgtgt ggaaaaaat ttcttcagga tgttttatct tggcctgac tttttacatt				586
tctgagccgg tctgtatcct tcaactctaca gtagtggttaa tttcagaaat ttagtagtat				646
aaaatattgt tgtccatatg ttaaaatcta tatgccacca ctaatttttt atccatgaat				706
actgggtggc aaaattaagc acctacaaat ttaaaatatt ttctaaatgt taagaacttt				766
ctgtcattaa atagtatttt gggataaatt ttctagaata ttctattaca tcctctttac				826
taagcatggg actaggtagg taattagaga atatgagcaa gattcatgtt atttattttt				886
aataaagcag gtattgctgt ctctaagcca gatctgggtca cctgtctgga gcaaggaaaa				946
gatccctgga atatgaaggg acacagtacg gtagtcaaac cccaggtag gtgagagtga				1006
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cagtagccgc tgaggggatt gcagataacc gcttcccgcga cggggaaagt ctaccctgcc	180
tgccactttc tgctcgccgt cagcgccgga gctcgccagc atg tct gtg gta ccg	235
	Met Ser Val Val Pro
	1 5
ccc aat cgc tgc cag acc ggc tgg ccc cgg ggg gtc act cag ttc ggc	283
Pro Asn Arg Ser Gln Thr Gly Trp Pro Arg Gly Val Thr Gln Phe Gly	
	10 15 20
aac aag tac atc cag cag acg aag ccc ctc acc ctg gag cgc acc atc	331
Asn Lys Tyr Ile Gln Gln Thr Lys Pro Leu Thr Leu Glu Arg Thr Ile	
	25 30 35
aac ctg tac cct ctt acc aat tat act ttt ggt aca aaa gag ccc ctc	379
Asn Leu Tyr Pro Leu Thr Asn Tyr Thr Phe Gly Thr Lys Glu Pro Leu	
	40 45 50

tac gag aag gac agc tct gtt gca gcc aga ttt cag cgc atg agg gaa Tyr Glu Lys Asp Ser Ser Val Ala Ala Arg Phe Gln Arg Met Arg Glu 55 60 65	427
gaa ttt gat aaa att gga atg agg agg act gta gaa ggg gtt ctg att Glu Phe Asp Lys Ile Gly Met Arg Arg Thr Val Glu Gly Val Leu Ile 70 75 80 85	475
gta cat gag cac cgg cta ccc cat gtg tta ctg ctg cag ctg gga aca. Val His Glu His Arg Leu Pro His Val Leu Leu Leu Gln Leu Gly Thr 90 95 100	523
act ttc ttc aaa cta cct ggt ggt gaa ctt aac cca gga gaa gat gaa Thr Phe Phe Lys Leu Pro Gly Gly Glu Leu Asn Pro Gly Glu Asp Glu 105 110 115	571
gtt gaa gga cta aaa cgc tta atg aca gag ata ctg ggt cgt cag gat Val Glu Gly Leu Lys Arg Leu Met Thr Glu Ile Leu Gly Arg Gln Asp 120 125 130	619
gga gtt ttg caa gac tgg gtc att gac gat tgc att ggt aac tgg tgg Gly Val Leu Gln Asp Trp Val Ile Asp Asp Cys Ile Gly Asn Trp Trp 135 140 145	667
aga cca aat ttt gaa cct cct cag tat cca tat att cct gca cat att Arg Pro Asn Phe Glu Pro Pro Gln Tyr Pro Tyr Ile Pro Ala His Ile 150 155 160 165	715
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aaa gcc ttg ttt gca gtc cct aaa aat tac aag ctg gta gct gca cca Lys Ala Leu Phe Ala Val Pro Lys Asn Tyr Lys Leu Val Ala Ala Pro 185 190 195	811
ttg ttt gaa ttg tat gac aat gca cca gga tat gga ccc atc att tct Leu Phe Glu Leu Tyr Asp Asn Ala Pro Gly Tyr Gly Pro Ile Ile Ser 200 205 210	859
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atctttgtga tgaagagctt ccattacttc tgaaaactat atttatctga gtgagtccaa	1387
ggtgcaactc ctaaataaat tgtgttgacag agaactccca gtataattca ctgaccagta	1447
cattttataa ccatccaggc cttgggttgc aagcaacaga ccttaaacat acaggaaact	1507



gct tct atg gca gga tat gcg gat ctg aaa aga aca att gct gtc ctt 713  
 Ala Ser Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu  
 75 80 85

ctg gat gac att ttg caa cga ttg gtg aag ctg gag aac aaa gtt gac 761  
 Leu Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp  
 90 95 100 105

tat att gtt gtg aat ggc tca gca gcc aac acc acc aat ggt act agt 809  
 Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr Ser  
 110 115 120

ggg aat ttg gtg cca gta acc aca aat aaa aga acg aat gtc tcg ggc 857  
 Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val Ser Gly  
 125 130 135

agt atc aga tag cag ttgaaaatca ccttggtgctg ctccatccac tgtggattat 912  
 Ser Ile Arg \*  
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 <222> (91) .. (1488)

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 Met Asp Gly Arg Met Met Arg  
 1 5

agc atg agg ctg aga gag gag gag tca ccc gga ccc agc cac aca gcg 159  
 Ser Met Arg Leu Arg Glu Glu Glu Ser Pro Gly Pro Ser His Thr Ala  
 10 15 20

tcc tgc ctc tgc ggc tct gcc ccc tgc atc ctg tgc agc tgc tgc ccc 207  
 Ser Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro  
 25 30 35

gcc agc cgc aac tcc acc gtg agc cgc ctc atc ttc acg ttc ttc ctc 255  
 Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe Leu  
 40 45 50 55

ttc ctg ggg gtg ctg gtg tcc atc att atg ctg agc ccg ggc gtg gag 303  
 Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly Val Glu  
 60 65 70

agt cag ctc tac aag ctg ccc tgg gtg tgt gag gag ggg gcc ggg atc 351  
 Ser Gln Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly Ala Gly Ile  
 75 80 85

ccc acc gtc ctg cag ggc cac atc gac tgt ggc tcc ctg ctt ggc tac 399



Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser	Leu	Leu	Gly	Tyr		
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cgc	gct	gtc	tac	cgc	atg	tgc	ttc	gcc	acg	gcg	gcc	ttc	ttc	ttc	ttt	447	
Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala	Ala	Phe	Phe	Phe	Phe		
	105					110					115						
ttc	acc	ctg	ctc	atg	ctc	tgc	gtg	agc	agc	agc	cgg	gac	ccc	cgg	gct	495	
Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	Ser	Ser	Arg	Asp	Pro	Arg	Ala		
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gcc	atc	cag	aat	ggg	ttt	tgg	ttc	ttt	aag	ttc	ctg	atc	ctg	gtg	ggc	543	
Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe	Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly		
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Leu	Thr	Val	Gly	Ala	Phe	Tyr	Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile		
			155					160					165				
tgg	ttc	tac	ttc	ggc	gtc	gtg	ggc	tcc	ttc	ctc	ttc	atc	ctc	atc	cag	639	
Trp	Phe	Tyr	Phe	Gly	Val	Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln		
		170					175					180					
ctg	gtg	ctg	ctc	atc	gac	ttt	gcg	cac	tcc	tgg	aac	cag	cgg	tgg	ctg	687	
Leu	Val	Leu	Leu	Ile	Asp	Phe	Ala	His	Ser	Trp	Asn	Gln	Arg	Trp	Leu		
	185					190					195						
ggc	aag	gcc	gag	gag	tgc	gat	tcc	cgt	gcc	tgg	tac	gca	ggc	ctc	ttc	735	
Gly	Lys	Ala	Glu	Glu	Cys	Asp	Ser	Arg	Ala	Trp	Tyr	Ala	Gly	Leu	Phe		
200					205					210					215		
ttc	ttc	act	ctc	ctc	ttc	tac	ttg	ctg	tgc	atc	gcg	gcc	gtg	gcg	ctg	783	
Phe	Phe	Thr	Leu	Leu	Phe	Tyr	Leu	Leu	Ser	Ile	Ala	Ala	Val	Ala	Leu		
				220					225					230			
atg	ttc	atg	tac	tac	act	gag	ccc	agc	ggc	tgc	cac	gag	ggc	aag	gtc	831	
Met	Phe	Met	Tyr	Tyr	Thr	Glu	Pro	Ser	Gly	Cys	His	Glu	Gly	Lys	Val		
			235					240					245				
ttc	atc	agc	ctc	aac	ctc	acc	ttc	tgt	gtc	tgc	gtg	tcc	atc	gct	gct	879	
Phe	Ile	Ser	Leu	Asn	Leu	Thr	Phe	Cys	Val	Cys	Val	Ser	Ile	Ala	Ala		
		250					255					260					
gtc	ctg	ccc	aag	gtc	cag	gac	gcc	cag	ccc	aac	tgc	ggt	ctg	ctg	cag	927	
Val	Leu	Pro	Lys	Val	Gln	Asp	Ala	Gln	Pro	Asn	Ser	Gly	Leu	Leu	Gln		
	265					270					275						
gcc	tgc	gtc	atc	acc	ctc	tac	acc	atg	ttt	gtc	acc	tgg	tca	gcc	cta	975	
Ala	Ser	Val	Ile	Thr	Leu	Tyr	Thr	Met	Phe	Val	Thr	Trp	Ser	Ala	Leu		
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Ser	Ser	Ile	Pro	Glu	Gln	Lys	Cys	Asn	Pro	His	Leu	Pro	Thr	Gln	Leu		
			300						305					310			
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Gly	Asn	Glu	Thr	Val	Val	Ala	Gly	Pro	Glu	Gly	Tyr	Glu	Thr	Gln	Trp		
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Trp	Asp	Ala	Pro	Ser	Ile	Val	Gly	Leu	Ile	Ile	Phe	Leu	Leu	Cys	Thr		
		330					335					340					
ctc	ttc	atc	agt	ctg	cgc	tcc	tca	gac	cac	cgg	cag	gtg	aac	agc	ctg	1167	

Leu	Phe	Ile	Ser	Leu	Arg	Ser	Ser	Asp	His	Arg	Gln	Val	Asn	Ser	Leu		
345						350					355						
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Met	Gln	Thr	Glu	Glu	Cys	Pro	Pro	Met	Leu	Asp	Ala	Thr	Gln	Gln	Gln		
360					365					370					375		
cag	cag	cag	gtg	gca	gcc	tgt	gag	ggc	cgg	gcc	ttt	gac	aac	gag	cag		1263
Gln	Gln	Gln	Val	Ala	Ala	Cys	Glu	Gly	Arg	Ala	Phe	Asp	Asn	Glu	Gln		
				380					385					390			
gac	ggc	gtc	acc	tac	agc	tac	tcc	ttc	ttc	cac	ttc	tgc	ctg	gtg	ctg		1311
Asp	Gly	Val	Thr	Tyr	Ser	Tyr	Ser	Phe	Phe	His	Phe	Cys	Leu	Val	Leu		
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gcc	tca	ctg	cac	gtc	atg	atg	acg	ctc	acc	aac	tgg	tac	aag	ccc	ggc		1359
Ala	Ser	Leu	His	Val	Met	Met	Thr	Leu	Thr	Asn	Trp	Tyr	Lys	Pro	Gly		
		410					415						420				
gag	acc	cgg	aag	atg	atc	agc	acg	tgg	acc	gcc	gtg	tgg	gtg	aag	atc		1407
Glu	Thr	Arg	Lys	Met	Ile	Ser	Thr	Trp	Thr	Ala	Val	Trp	Val	Lys	Ile		
	425					430					435						
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Cys	Ala	Ser	Trp	Ala	Gly	Leu	Leu	Leu	Tyr	Leu	Trp	Thr	Leu	Val	Ala		
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cca	ctc	ctc	ctg	cgc	aac	cgc	gac	ttc	agc	tga	ggcagcct	cacagcctgc					1506
Pro	Leu	Leu	Leu	Arg	Asn	Arg	Asp	Phe	Ser	*							
			460					465									
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&lt;211&gt; 2389

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (136)..(1347)

&lt;400&gt; 293

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Gln Val Leu Thr Phe Leu Leu Leu Phe Val Ile Thr Ser Val Ala Ser	
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Glu Asn Ala Ser Thr Ser Arg Gly Cys Gly Leu Asp Leu Leu Pro Gln	
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Tyr Val Ser Leu Cys Asp Leu Asp Ala Ile Trp Gly Ile Val Val Glu	
45 50 55 60	
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Ala Val Ala Gly Ala Gly Ala Leu Ile Thr Leu Leu Leu Met Leu Ile	
65 70 75	
ctc ctg gtg cgg ctg ccc ttc atc aag gag aag gag aag aag agc cct	411
Leu Leu Val Arg Leu Pro Phe Ile Lys Glu Lys Glu Lys Lys Ser Pro	
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Val Gly Leu His Phe Leu Phe Leu Leu Gly Thr Leu Gly Leu Phe Gly	
95 100 105	
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Leu Thr Phe Ala Phe Ile Ile Gln Glu Asp Glu Thr Ile Cys Ser Val	
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cgc cgc ttc ctc tgg ggc gtc ctc ttt gcg ctc tgc ttc tcc tgc ctg	555
Arg Arg Phe Leu Trp Gly Val Leu Phe Ala Leu Cys Phe Ser Cys Leu	
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Pro Ala Gly Trp Gln Leu Val Gly Leu Ala Leu Cys Leu Met Leu Val	
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Gln Val Ile Ile Ala Val Glu Trp Leu Val Leu Thr Val Leu Arg Asp	
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Thr Arg Pro Ala Cys Ala Tyr Glu Pro Met Asp Phe Val Met Ala Leu	
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Ile Tyr Asp Met Val Leu Leu Val Val Thr Leu Gly Leu Ala Leu Phe	
205 210 215 220	
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Thr Leu Cys Gly Lys Phe Lys Arg Trp Lys Leu Asn Gly Ala Phe Leu	
225 230 235	
ctc atc aca gcc ttc ctc tct gtg ctc atc tgg gtg gcc tgg atg acc	891
Leu Ile Thr Ala Phe Leu Ser Val Leu Ile Trp Val Ala Trp Met Thr	
240 245 250	

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Met Tyr Leu Phe Gly Asn Val Lys Leu Gln Gln Gly Asp Ala Trp Asn	
255 260 265	
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Asp Pro Thr Leu Ala Ile Thr Leu Ala Ala Ser Gly Trp Val Phe Val	
270 275 280	
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Ile Phe His Ala Ile Pro Glu Ile His Cys Thr Leu Leu Pro Ala Leu	
285 290 295 300	
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Gln Glu Asn Thr Pro Asn Tyr Phe Asp Thr Ser Gln Pro Arg Met Arg	
305 310 315	
gag acg gcc ttc gag gag gac gtg cag ctg ccg cgg gcc tat atg gag	1131
Glu Thr Ala Phe Glu Glu Asp Val Gln Leu Pro Arg Ala Tyr Met Glu	
320 325 330	
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Asn Lys Ala Phe Ser Met Asp Glu His Asn Ala Ala Leu Arg Thr Ala	
335 340 345	
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Gly Phe Pro Asn Gly Ser Leu Gly Lys Arg Pro Ser Gly Ser Leu Gly	
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Lys Arg Pro Ser Ala Pro Phe Arg Ser Asn Val Tyr Gln Pro Thr Glu	
365 370 375 380	
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Met Ala Val Val Leu Asn Gly Gly Thr Ile Pro Thr Ala Pro Pro Ser	
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His Thr Gly Arg His Leu Trp *	
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tggggctctt gctctagtgt ctatggtgag aacacaggcc ccgccccctc cctttagtag	2097



Gln Lys Lys Arg Asn  
140

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ctgccctttt attcactttt agcctctttt ttttaattttt aaaatttaaa gatatgcata 732  
ctgaaaagta tataacatgt acgtacaatt taaagaataa ttttaaagtg aatactacgt 792  
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ccccgcaccg acggggagaa cgtatttacc gggcagtcaa agatctattc ctacatgagc 300  
ccgaacaaat gctctggaat gcgtttcccc cttcaggaag agaactcagt tacacatcac 360  
gaagtcaaat gccaggggaa accattagcc ggaatctaca ggaaacgaga agagaaaaga 420  
aatgctggga acgcagtacg gagcgcc atg aag tcc gag gaa cag aag atc 471  
Met Lys Ser Glu Glu Gln Lys Ile  
1 5  
aaa gac gcc agg aaa ggt ccc ctg gta cct ttt cca aac caa aaa tct 519  
Lys Asp Ala Arg Lys Gly Pro Leu Val Pro Phe Pro Asn Gln Lys Ser  
10 15 20  
gaa gca gca gaa cct cca aaa act cca ccc tca tct tgt gat tcc acc 567  
Glu Ala Ala Glu Pro Pro Lys Thr Pro Pro Ser Ser Cys Asp Ser Thr  
25 30 35 40



aat gca gcc atc gcc aag caa gcc ctg aaa aag ccc atc aag ggc aaa Asn Ala Ala Ile Ala Lys Gln Ala Leu Lys Lys Pro Ile Lys Gly Lys	615
45 50 55	
cag gcc ccc cga aaa aaa gct caa gga aaa acg caa cag aat cgc aaa Gln Ala Pro Arg Lys Lys Ala Gln Gly Lys Thr Gln Gln Asn Arg Lys	663
60 65 70	
ctt acg gat ttc tac cct gtc cga agg agc tcc agg aag agc aaa gcc Leu Thr Asp Phe Tyr Pro Val Arg Arg Ser Ser Arg Lys Ser Lys Ala	711
75 80 85	
gag ctg cag tct gaa gaa agg aaa aga ata gat gaa ttg att gaa agt Glu Leu Gln Ser Glu Glu Arg Lys Arg Ile Asp Glu Leu Ile Glu Ser	759
90 95 100	
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105 110 115 120	
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125 130 135	
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170 175 180	
cta gga aga ctg atc aat cac agc aaa tgt ggg aac tgc caa acc aaa Leu Gly Arg Leu Ile Asn His Ser Lys Cys Gly Asn Cys Gln Thr Lys	1047
185 190 195 200	
ctg cac gac atc gac ggc gta cct cac ctc atc ctc atc gcc tcc cga Leu His Asp Ile Asp Gly Val Pro His Leu Ile Leu Ile Ala Ser Arg	1095
205 210 215	
gac atc gcg gct ggg gag gag ctc ctg tat gac tat ggg gac cgc agc Asp Ile Ala Ala Gly Glu Glu Leu Leu Tyr Asp Tyr Gly Asp Arg Ser	1143
220 225 230	
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235 240	
cgtagccctcc ccgcccact ttcccttctt caaaggacaa agtgcctca aagggaattg	1253
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<223> n = a,t,c or g

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Met Thr Cys
1

tgg ctg cgg ggc gtc acg gcg acg ttc ggg cga cct gcc gag tgg cca 162
Trp Leu Arg Gly Val Thr Ala Thr Phe Gly Arg Pro Ala Glu Trp Pro
5 10 15

ggc tac ctc agt cac ctg tgt ggt cgc agt gct gcc atg gac ctg gga 210
Gly Tyr Leu Ser His Leu Cys Gly Arg Ser Ala Ala Met Asp Leu Gly
20 25 30 35

ccc atg cgc aag agt tac cgc ggg gac cga gag gca ttt gag gag act 258
Pro Met Arg Lys Ser Tyr Arg Gly Asp Arg Glu Ala Phe Glu Glu Thr
40 45 50

cat ctg acc tcc ctt gac cca gtg aaa cag ttt gct gcc tgg ttt gag 306
His Leu Thr Ser Leu Asp Pro Val Lys Gln Phe Ala Ala Trp Phe Glu
55 60 65

gag gct gtt cag tgt cct gac ata ggg gaa gcc aat gcc atg tgt ctg 354
Glu Ala Val Gln Cys Pro Asp Ile Gly Glu Ala Asn Ala Met Cys Leu
70 75 80

gct acc tgc acc aga gat gga aaa ccc tct gct cgc atg ttg ctg ctg 402
Ala Thr Cys Thr Arg Asp Gly Lys Pro Ser Ala Arg Met Leu Leu Leu
85 90 95

aag ggc ttc ggg aaa gat ggc ttc cgc ttc ttc act aac ttc gag agt 450
Lys Gly Phe Gly Lys Asp Gly Phe Arg Phe Phe Thr Asn Phe Glu Ser

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Arg Lys Gly Lys Glu Leu Asp Ser Asn Pro Phe Ala Ser Leu Val Phe				
	120	125	130	
tac tgg gag cca ctt aac cgt cag gtg cgt gtg gaa ggc cct gtg aag				546
Tyr Trp Glu Pro Leu Asn Arg Gln Val Arg Val Glu Gly Pro Val Lys				
	135	140	145	
aaa ctg cct gag gag gag gct gaa gtt gct act ttc cac ttc ccc ggc				594
Lys Leu Pro Glu Glu Glu Ala Glu Val Ala Thr Phe His Phe Pro Gly				
	150	155	160	
ccc aag agc agc cag att ggg gct gtg gtc agc cac cag agt tct gtg				642
Pro Lys Ser Ser Gln Ile Gly Ala Val Val Ser His Gln Ser Ser Val				
	165	170	175	
atc cct gat cgg gag tat ctg aga aag aaa aat gag gaa ctg gaa cag				690
Ile Pro Asp Arg Glu Tyr Leu Arg Lys Lys Asn Glu Glu Leu Glu Gln				
	180	185	190	195
ctc tac cag gat caa gag gtg ccc aag cca aaa tcc tgg ggt ggc tat				738
Leu Tyr Gln Asp Gln Glu Val Pro Lys Pro Lys Ser Trp Gly Gly Tyr				
	200	205	210	
gtc ctg tac cct cag gtg atg gag ttc tgg caa ggt caa acc aac cgc				786
Val Leu Tyr Pro Gln Val Met Glu Phe Trp Gln Gly Gln Thr Asn Arg				
	215	220	225	
ctg cat gac cgg ata gtc ttt cgg cgg ggc cta ccc aca gga gat tcc				834
Leu His Asp Arg Ile Val Phe Arg Arg Gly Leu Pro Thr Gly Asp Ser				
	230	235	240	
cct ttg ggg ccc atg acc cac cgc ggg gag gaa gac tgg ctc tat gag				882
Pro Leu Gly Pro Met Thr His Arg Gly Glu Glu Asp Trp Leu Tyr Glu				
	245	250	255	
aga ctt gca cct taa ctctgggacc tgctggccca gaggtagct agggctaggt				937
Arg Leu Ala Pro				
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      Met Glu Val Lys Pro Pro Pro Gly Arg Pro Gln
              1              5              10

ccc gac tcc ggc cgt cgc cgt cgc cgc cgg ggg gag gag ggc cat gat      158
Pro Asp Ser Gly Arg Arg Arg Arg Arg Arg Gly Glu Glu Gly His Asp
              15              20              25

cca aag gaa cca gag cag ttg aga aaa ctg ttt att ggt ggt ctg agc      206
Pro Lys Glu Pro Glu Gln Leu Arg Lys Leu Phe Ile Gly Gly Leu Ser
              30              35              40

ttt gaa act aca gat gat agt tta cga gaa cat ttt gag aaa tgg ggc      254
Phe Glu Thr Thr Asp Asp Ser Leu Arg Glu His Phe Glu Lys Trp Gly
              45              50              55

aca ctc aca gat tgt gtg gta atg aga gac ccc caa aca aaa cgt tcc      302
Thr Leu Thr Asp Cys Val Val Met Arg Asp Pro Gln Thr Lys Arg Ser
              60              65              70              75

agg ggc ttt ggt ttt gtg act tat tct tgt gtt gaa gag gtg gat gca      350
Arg Gly Phe Gly Phe Val Thr Tyr Ser Cys Val Glu Glu Val Asp Ala
              80              85              90

gca atg tgt gct cga cca cac aag gtt gat ggg cgt gta gtg gaa cca      398
Ala Met Cys Ala Arg Pro His Lys Val Asp Gly Arg Val Val Glu Pro
              95              100              105

aag aga gct gtt tct aga gag gat tct gta aag cct ggt gcc cat cta      446
Lys Arg Ala Val Ser Arg Glu Asp Ser Val Lys Pro Gly Ala His Leu
              110              115              120

aca gtg aag aaa att ttt gtt ggt ggt att aaa gaa gat aca gaa gaa      494
Thr Val Lys Lys Ile Phe Val Gly Gly Ile Lys Glu Asp Thr Glu Glu
              125              130              135

tat aat ttg aga gac tac ttt gaa aag tat ggc aag att gaa acc ata      542
Tyr Asn Leu Arg Asp Tyr Phe Glu Lys Tyr Gly Lys Ile Glu Thr Ile
              140              145              150              155

gaa gtt atg gaa gac agg cag agt gga aaa aag aga gga ttt gct ttt      590
Glu Val Met Glu Asp Arg Gln Ser Gly Lys Lys Arg Gly Phe Ala Phe
              160              165              170

gta act ttt gat gat cat gat aca gtt gat aaa att gtt gtt cag aaa      638
Val Thr Phe Asp Asp His Asp Thr Val Asp Lys Ile Val Val Gln Lys
              175              180              185

tac cac act att aat ggg cat aac tgt gaa gtg aaa aag gcc ctt gct      686
Tyr His Thr Ile Asn Gly His Asn Cys Glu Val Lys Lys Ala Leu Ala
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aaa caa gtg atg cag ccg gct gga tca cag agg ggt cgt gga ggt gga      734

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Ser	Gly	Asn	Cys	Met	Gly	His	Arg	Gly	Asn	Phe	Gly	Gly	Gly	Gly	Gly	
220					225				230					235		
aat	ttt	ggc	cgt	gat	gga	aac	ttt	ggg	gga	aga	gga	ggc	tat	ggg	ggg	830
Asn	Phe	Gly	Arg	Asp	Gly	Asn	Phe	Gly	Gly	Arg	Gly	Gly	Tyr	Gly	Gly	
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gga	ggt	ggg	ggc	agc	aga	ggg	agt	tat	gga	gga	ggt	gat	ggg	gga	tat	878
Gly	Gly	Gly	Gly	Ser	Arg	Gly	Ser	Tyr	Gly	Gly	Gly	Asp	Gly	Gly	Tyr	
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Asn	Gly	Phe	Gly	Gly	Asp	Gly	Gly	Asn	Tyr	Gly	Gly	Gly	Pro	Gly	Tyr	
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agt	agt	aga	ggg	ggc	tat	ggg	ggg	ggg	gga	cca	gga	tat	gga	aac	caa	974
Ser	Ser	Arg	Gly	Gly	Tyr	Gly	Gly	Gly	Gly	Pro	Gly	Tyr	Gly	Asn	Gln	
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Gly	Gly	Gly	Tyr	Gly	Gly	Gly	Gly	Gly	Tyr	Asp	Gly	Tyr	Asn	Glu	Gly	
300				305				310						315		
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Gly	Asn	Phe	Gly	Gly	Gly	Asn	Tyr	Gly	Gly	Gly	Gly	Asn	Tyr	Asn	Asp	
			320			325						330				
ttt	gga	aat	tat	agt	gga	caa	cag	caa	tca	aat	tat	gga	ccc	atg	aaa	1118
Phe	Gly	Asn	Tyr	Ser	Gly	Gln	Gln	Gln	Ser	Asn	Tyr	Gly	Pro	Met	Lys	
		335				340						345				
ggg	ggc	agt	ttt	ggg	gga	aga	agc	tgc	ggc	agt	ccc	tat	ggg	ggg	ggg	1166
Gly	Gly	Ser	Phe	Gly	Gly	Arg	Ser	Ser	Gly	Ser	Pro	Tyr	Gly	Gly	Gly	
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tat	gga	tct	ggg	ggg	gga	agt	ggg	gga	tat	ggg	agc	aga	agg	ttc	taa	1214
Tyr	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Tyr	Gly	Ser	Arg	Arg	Phe	*	
	365				370					375						
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aaattaagga	atttttaact	tttcaatatt	tgtgtagttc	agtttttcta	catttttagta											1634
cagaaacttt	aacaaaatgc	agtttcgaag	gtgtttcctt	gtgagttaac	aagtaaagaa											1694
gatcattgtt	aattactatt	ttgtatgaat	tttgctaaag	ttaactgtaa	agaaacacct											1754
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777



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gct caa aaa att ggg ttc tgc cct cca cgt ttg gtc act gcc aat ctc Ala Gln Lys Ile Gly Phe Cys Pro Pro Arg Leu Val Thr Ala Asn Leu 220 225 230 235			782
att aca att caa aac aag gaa ctg gaa aga gtt atc ggt gac tgt cgt Ile Thr Ile Gln Asn Lys Glu Leu Glu Arg Val Ile Gly Asp Cys Arg 240 245 250			830
ttt gtt tct gca aca ttt cgc ctc ttc aaa cac tct aag aca gga cca Phe Val Ser Ala Thr Phe Arg Leu Phe Lys His Ser Lys Thr Gly Pro 255 260 265			878
acc aag aga tgc caa gtt att tac aat gga gga att aca gga cat gaa Thr Lys Arg Cys Gln Val Ile Tyr Asn Gly Gly Ile Thr Gly His Glu 270 275 280			926
aaa gaa cta atg ttt gat gcc aat ttt aca ttt aag gaa ggt gaa att Lys Glu Leu Met Phe Asp Ala Asn Phe Thr Phe Lys Glu Gly Glu Ile 285 290 295			974
ggt gaa gtg gat gaa gaa aca gca gct atc ttg aag aat tca aga ttt Val Glu Val Asp Glu Glu Thr Ala Ala Ile Leu Lys Asn Ser Arg Phe 300 305 310 315			1022
gct caa gat ttt ctg atc aga cca att gga gag aag ttg cca aca tct Ala Gln Asp Phe Leu Ile Arg Pro Ile Gly Glu Lys Leu Pro Thr Ser 320 325 330			1070
gga ggc tgt tct gct ttg gag tta aag gat ata atc aca cat cca ttt Gly Gly Cys Ser Ala Leu Glu Leu Lys Asp Ile Ile Thr His Pro Phe 335 340 345			1118
aag ctt gca gaa aag ttt gac cct atg aat tcc aca cga gcc cct gat Lys Leu Ala Glu Lys Phe Asp Pro Met Asn Ser Thr Arg Ala Pro Asp 350 355 360			1166
gct tct taa ggctgct gtgtatcaaa aaatagctgc tgaagccatt gcctaccacg Ala Ser *			1222
			365
tgaccactca agtgtgcggg aaagcacctc ctgagtatga acccagtttc ccccttaccg			1282
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                      Met Ala Ala Leu Arg Asp Ala Glu Ile Gln Lys
                      1           5           10

gac gtg cag acc tac tac ggg cag gtg ctg aag aga tcg gca gac ctc      158
Asp Val Gln Thr Tyr Tyr Gly Gln Val Leu Lys Arg Ser Ala Asp Leu
                      15           20           25

cag acc aac ggc tgt gtc acc aca gcc agg ccg gtc ccc aag cac atc      206
Gln Thr Asn Gly Cys Val Thr Thr Ala Arg Pro Val Pro Lys His Ile
                      30           35           40

cgg gaa gcc ttg caa aat gta cac gaa gaa gta gcc cta aga tat tat      254
Arg Glu Ala Leu Gln Asn Val His Glu Glu Val Ala Leu Arg Tyr Tyr
                      45           50           55

ggc tgt ggt ctg gtg atc cct gag cat cta gaa aac tgc tgg att ttg      302
Gly Cys Gly Leu Val Ile Pro Glu His Leu Glu Asn Cys Trp Ile Leu
                      60           65           70           75

gat ctg ggt agt gga agt ggc aga gat tgc tat gta ctt agc cag ctg      350
Asp Leu Gly Ser Gly Ser Gly Arg Asp Cys Tyr Val Leu Ser Gln Leu
                      80           85           90

gtt ggt gaa aaa gga cac gtg act gga ata gac atg acc aaa ggc cag      398
Val Gly Glu Lys Gly His Val Thr Gly Ile Asp Met Thr Lys Gly Gln
                      95           100           105

gtg gaa gtg gct gaa aag tat ctt gac tat cac atg gaa aaa tat ggc      446
Val Glu Val Ala Glu Lys Tyr Leu Asp Tyr His Met Glu Lys Tyr Gly
                      110           115           120

ttc cag gca tct aat gtg act ttt att cat ggc tac att gag aag ttg      494
Phe Gln Ala Ser Asn Val Thr Phe Ile His Gly Tyr Ile Glu Lys Leu
                      125           130           135

gga gag gct gga atc aag aat gag agc cat gat att gtt gta tca aac      542
Gly Glu Ala Gly Ile Lys Asn Glu Ser His Asp Ile Val Val Ser Asn
                      140           145           150           155

tgt gtt att aac ctt gtg cct gat aaa caa caa gtg ctt cag gag gca      590
Cys Val Ile Asn Leu Val Pro Asp Lys Gln Gln Val Leu Gln Glu Ala
                      160           165           170

tat cgg gtg ctg aag gtt gca aaa ggt agt aaa tcc gag gtg aca gtt      638
Tyr Arg Val Leu Lys Val Ala Lys Gly Ser Lys Ser Glu Val Thr Val
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gtc act gaa tgt gtt aag cat ggt ggg gag tta tat ttc agt gac gtc      686
Val Thr Glu Cys Val Lys His Gly Gly Glu Leu Tyr Phe Ser Asp Val
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tat acg agc ctt gaa ctg cca gaa gaa atc agg aca cac aaa gtt tta      734
Tyr Thr Ser Leu Glu Leu Pro Glu Glu Ile Arg Thr His Lys Val Leu
                      205           210           215

tgg ggt gag tgt ctg ggt ggt gct tta tac tgg aag gaa ctt gct gtc      782
Trp Gly Glu Cys Leu Gly Gly Ala Leu Tyr Trp Lys Glu Leu Ala Val
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ctt gct caa aaa att ggg ttc tgc cct cca cgt ttg gtc act gcc aat      830

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Leu Ala Gln Lys Ile Gly Phe Cys Pro Pro Arg Leu Val Thr Ala Asn  
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 Leu Ile Thr Ile Gln Asn Lys Glu Leu Glu Arg Val Ile Gly Asp Cys  
 255 260 265  
 cgt ttt gtt tct gca aca ttt cgc ctg ttc aaa cac tct aag aca gga 926  
 Arg Phe Val Ser Ala Thr Phe Arg Leu Phe Lys His Ser Lys Thr Gly  
 270 275 280  
 cca acc aag aga tgc caa gtt att tac aat gga gga att aca gga cat 974  
 Pro Thr Lys Arg Cys Gln Val Ile Tyr Asn Gly Gly Ile Thr Gly His  
 285 290 295  
 gaa aaa gaa cta atg ttt gat gcc aat ttt aca ttt aag gaa ggt gaa 1022  
 Glu Lys Glu Leu Met Phe Asp Ala Asn Phe Thr Phe Lys Glu Gly Glu  
 300 305 310 315  
 att gtt gaa gtg gat gaa gaa aca gca gct atc ttg aag aat tca aga 1070  
 Ile Val Glu Val Asp Glu Glu Thr Ala Ala Ile Leu Lys Asn Ser Arg  
 320 325 330  
 ttt gct caa gat ttt ctg atc aga cca att gga gag aag ttg cca aca 1118  
 Phe Ala Gln Asp Phe Leu Ile Arg Pro Ile Gly Glu Lys Leu Pro Thr  
 335 340 345  
 tct gga ggc tgt tct gct ttg gag tta aag gat ata atc aca cat cca 1166  
 Ser Gly Gly Cys Ser Ala Leu Glu Leu Lys Asp Ile Ile Thr His Pro  
 350 355 360  
 ttt aag ctt gca gaa aag ttt gac cct atg aat tcc aca cga gcc cct 1214  
 Phe Lys Leu Ala Glu Lys Phe Asp Pro Met Asn Ser Thr Arg Ala Pro  
 365 370 375  
 gat gct tct taa ggc tgctgtgtat caaaaaatag ctgctgaagc cattgcctac 1269  
 Asp Ala Ser \*  
 380  
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 1 5 10 15  
 cgc gtc cgc ctg ggt tcg aac acg gca ccc gca ctg cgc gtc atg gtg 96  
 Arg Val Arg Leu Gly Ser Asn Thr Ala Pro Ala Leu Arg Val Met Val

20	25	30	
cag gcc tgg tat atg gac gac gcc ccg ggc gac ccg cgg caa ccc cac Gln Ala Trp Tyr Met Asp Asp Ala Pro Gly Asp Pro Arg Gln Pro His 35 40 45			144
cgc ccc gac ccc ggc cgc cca gtg ggc ctg gag cag ctg cgg cgg ctc Arg Pro Asp Pro Gly Arg Pro Val Gly Leu Glu Gln Leu Arg Arg Leu 50 55 60			192
ggg gtg ctc tac tgg aag ctg gat gct gac aaa tat gag aat gat cca Gly Val Leu Tyr Trp Lys Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro 65 70 75 80			240
gaa tta gaa aag atc cga aga gag agg aac tac tcc tgg atg gac atc Glu Leu Glu Lys Ile Arg Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile 85 90 95			288
ata acc ata tgc aaa gat aaa cta cca aat tat gaa gaa aag att aag Ile Thr Ile Cys Lys Asp Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys 100 105 110			336
atg ttc tac gag gag cat ttg cac ttg gac gat gag atc cgc tac atc Met Phe Tyr Glu Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile 115 120 125			384
ctg gat ggc agt ggg tac ttc gat gtg agg gac aag gag gac cag tgg Leu Asp Gly Ser Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp Gln Trp 130 135 140			432
atc cgg atc ttc atg gag aag gga gac atg gtg acg ctc ccc gcg ggg Ile Arg Ile Phe Met Glu Lys Gly Asp Met Val Thr Leu Pro Ala Gly 145 150 155 160			480
atc tat cac cgc ttc acg gtg gac gag aag aac tac acg aag gcc atg Ile Tyr His Arg Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys Ala Met 165 170 175			528
cgg ctg ttt gtg gga gaa ccg gtg tgg aca gcg tac aac cgg ccc gct Arg Leu Phe Val Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala 180 185 190			576
gac cat ttt gaa gcc cgc ggg cag tac gtg aaa ttt ctg gca cag acc Asp His Phe Glu Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr 195 200 205			624
gcc tagc agtgctgcct gggaactaac acgcgcctcg taaagggtccc caatgtaatg Ala			681
actgagcaga aaatcaatca ctttctcttt gcttttagag gatagccttg aggctagggt			741
atcttttcctt tgtaagatta tttgatcaga atatttttgta atgaaaggat ctagaaagca			801
acttggaagt gtaaagagtc accttcattt tctgtaactc aatcaagact ggtgggtcca			861
tggccctgtg ttagttcatg cattcagttg agtcccaaata gaaagtttca tctcccgaaa			921
tgcagttcct tagatgccca tctggacgtg atgccgcgcc tgccatgtaa gaagggtgcaa			981
tcttagataa cacagctagc cagatagaag acactttttt ctccaaaatg atgccttggtg			1041
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 ggaaaaggcg ctccgtc atg ggg atc cag acg agc ccc gtc ctg ctg gcc 170  
 Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala  
 1 5 10  
 tcc ctg ggg gtg ggg ctg gtc act ctg ctc ggc ctg gct gtg ggc tcc 218  
 Ser Leu Gly Val Gly Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser  
 15 20 25  
 tac ttg gtt cgg agg tcc cgc cgg cct cag gtc act ctc ctg gac ccc 266  
 Tyr Leu Val Arg Arg Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro  
 30 35 40  
 aat gaa aag tac ctg cta cga ctg cta gac aag acg act gtg agc cac 314  
 Asn Glu Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His  
 45 50 55  
 aac acc aag agg ttc cgc ttt gcc ctg ccc acc gcc cac cac act ctg 362  
 Asn Thr Lys Arg Phe Arg Phe Ala Leu Pro Thr Ala His His Thr Leu  
 60 65 70 75  
 ggg ctg cct gtg ggc aaa cat atc tac ctc tcc acc cga att gat ggc 410  
 Gly Leu Pro Val Gly Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly  
 80 85 90  
 agc ctg gtc atc agg cca tac act cct gtc acc agt gat gag gat caa 458

Ser	Leu	Val	Ile	Arg	Pro	Tyr	Thr	Pro	Val	Thr	Ser	Asp	Glu	Asp	Gln	
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Gly	Tyr	Val	Asp	Leu	Val	Ile	Lys	Val	Tyr	Leu	Lys	Gly	Val	His	Pro	
		110					115					120				
aaa	ttt	cct	gag	gga	ggg	aag	atg	tct	cag	tac	ctg	gat	agc	ctg	aag	554
Lys	Phe	Pro	Glu	Gly	Gly	Lys	Met	Ser	Gln	Tyr	Leu	Asp	Ser	Leu	Lys	
		125				130					135					
gtt	ggg	gat	gtg	gtg	gag	ttt	cgg	ggg	cca	agc	ggg	ttg	ctc	act	tac	602
Val	Gly	Asp	Val	Val	Glu	Phe	Arg	Gly	Pro	Ser	Gly	Leu	Leu	Thr	Tyr	
140					145				150						155	
act	gga	aaa	ggg	cat	ttt	aac	att	cag	ccc	aac	aag	aaa	tct	cca	cca	650
Thr	Gly	Lys	Gly	His	Phe	Asn	Ile	Gln	Pro	Asn	Lys	Lys	Ser	Pro	Pro	
				160				165						170		
gaa	ccc	cga	gtg	gcg	aag	aaa	ctg	gga	atg	att	gcc	ggc	ggg	aca	gga	698
Glu	Pro	Arg	Val	Ala	Lys	Lys	Leu	Gly	Met	Ile	Ala	Gly	Gly	Thr	Gly	
			175				180					185				
atc	acc	cca	atg	cta	cag	ctg	atc	cgg	gcc	atc	ctg	aaa	gtc	cct	gaa	746
Ile	Thr	Pro	Met	Leu	Gln	Leu	Ile	Arg	Ala	Ile	Leu	Lys	Val	Pro	Glu	
		190				195					200					
gat	cca	acc	cag	tgc	ttt	ctg	ctt	ttt	gcc	aac	cag	aca	gaa	aag	gat	794
Asp	Pro	Thr	Gln	Cys	Phe	Leu	Leu	Phe	Ala	Asn	Gln	Thr	Glu	Lys	Asp	
		205				210					215					
atc	atc	ttg	cgg	gag	gac	tta	gag	gaa	ctg	cag	gcc	cgc	tat	ccc	aat	842
Ile	Ile	Leu	Arg	Glu	Asp	Leu	Glu	Glu	Leu	Gln	Ala	Arg	Tyr	Pro	Asn	
220				225					230					235		
cgc	ttt	aag	ctc	tgg	ttc	act	ctg	gat	cat	ccc	cca	aaa	gat	tgg	gcc	890
Arg	Phe	Lys	Leu	Trp	Phe	Thr	Leu	Asp	His	Pro	Pro	Lys	Asp	Trp	Ala	
			240				245						250			
tac	agc	aag	ggc	ttt	gtg	act	gcc	gac	atg	atc	cgg	gaa	cac	ctg	ccc	938
Tyr	Ser	Lys	Gly	Phe	Val	Thr	Ala	Asp	Met	Ile	Arg	Glu	His	Leu	Pro	
		255					260					265				
gct	cca	ggg	gat	gat	gtg	ctg	gta	ctg	ctt	tgt	ggg	cca	ccc	cca	atg	986
Ala	Pro	Gly	Asp	Asp	Val	Leu	Val	Leu	Leu	Cys	Gly	Pro	Pro	Pro	Met	
		270				275					280					
gtg	cag	ctg	gcc	tgc	cat	ccc	aac	ttg	gac	aaa	ctg	ggc	tac	tca	caa	1034
Val	Gln	Leu	Ala	Cys	His	Pro	Asn	Leu	Asp	Lys	Leu	Gly	Tyr	Ser	Gln	
		285				290					295					
aag	atg	cga	ttc	acc	tac	tga	gc	atcctccagc	ttccctgggtg	ctgttcgctg						1087
Lys	Met	Arg	Phe	Thr	Tyr	*										
300					305											
cagttgttcc	ccatcagttac	tcaagcacta	taagccttag	attcctttcc	tcagagtttc											1147
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gtggcaacag	gtccaggaga	ggcccatgga	gcagtctctt	ccatggagta	agaaggaagg											1327
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atatcatatt tctgtgtgtg tctctctcag cccctgcccc ggctagaggg aaacagctac 1627
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<223> n = a,t,c or g

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tccgac atg tct atg ctg gct gaa cgt cgg cgg aag cag aag tgg gct 168
      Met Ser Met Leu Ala Glu Arg Arg Arg Lys Gln Lys Trp Ala
        1             5             10

gtg gat cct cag aac act gcc tgg agt aat gac gat tcc aag ttt ggc 216
Val Asp Pro Gln Asn Thr Ala Trp Ser Asn Asp Asp Ser Lys Phe Gly
  15             20             25             30

cag cgg atg cta gag aag atg ggg tgg tct aaa gga aag ggt tta ggg 264
Gln Arg Met Leu Glu Lys Met Gly Trp Ser Lys Gly Lys Gly Leu Gly
        35             40             45

gct cag gag caa gga gcc aca gat cat att aaa gtt caa gtg aaa aat 312
Ala Gln Glu Gln Gly Ala Thr Asp His Ile Lys Val Gln Val Lys Asn
        50             55             60

aac cac ctg gga ctc gga gct acc atc aat aat gaa gac aac tgg att 360
Asn His Leu Gly Leu Gly Ala Thr Ile Asn Asn Glu Asp Asn Trp Ile
        65             70             75

gcc cat cag gat gat ttt aac cag ctt ctg gcc gaa ctg aac act tgc 408
Ala His Gln Asp Asp Phe Asn Gln Leu Leu Ala Glu Leu Asn Thr Cys
        80             85             90

cat ggg cag gaa acc aca gat tcc tcg gac aag aag gaa aag aaa tct 456
His Gly Gln Glu Thr Thr Asp Ser Ser Asp Lys Lys Glu Lys Lys Ser
        95             100             105             110

ttt agc ctt gag gaa aag tcc aaa atc tcc aaa aac cgt gtt cac tat 504

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Phe	Ser	Leu	Glu	Glu	Lys	Ser	Lys	Ile	Ser	Lys	Asn	Arg	Val	His	Tyr	
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Met	Lys	Phe	Thr	Lys	Gly	Lys	Asp	Leu	Ser	Ser	Arg	Ser	Lys	Thr	Asp	
			130					135						140		
ctt	gac	tgc	att	ttt	ggg	aaa	aga	cag	agt	aag	aag	act	ccc	gag	ggc	600
Leu	Asp	Cys	Ile	Phe	Gly	Lys	Arg	Gln	Ser	Lys	Lys	Thr	Pro	Glu	Gly	
			145					150						155		
gat	gcc	agt	ccc	tcc	act	cca	gag	gag	aac	gaa	acc	acg	aca	acc	agc	648
Asp	Ala	Ser	Pro	Ser	Thr	Pro	Glu	Glu	Asn	Glu	Thr	Thr	Thr	Thr	Ser	
			160					165						170		
gcc	ttc	acc	atc	cag	gag	tac	ttt	gcc	aag	cgg	atg	gca	gca	ctg	aag	696
Ala	Phe	Thr	Ile	Gln	Glu	Tyr	Phe	Ala	Lys	Arg	Met	Ala	Ala	Leu	Lys	
					180					185					190	
aac	aag	ccc	cag	gtt	cca	gtt	cca	ggg	tct	gac	att	tct	gag	acg	cag	744
Asn	Lys	Pro	Gln	Val	Pro	Val	Pro	Gly	Ser	Asp	Ile	Ser	Glu	Thr	Gln	
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gtg	gaa	cgt	aaa	agg	ggg	aag	aaa	aga	aat	aaa	gag	gcc	aca	ggt	aaa	792
Val	Glu	Arg	Lys	Arg	Gly	Lys	Lys	Arg	Asn	Lys	Glu	Ala	Thr	Gly	Lys	
			210					215						220		
gat	gtg	gaa	agt	tac	ctc	cag	cct	aag	gcc	aag	agg	cac	acg	gag	gga	840
Asp	Val	Glu	Ser	Tyr	Leu	Gln	Pro	Lys	Ala	Lys	Arg	His	Thr	Glu	Gly	
			225					230						235		
aag	ccc	gag	agg	gcc	gag	gcc	cag	gag	cga	gtg	gcc	aag	aag	aag	agc	888
Lys	Pro	Glu	Arg	Ala	Glu	Ala	Gln	Glu	Arg	Val	Ala	Lys	Lys	Lys	Ser	
			240					245						250		
gcg	cca	gca	gaa	gag	cag	ctc	aga	ggc	ccc	tgc	tgg	gac	cag	agt	tcc	936
Ala	Pro	Ala	Glu	Glu	Gln	Leu	Arg	Gly	Pro	Cys	Trp	Asp	Gln	Ser	Ser	
					260					265					270	
aag	gcc	tct	gct	cag	gat	gca	ggg	gac	cat	gtg	cag	ccg	cct	gag	ggc	984
Lys	Ala	Ser	Ala	Gln	Asp	Ala	Gly	Asp	His	Val	Gln	Pro	Pro	Glu	Gly	
				275					280						285	
cgg	gac	ttc	acc	ctg	aag	ccc	aaa	aag	agg	aga	ggg	aag	aaa	aag	ctg	1032
Arg	Asp	Phe	Thr	Leu	Lys	Pro	Lys	Lys	Arg	Arg	Gly	Lys	Lys	Lys	Leu	
			290					295						300		
caa	aaa	cca	gta	gag	ata	gca	gag	gac	gct	aca	cta	gaa	gaa	acg	cta	1080
Gln	Lys	Pro	Val	Glu	Ile	Ala	Glu	Asp	Ala	Thr	Leu	Glu	Glu	Thr	Leu	
			305					310						315		
gtg	aaa	aag	aag	aag	aag	aaa	gat	tcc	aaa	t	gaatccttcc	cagccggggc				1131
Val	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Asp	Ser	Lys						
			320					325								
cttccgacca	ctcagctgtc	aggggcactgc	gggggcagac	acctctggcc	tgaagtcaca											1191
gcagagttca	ccccagagcg	cctgggcgca	tcttgtggca	tgcccatggg	ctgccgagtc											1251
ctgccctctc	gccacatttc	ccccaaagtta	cattcccagg	aggacctttt	taatgttctc											1311
aatcgtggct	ctcagacaca	aataaatttt	tttgtaaact	ctgagccctt	cagcaagaga											1371
gtttaattat	aatcattaca	aatacatgca	ttcatgtaag	tgtgcacacg	tgtgtgtgca											1431

tgtgcgcatac tgtgtgtgtg tgtgtgtgtc actatctccg tttgctctcg gttcccttca 1491  
 ataacaatga atggtgcttt cttctgaaag actcagccta attaaaggat taagaggcaa 1551  
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 agtatcccag catacgtgag cgta 1635

<210> 303  
 <211> 566  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (110)..(361)

<400> 303  
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 ttcccgcgcg gacgccggcg ctgccaacgg aagggcgggc tctgctgcc atg aag 115  
 Met Lys  
 1  
 gtg aag att aag tgc tgg aac ggc gtg gcc act tgg ctc tgg gtg gcc 163  
 Val Lys Ile Lys Cys Trp Asn Gly Val Ala Thr Trp Leu Trp Val Ala  
 5 10 15  
 aac gat gag aac tgt ggc atc tgc agg atg gca ttt aac gga tgc tgc 211  
 Asn Asp Glu Asn Cys Gly Ile Cys Arg Met Ala Phe Asn Gly Cys Cys  
 20 25 30  
 cct gac tgc aag gtg ccc ggc gac gac tgc ccg ctg gtg tgg ggc cag 259  
 Pro Asp Cys Lys Val Pro Gly Asp Asp Cys Pro Leu Val Trp Gly Gln  
 35 40 45 50  
 tgc tcc cac tgc ttc cac atg cat tgc atc ctc aag tgg ctg cac gca 307  
 Cys Ser His Cys Phe His Met His Cys Ile Leu Lys Trp Leu His Ala  
 55 60 65  
 cag cag gtg cag cag cac tgc ccc atg tgc cgc cag gaa tgg aag ttc 355  
 Gln Gln Val Gln Gln His Cys Pro Met Cys Arg Gln Glu Trp Lys Phe  
 70 75 80  
 aag gag tgaggcccga cctggctctc gctggagggg catcctgaga ctccttcctc 411  
 Lys Glu  
 atgctggcgc cgatggctgc tggggacagc gccctgagc tgcaacaagg tggaaacaag 471  
 ggctggagct gcgtttgttt tgccatcact atgttgacac ttttatccaa taagtgaaaa 531  
 ctcattaaac tactcaaatac ttgaaaaaaaa aaaaa 566

<210> 304  
 <211> 2172  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (415) .. (669)

&lt;400&gt; 304

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ttttggccga agcggcctac ggctgcgaga agacgacaga aggggtacggc tgcgagaaga      120
cgacagaagg gtacggctgc gagaagacga cagaagggtta cggctgcgag aagacgacag      180
aagggtacgg ctgcgagaag acgacagaag ggtacggctg cgagaagacg acagaagggt      240
acggctgcga gaagacgaca gaagggtacg gctgcgagaa gacgacagaa ggggtacggct      300
gcgagaagac gacagaaggg tacggctgcg agaagacgac agaagggggac actagaggaa      360
gtcgtgctac ccccgcgag tggtcgtgtg ttctggattc attccggcac cacc  atg      417
                                     Met
                                     1

tcg aag gtt tcc ttt aag atc acg ctg acg tcg gac cca cgg ctg ccg      465
Ser Lys Val Ser Phe Lys Ile Thr Leu Thr Ser Asp Pro Arg Leu Pro
          5              10              15

tac aaa gta ctc agt gtt cct gaa agt aca cct ttc aca gca gtc tta      513
Tyr Lys Val Leu Ser Val Pro Glu Ser Thr Pro Phe Thr Ala Val Leu
          20              25              30

aag ttt gca gca gaa gaa ttt aaa gtt cct gct gca aca agt gca att      561
Lys Phe Ala Ala Glu Glu Phe Lys Val Pro Ala Ala Thr Ser Ala Ile
          35              40              45

att acc aat gat gga ata gga ata aat cct gca cag act gct gga aat      609
Ile Thr Asn Asp Gly Ile Gly Ile Asn Pro Ala Gln Thr Ala Gly Asn
          50              55              60              65

gtt ttt cta aaa cat ggt tca gaa ctg cgg att att cct aga gat cgt      657
Val Phe Leu Lys His Gly Ser Glu Leu Arg Ile Ile Pro Arg Asp Arg
          70              75              80

gtt gga agt tgt taa tatctgctac ttggaacata cgattgcctt tcagaataaa      712
Val Gly Ser Cys
          85

tattggtatt ttttggtggt gtaaaattga aatcaggcat ttaacatact atgaaaacac      772
caggagtcaa tgattaatga aagggtgactc atctgtccct ttttggtgtc catactcttc      832
ctatgaagag ggaatgcgta tgaattaagg ctactactgt cacagaagat catagtcttt      892
gatgctacct cacaacacaa acaggtagtt cgttgggggc aaatgaatta gccaaactgtt      952
aactggaagc ttttgataat tttttttttt agaacaattt ggaacattaa aatttactga     1012
atcgatatata ttcacttgag ataaaaatat aaaaagaatt atggaccctg gatggcaatt     1072
tgcttgatag catctgattt gcagactcat aatttgattt ttaattaaat atataggtta     1132
tgatgaagtg aatagacata tcagtgaaca gttaactata ttaaattttt atcatttact     1192
ttttttaaga ttcagacctc agttatataa atttcagttt aatatcaacc aaaaaattaa     1252

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aattttaatc taacccttat gtgtataaat tgggtgtccca taccagcttt taatggtgga 1312
cctatagaat ccagtacttt taatggtggg aatttacagt agaagcatcc tttgctgagt 1372
tatacattcc tttatcaatc tcttttgata caacatttaa aacaagtagc ttcaagaaac 1432
cactggtggt ttgaggatag tattttctaaa tagcattcag gaacagagta ttattgcaca 1492
gatctgaaga tcaaaaaaaaa gctcaaggaa atacagatcg gaagtgctga tgagttatat 1552
ttattgaaaa cccaactttt aaggaagtgc taagatcagt cacccatgtg aataagaagc 1612
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gaggaaacag tgaaggggaa cagaaggggg tagcaaagtg ttacagaaaa gcggactgga 1732
tagacaaaac tgcagaaggt gtatgttggg gagaactgaa agggaaaaca aaataactga 1792
catagtctta agtagaagaa ggcagttaga gaaaacaaag tatctactgg ctttgtcaac 1852
atacagactt caaaataccc cttatgagaa tccaaagaat gatgtgtgta agggaagatt 1912
ttatttgccc ttccggaaga aatcagtatc tatgcaaac ttgaaagacg aaatcaaagc 1972
ccattaatga ttcagaatca gtgcttgacc tcctgtattc tgaatggtga actctggaag 2032
cagggattgt gtctggctct ttttagagct ggaaatgtag tggctttcat taaatacttg 2092
ctgtaaagtc tttctaagac caattattat cttagcatgt ttcagtatct tctctatcat 2152
aggccctaag ttcattgggg 2172

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<210> 305
<211> 1509
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (69)..(1214)

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atttctgg atg gtc atg gtt gtt cgg aat cct ata att gaa aaa cag agt 110
      Met Val Met Val Val Arg Asn Pro Ile Ile Glu Lys Gln Ser
        1              5              10

aaa gat gga aaa cca gtt att gaa tat caa gag gag gag ttg ttg gac 158
Lys Asp Gly Lys Pro Val Ile Glu Tyr Gln Glu Glu Glu Leu Leu Asp
  15              20              25              30

aag gtt tat agc tcg gtg ctg cgg cag tgc tac agc atg tac aag ctt 206
Lys Val Tyr Ser Ser Val Leu Arg Gln Cys Tyr Ser Met Tyr Lys Leu
        35              40              45

ttt aat ggt aca ttt ctg aaa gcc atg gaa gac gga ggc gtc aag ctt 254
Phe Asn Gly Thr Phe Leu Lys Ala Met Glu Asp Gly Gly Val Lys Leu
        50              55              60

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ctg aaa gaa aga tta gag aaa ttc ttc cat cgg tat ttg caa acg cta	302
Leu Lys Glu Arg Leu Glu Lys Phe Phe His Arg Tyr Leu Gln Thr Leu	
65 70 75	
cat ttg cag tca tgt gac cta ctt gac att ttt ggt gga atc agc ttc	350
His Leu Gln Ser Cys Asp Leu Leu Asp Ile Phe Gly Gly Ile Ser Phe	
80 85 90	
ttc ccg ttg gat aaa atg act tat ttg aaa atc cag tcc ttt att aat	398
Phe Pro Leu Asp Lys Met Thr Tyr Leu Lys Ile Gln Ser Phe Ile Asn	
95 100 105 110	
aga atg gag gaa agc ctg aat ata gtc aaa tac act gct ttt ctc tat	446
Arg Met Glu Glu Ser Leu Asn Ile Val Lys Tyr Thr Ala Phe Leu Tyr	
115 120 125	
aac gat cag ctt atc tgg agt gga tta gaa caa gat gac atg aga att	494
Asn Asp Gln Leu Ile Trp Ser Gly Leu Glu Gln Asp Asp Met Arg Ile	
130 135 140	
tta tac aaa tac ctt acc acc tcc ctt ttc cca agg cac atc gaa cct	542
Leu Tyr Lys Tyr Leu Thr Thr Ser Leu Phe Pro Arg His Ile Glu Pro	
145 150 155	
gag tta gca gga agg gat tct cca ata aga gca gaa atg cca gga aat	590
Glu Leu Ala Gly Arg Asp Ser Pro Ile Arg Ala Glu Met Pro Gly Asn	
160 165 170	
ctt caa cac tat gga aga ttt ctt acc gga ccc ttg aac ctc aat gat	638
Leu Gln His Tyr Gly Arg Phe Leu Thr Gly Pro Leu Asn Leu Asn Asp	
175 180 185 190	
cca gat gca aaa tgc aga ttc ccc aaa att ttt gta aat aca gat gac	686
Pro Asp Ala Lys Cys Arg Phe Pro Lys Ile Phe Val Asn Thr Asp Asp	
195 200 205	
act tat gaa gag ctc cat tta atc gtt tat aag gcc atg agt gcg gct	734
Thr Tyr Glu Glu Leu His Leu Ile Val Tyr Lys Ala Met Ser Ala Ala	
210 215 220	
gtg tgc ttt atg atc gac gcc tct gtc cac cca acg ttg gat ttt tgc	782
Val Cys Phe Met Ile Asp Ala Ser Val His Pro Thr Leu Asp Phe Cys	
225 230 235	
cga aga ctg gac agc atc gtt ggg ccc cag ctc aca gtg ctg gcc tct	830
Arg Arg Leu Asp Ser Ile Val Gly Pro Gln Leu Thr Val Leu Ala Ser	
240 245 250	
gac atc tgt gaa cag ttt aac atc aac aag agg atg tcc ggg tct gag	878
Asp Ile Cys Glu Gln Phe Asn Ile Asn Lys Arg Met Ser Gly Ser Glu	
255 260 265 270	
aaa gaa ccc cag ttt aag ttt atc tac ttc aac cac atg aat ctc gcc	926
Lys Glu Pro Gln Phe Lys Phe Ile Tyr Phe Asn His Met Asn Leu Ala	
275 280 285	
gag aag agc aca gtt cac atg agg aaa acg ccc agc gtg tcg ctc act	974
Glu Lys Ser Thr Val His Met Arg Lys Thr Pro Ser Val Ser Leu Thr	
290 295 300	
tcc gtg cac ccg gat tta atg aag att ctc ggt gac atc aac agt gac	1022
Ser Val His Pro Asp Leu Met Lys Ile Leu Gly Asp Ile Asn Ser Asp	
305 310 315	



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ttt acc aga gtg gat gaa gat gag gag atc att gtg aag gcc atg agt      1070
Phe Thr Arg Val Asp Glu Asp Glu Glu Ile Ile Val Lys Ala Met Ser
      320                      325                      330

gat tac tgg gtt gtt gga aag aag tct gat cgg cgg gag ctc tat gtt      1118
Asp Tyr Trp Val Val Gly Lys Lys Ser Asp Arg Arg Glu Leu Tyr Val
335                      340                      345                      350

att ttg aat caa aaa aat gca aac ctg att gaa gta aat gaa gag gtc      1166
Ile Leu Asn Gln Lys Asn Ala Asn Leu Ile Glu Val Asn Glu Glu Val
      355                      360                      365

aag aaa ctt tgt gca aca cag ttc aac aac atc ttc ttc ttg gat tga      1214
Lys Lys Leu Cys Ala Thr Gln Phe Asn Asn Ile Phe Phe Leu Asp *
      370                      375                      380

cggatgacgg ctactgaga gcatacttaa aaaacactct gcaaacattt ggtcacatgc      1274

aagttagtgg tcatatgacg gactgcattc aggacaaggg taaagcaata cttgctttga      1334

agaatcacat ttcgactcgg tctgctgacg tgagggttttt agatttttaa tatttatgtg      1394

gaattaatta aaggtagttg gctatatcgc tatcatttca ttcttttgac attatgtgaa      1454

tattttactg gaaaataaga ctaataaatt gttaaaagtt tttaaaaaaa aaaaa      1509

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&lt;210&gt; 306

&lt;211&gt; 1919

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (198)..(1622)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1919)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 306

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ccggaattcc cgggtcgacg atttcgtcgt gtggtgagc ctacagaagc ggccttcagc      120

tggaccttgg tctccccgcc ggacttcgag ggtgtcatcg ccgcccctgt tgggggtgag      180

cgccgcgcgg ctgcagc   atg cct cac agg aag aaa aag ccc ttt ata gag      230
                    Met Pro His Arg Lys Lys Lys Pro Phe Ile Glu
                        1             5             10

aag aag aaa gct gtg tct ttt cac ttg gtc cac cgg agc caa cga gat      278
Lys Lys Lys Ala Val Ser Phe His Leu Val His Arg Ser Gln Arg Asp
      15                      20                      25

cct tta gca gca gat gag agt gca ccc cag agg gtt cta ttg ccc aca      326
Pro Leu Ala Ala Asp Glu Ser Ala Pro Gln Arg Val Leu Leu Pro Thr
      30                      35                      40

caa aaa ata gac aat gaa gaa agg cga gca gaa cag agg aag tat gga      374
Gln Lys Ile Asp Asn Glu Glu Arg Arg Ala Glu Gln Arg Lys Tyr Gly

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45	50	55	
gtg ttc ttt gat gac gac tat gac tac ctg cag cac ctg aag gaa cca Val Phe Phe Asp Asp Asp Tyr Asp Tyr Leu Gln His Leu Lys Glu Pro 60 65 70 75			422
tct ggg cct tca gag ctt att ccc tca agt acc ttc agt gca cac aac Ser Gly Pro Ser Glu Leu Ile Pro Ser Ser Thr Phe Ser Ala His Asn 80 85 90			470
agg aga gag gag aaa gaa gaa acg cta gta att cca agc act gga att Arg Arg Glu Glu Lys Glu Glu Thr Leu Val Ile Pro Ser Thr Gly Ile 95 100 105			518
aag ttg cct tca tca gtg ttt gct tca gag ttt gag gaa gat gtt gga Lys Leu Pro Ser Ser Val Phe Ala Ser Glu Phe Glu Glu Asp Val Gly 110 115 120			566
ttg tta aat aaa gca gct cca gtt tca gga cct cga ctg gat ttt gat Leu Leu Asn Lys Ala Ala Pro Val Ser Gly Pro Arg Leu Asp Phe Asp 125 130 135			614
cct gac att gtt gca gct ctt gat gat gat ttt gac ttt gat gat cca Pro Asp Ile Val Ala Ala Leu Asp Asp Asp Phe Asp Phe Asp Asp Pro 140 145 150 155			662
gat aat ctg ctt gag gat gac ttt att ctt cag gcc aat aag gca aca Asp Asn Leu Leu Glu Asp Asp Phe Ile Leu Gln Ala Asn Lys Ala Thr 160 165 170			710
gga gag gaa gag gga atg gat ata cag aaa tct gag aat gaa gat gac Gly Glu Glu Glu Gly Met Asp Ile Gln Lys Ser Glu Asn Glu Asp Asp 175 180 185			758
agc gag tgg gaa gat gtg gat gat gag aag gga gat agc aat gat gac Ser Glu Trp Glu Asp Val Asp Asp Glu Lys Gly Asp Ser Asn Asp Asp 190 195 200			806
tat gac tct gca ggc cta ttg tca gat gaa gac tgt atg tct gtg ccc Tyr Asp Ser Ala Gly Leu Leu Ser Asp Glu Asp Cys Met Ser Val Pro 205 210 215			854
gga aaa act cac aga gct ata gca gat cac ttg ttc tgg agt gag gaa Gly Lys Thr His Arg Ala Ile Ala Asp His Leu Phe Trp Ser Glu Glu 220 225 230 235			902
aca aag agt cgc ttc acg gag tat tcg atg act tcc tca gtc atg agg Thr Lys Ser Arg Phe Thr Glu Tyr Ser Met Thr Ser Ser Val Met Arg 240 245 250			950
aga aat gaa cag ctg acc cta cat gat gag agg ttt gag aag ttt tat Arg Asn Glu Gln Leu Thr Leu His Asp Glu Arg Phe Glu Lys Phe Tyr 255 260 265			998
gag caa tat gat gat gat gaa att gga gct ctg gat aat gca gaa ttg Glu Gln Tyr Asp Asp Asp Glu Ile Gly Ala Leu Asp Asn Ala Glu Leu 270 275 280			1046
gaa ggt tct att caa gtg gac agc aat cgc tta cag gaa gtt ttg aat Glu Gly Ser Ile Gln Val Asp Ser Asn Arg Leu Gln Glu Val Leu Asn 285 290 295			1094
gac tac tat aaa gag aag gca gag aat tgt gta aaa ttg aat acc ctt Asp Tyr Tyr Lys Glu Lys Ala Glu Asn Cys Val Lys Leu Asn Thr Leu			1142

300	305	310	315	
gaa ccc ttg gag gat caa gac ctg cca atg aat gag ctt gat gag tct				1190
Glu Pro Leu Glu Asp Gln Asp Leu Pro Met Asn Glu Leu Asp Glu Ser				
	320	325	330	
gag gag gaa gaa atg att act gta gtc ctt gaa gaa gcc aaa gag aag				1238
Glu Glu Glu Glu Met Ile Thr Val Val Leu Glu Glu Ala Lys Glu Lys				
	335	340	345	
tgg gat tgt gaa tct att tgt agt aca tac tca aat tta tat aac cat				1286
Trp Asp Cys Glu Ser Ile Cys Ser Thr Tyr Ser Asn Leu Tyr Asn His				
	350	355	360	
cca cag ctt atc aag tat caa cca aag ccc aaa caa att cga ata tct				1334
Pro Gln Leu Ile Lys Tyr Gln Pro Lys Pro Lys Gln Ile Arg Ile Ser				
	365	370	375	
tct aaa aca gga ata cct ctc aat gtc tta cca aag aaa gga ctc aca				1382
Ser Lys Thr Gly Ile Pro Leu Asn Val Leu Pro Lys Lys Gly Leu Thr				
	380	385	390	395
gca aag caa act gaa aga ata cag atg att aat ggc agt gat ctt cct				1430
Ala Lys Gln Thr Glu Arg Ile Gln Met Ile Asn Gly Ser Asp Leu Pro				
	400	405	410	
aaa gta tca act cag cca cgt tct aaa aat gaa agc aaa gaa gat aaa				1478
Lys Val Ser Thr Gln Pro Arg Ser Lys Asn Glu Ser Lys Glu Asp Lys				
	415	420	425	
aga gca aga aag caa gct ata aaa gaa gag cgc aag gaa cga aga gtg				1526
Arg Ala Arg Lys Gln Ala Ile Lys Glu Glu Arg Lys Glu Arg Arg Val				
	430	435	440	
gag aag aaa gct aac aaa tta gca ttt aaa ctg gag aaa aga agg caa				1574
Glu Lys Lys Ala Asn Lys Leu Ala Phe Lys Leu Glu Lys Arg Arg Gln				
	445	450	455	
gaa aaa gag ctg ctg aac ttg aag aag aat gtt gag ggt cta aag cta				1622
Glu Lys Glu Leu Leu Asn Leu Lys Lys Asn Val Glu Gly Leu Lys Leu				
	460	465	470	475
tagacagtgg agcatacagg gcaaggcact ttattagggg ctccatcatct ttgggttattg				1682
actagaaact tcagaaagac aaaactgttt gccattttta ctggcagata agaggaaaat				1742
acaatatattg tattattttt atactagtaa gtgtcccctg ccaaccatct tgtaaatatt				1802
gtaatacttt aatttttaat attataagct tacatttgct ctgaagtaaa tgacttcatg				1862
aatgtgaaat gtttgataaa ttaaaggaaa atatcttcat aacgtggaaa aaaaaaa				1919

<210> 307  
 <211> 2138  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (224)..(1180)

&lt;400&gt; 307

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attggctata aaatataaat gatggtatatt ctgaaagggtt agcaatgcat gcctgtctcg	180
tttccctctt tctctctctc tctctgatag tcacttcaat caa atg gaa cca gga	235
	Met Glu Pro Gly
	1
aat gat aca caa att tca gaa ttt ctt ctt ctg gga ttt tca caa gaa	283
Asn Asp Thr Gln Ile Ser Glu Phe Leu Leu Leu Gly Phe Ser Gln Glu	
5 10 15 20	
cct gga ctg caa ccc ttc ctc ttt ggg ctg ttc ctg tcc atg tac ctg	331
Pro Gly Leu Gln Pro Phe Leu Phe Gly Leu Phe Leu Ser Met Tyr Leu	
25 30 35	
gtc act gtg ctc ggg aac ctg ctc atc atc ctg gcc aca atc tca gac	379
Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Thr Ile Ser Asp	
40 45 50	
tcc cac ctc cac acc ccc atg tac ttc ttc ctc tcc aac ctg tcc ttt	427
Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe	
55 60 65	
gct gac att tgt gtt act tcc acc acc att cca aaa atg ctg atg aac	475
Ala Asp Ile Cys Val Thr Ser Thr Thr Ile Pro Lys Met Leu Met Asn	
70 75 80	
atc cag aca cag aac aaa gtc atc acc tac ata gcc tgc ctc atg cag	523
Ile Gln Thr Gln Asn Lys Val Ile Thr Tyr Ile Ala Cys Leu Met Gln	
85 90 95 100	
atg tat ttt ttc ata ctc ttt gct gga ttt gaa aac ttc ctc ctg tcc	571
Met Tyr Phe Phe Ile Leu Phe Ala Gly Phe Glu Asn Phe Leu Leu Ser	
105 110 115	
gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac ccc ctg cac tac	619
Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His Tyr	
120 125 130	
atg gtc att atg aac cct cac ctc tgt gga ctg ctg gtt cta gca tcc	667
Met Val Ile Met Asn Pro His Leu Cys Gly Leu Leu Val Leu Ala Ser	
135 140 145	
tgg acc atg agt gct ctg tat tcc ttg cta caa atc tta atg gta gta	715
Trp Thr Met Ser Ala Leu Tyr Ser Leu Leu Gln Ile Leu Met Val Val	
150 155 160	
cgg ctg tcc ttc tgc aca gcc tta gaa atc ccc cac ttt ttc tgt gaa	763
Arg Leu Ser Phe Cys Thr Ala Leu Glu Ile Pro His Phe Phe Cys Glu	
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acg gct aca ctg ata gat gag ccc act gag gtg gat gac ccc tgg aac Thr Ala Thr Leu Ile Asp Glu Pro Thr Glu Val Asp Asp Pro Trp Asn 60 65 70			243
cta ccc act ctt cag gac tcg ggg atc aag tgg tca gag aga gac acc Leu Pro Thr Leu Gln Asp Ser Gly Ile Lys Trp Ser Glu Arg Asp Thr 75 80 85			291
aaa ggg aag att ctc tgt ttc ttc caa ggg att ggg aga ttg att tta Lys Gly Lys Ile Leu Cys Phe Phe Gln Gly Ile Gly Arg Leu Ile Leu 90 95 100			339
ctt ctc gga ttt ctc tac ttt ttc gtg tgc tcc ctg gat att ctt agt Leu Leu Gly Phe Leu Tyr Phe Phe Val Cys Ser Leu Asp Ile Leu Ser 105 110 115			387
agc gcc ttc cag ctg gtt gga gga aaa atg gca gga cag ttc ttc agc Ser Ala Phe Gln Leu Val Gly Gly Lys Met Ala Gly Gln Phe Phe Ser 120 125 130 135			435
aac agc tct att atg tcc aac cct ttg ttg ggg ctg gtg atc ggg gtg Asn Ser Ser Ile Met Ser Asn Pro Leu Leu Gly Leu Val Ile Gly Val 140 145 150			483
ctg gtg acc gtc ttg gtg cag agc tcc agc acc tca acg tcc atc gtt Leu Val Thr Val Leu Val Gln Ser Ser Ser Thr Ser Thr Ser Ile Val 155 160 165			531
gtc agc atg gtg tcc tct tca ttg ctc act gtt cgg gct gcc atc ccc Val Ser Met Val Ser Ser Ser Leu Leu Thr Val Arg Ala Ala Ile Pro 170 175 180			579
att atc atg ggg gcc aac att gga acg tca atc acc aac act att gtt Ile Ile Met Gly Ala Asn Ile Gly Thr Ser Ile Thr Asn Thr Ile Val 185 190 195			627
gcg ctc atg cag gtg gga gat cgg agt gag ttc aga aga gct ttt gca Ala Leu Met Gln Val Gly Asp Arg Ser Glu Phe Arg Arg Ala Phe Ala 200 205 210 215			675
gga gcc act gtc cat gac ttc ttc aac tgg ctg tcc gtg ttg gtg ctc Gly Ala Thr Val His Asp Phe Phe Asn Trp Leu Ser Val Leu Val Leu 220 225 230			723
ttg ccc gtg gag gtg gcc acc cat tac ctc gag atc ata acc cag ctt Leu Pro Val Glu Val Ala Thr His Tyr Leu Glu Ile Ile Thr Gln Leu 235 240 245			771
ata gtg gag agc ttc cac ttc aag aat gga gaa gat gcc cca gat ctt Ile Val Glu Ser Phe His Phe Lys Asn Gly Glu Asp Ala Pro Asp Leu 250 255 260			819
ctg aaa gtc atc act aag ccc ttc aca aag ctc att gtc cag ctg gat Leu Lys Val Ile Thr Lys Pro Phe Thr Lys Leu Ile Val Gln Leu Asp 265 270 275			867
aaa aaa gtt atc agc caa att gca atg aac gat gaa aaa gcg aaa aac Lys Lys Val Ile Ser Gln Ile Ala Met Asn Asp Glu Lys Ala Lys Asn			915



280	285	290	295	
aag agt ctt gtc aag att tgg tgc aaa act ttt acc aac aag acc cag				963
Lys Ser Leu Val Lys Ile Trp Cys Lys Thr Phe Thr Asn Lys Thr Gln				
	300	305	310	
att aac gtc act gtt ccc tcg act gct aac tgc acc tcc cct tcc ctc				1011
Ile Asn Val Thr Val Pro Ser Thr Ala Asn Cys Thr Ser Pro Ser Leu				
	315	320	325	
tgt tgg acg gat ggc atc caa aac tgg acc atg aag aat gtg acc tac				1059
Cys Trp Thr Asp Gly Ile Gln Asn Trp Thr Met Lys Asn Val Thr Tyr				
	330	335	340	
aag gag aac atc gcc aaa tgc cag cat atc ttt gtg aat ttc cac ctc				1107
Lys Glu Asn Ile Ala Lys Cys Gln His Ile Phe Val Asn Phe His Leu				
	345	350	355	
ccg gat ctt gct gtg ggc acc atc ttg ctc ata ctc tcc ctg ctg gtc				1155
Pro Asp Leu Ala Val Gly Thr Ile Leu Leu Ile Leu Ser Leu Leu Val				
	360	365	370	375
ctc tgt ggt tgc ctg atc atg att gtc aag atc ctg ggc tct gtg ctc				1203
Leu Cys Gly Cys Leu Ile Met Ile Val Lys Ile Leu Gly Ser Val Leu				
	380	385	390	
aag ggg cag gtc gcc act gtc atc aag aag acc atc aac act gat ttc				1251
Lys Gly Gln Val Ala Thr Val Ile Lys Lys Thr Ile Asn Thr Asp Phe				
	395	400	405	
ccc ttt ccc ttt gca tgg ttg act ggc tac ctg gcc atc ctc gtc ggg				1299
Pro Phe Pro Phe Ala Trp Leu Thr Gly Tyr Leu Ala Ile Leu Val Gly				
	410	415	420	
gca ggc atg acc ttc atc gta cag agc agc tct gtg ttc acg tcg gcc				1347
Ala Gly Met Thr Phe Ile Val Gln Ser Ser Ser Val Phe Thr Ser Ala				
	425	430	435	
ttg acc ccc ctg att gga atc ggc gtg ata acc att gag agg gct tat				1395
Leu Thr Pro Leu Ile Gly Ile Gly Val Ile Thr Ile Glu Arg Ala Tyr				
	440	445	450	455
cca ctc acg ctg ggc tcc aac atc ggc acc acc acc acc gcc atc ctg				1443
Pro Leu Thr Leu Gly Ser Asn Ile Gly Thr Thr Thr Thr Ala Ile Leu				
	460	465	470	
gcc gcc tta gcc agc cct ggc aat gca ttg agg agt tca ctc cag atc				1491
Ala Ala Leu Ala Ser Pro Gly Asn Ala Leu Arg Ser Ser Leu Gln Ile				
	475	480	485	
gcc ctg tgc cac ttt ttc ttc aac atc tcc ggc atc ttg ctg tgg tac				1539
Ala Leu Cys His Phe Phe Phe Asn Ile Ser Gly Ile Leu Leu Trp Tyr				
	490	495	500	
ccg atc ccg ttc act cgc ctg ccc atc cgc atg gcc aag ggg ctg ggc				1587
Pro Ile Pro Phe Thr Arg Leu Pro Ile Arg Met Ala Lys Gly Leu Gly				
	505	510	515	
aac atc tct gcc aag tat cgc tgg ttc gcc gtc ttc tac ctg atc atc				1635
Asn Ile Ser Ala Lys Tyr Arg Trp Phe Ala Val Phe Tyr Leu Ile Ile				
	520	525	530	535
ttc ttc ttc ctg atc ccg ctg acg gtg ttt ggc ctc tcg ctg gcc ggc				1683
Phe Phe Phe Leu Ile Pro Leu Thr Val Phe Gly Leu Ser Leu Ala Gly				

540	545	550	
tgg cgg gtg ctg gtt ggt gtc ggg gtt ccc gtc gtc ttc atc atc atc			1731
Trp Arg Val Leu Val Gly Val Gly Val Pro Val Val Phe Ile Ile Ile			
555	560	565	
ctg gta ctg tgc ctc cga ctc ctg cag tct cgc tgc cca cgc gtc ctg			1779
Leu Val Leu Cys Leu Arg Leu Leu Gln Ser Arg Cys Pro Arg Val Leu			
570	575	580	
ccg aag aaa ctc cag aac tgg aac ttc ctg ccg ctg tgg atg cgc tcg			1827
Pro Lys Lys Leu Gln Asn Trp Asn Phe Leu Pro Leu Trp Met Arg Ser			
585	590	595	
ctg aag ccc tgg gat gcc gtc gtc tcc aag ttc acc ggc tgc ttc cag			1875
Leu Lys Pro Trp Asp Ala Val Val Ser Lys Phe Thr Gly Cys Phe Gln			
600	605	610	615
atg cgc tgc tgc tgc tgc tgc cgc gtg tgc tgc cgc gcg tgc tgc ttg			1923
Met Arg Cys Cys Cys Cys Cys Arg Val Cys Cys Arg Ala Cys Cys Leu			
620	625	630	
ctg tgt ggc tgc ccc aag tgc tgc cgc tgc agc aag tgc tgc gag gac			1971
Leu Cys Gly Cys Pro Lys Cys Cys Arg Cys Ser Lys Cys Cys Glu Asp			
635	640	645	
ttg gag gag gcg cag gag ggg cag gat gtc cct gtc aag gct cct gag			2019
Leu Glu Glu Ala Gln Glu Gly Gln Asp Val Pro Val Lys Ala Pro Glu			
650	655	660	
acc ttt gat aac ata acc att agc aga gag gct cag ggt gag gtc cct			2067
Thr Phe Asp Asn Ile Thr Ile Ser Arg Glu Ala Gln Gly Glu Val Pro			
665	670	675	
gcc tcg gac tca aag acc gaa tgc acg gcc ttg taggggac gccccagatt			2118
Ala Ser Asp Ser Lys Thr Glu Cys Thr Ala Leu			
680	685	690	
gtcagggatt gggggatggt ccttgagttt tgcattgctct cctccctccc acttctgcac			2178
cctttcacca cctcgaggag atttgctccc cattagcgaa tgaaattgat gcagtcctac			2238
ctaactcgat tccctttggc ttggtgggta ggctgcagg gcacttttat tccaaccct			2298
ggtcactcag taatctttta ctccaggaag gcacaggatg gtacctaaag agaattagag			2358
aatgaacctg gcgggacgga tg			2380

<210> 310  
 <211> 1710  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (194) .. (1405)

<400> 310	
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aagccagcag ggaagccagc cccacaggca agggcccccc agcctcctca cagctcccca	120

804

Phe	Asn	Val	Leu	Thr	Ala	Cys	Arg	Leu	Arg	Gln	Pro	Gly	Gln	Pro	Lys	
			240					245					250			
agc	cgg	cgc	cac	tgc	ttg	ctg	ctg	tgc	gcc	tac	gtg	gcc	gtc	ttt	gtc	997
Ser	Arg	Arg	His	Cys	Leu	Leu	Leu	Cys	Ala	Tyr	Val	Ala	Val	Phe	Val	
		255					260					265				
atg	tgc	tgg	ctg	ccc	tat	cat	gtg	acc	ctg	ctg	ctg	ctc	aca	ctg	cat	1045
Met	Cys	Trp	Leu	Pro	Tyr	His	Val	Thr	Leu	Leu	Leu	Leu	Thr	Leu	His	
		270				275					280					
ggg	acc	cac	atc	tcc	ctc	cac	tgc	cac	ctg	gtc	cac	ctg	ctc	tac	ttc	1093
Gly	Thr	His	Ile	Ser	Leu	His	Cys	His	Leu	Val	His	Leu	Leu	Tyr	Phe	
285					290					295					300	
ttc	tat	gat	gtc	att	gac	tgc	ttc	tcc	atg	ctg	cac	tgt	gtc	atc	aac	1141
Phe	Tyr	Asp	Val	Ile	Asp	Cys	Phe	Ser	Met	Leu	His	Cys	Val	Ile	Asn	
				305				310						315		
ccc	atc	ctt	tac	aac	ttt	ctc	agc	cca	cac	ttc	cgg	ggc	cgg	ctc	ctg	1189
Pro	Ile	Leu	Tyr	Asn	Phe	Leu	Ser	Pro	His	Phe	Arg	Gly	Arg	Leu	Leu	
			320					325					330			
aat	gct	gta	gtc	cat	tac	ctt	cct	aag	gac	cag	acc	aag	gcg	ggc	aca	1237
Asn	Ala	Val	Val	His	Tyr	Leu	Pro	Lys	Asp	Gln	Thr	Lys	Ala	Gly	Thr	
		335					340					345				
tgc	gcc	tcc	tct	tcc	tcc	tgt	tcc	acc	cag	cat	tcc	atc	atc	atc	acc	1285
Cys	Ala	Ser	Ser	Ser	Ser	Cys	Ser	Thr	Gln	His	Ser	Ile	Ile	Ile	Thr	
	350					355					360					
aag	ggt	gat	agc	cag	cct	gct	gca	gca	gcc	ccc	cac	cct	gag	cca	agc	1333
Lys	Gly	Asp	Ser	Gln	Pro	Ala	Ala	Ala	Ala	Pro	His	Pro	Glu	Pro	Ser	
365					370					375					380	
ctg	agc	ttt	cag	gca	cac	cat	ttg	ctt	cca	aat	act	tcc	ccc	atc	tct	1381
Leu	Ser	Phe	Gln	Ala	His	His	Leu	Leu	Pro	Asn	Thr	Ser	Pro	Ile	Ser	
				385					390					395		
ccc	act	cag	cct	ctt	aca	ccc	agc	tgaggtagag	gccagactcc	tccaacagtg						1435
Pro	Thr	Gln	Pro	Leu	Thr	Pro	Ser									
				400												
aaggaaaagg	cacagatcac	cttagaggcc	acgctcccaa	gattagttat	caccctggca											1495
gtatgaatac	ttccctaagg	cctcccatcc	atggagggga	agagtgggaa	ccagctgtta											1555
cactcagcat	ctactgagca	ctgatgggag	ccctgcctgg	gccatgtgct	gtggggccaa											1615
atggacatca	ctccctaact	tcttgaggtc	tgtctcctct	gtggattcac	gcatgtatca											1675
acctcattaa	actatgccaa	acttttaaaaa	aaaaa													1710

<210> 311  
 <211> 1424  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (212) .. (1102)

<400> 311

ccgagacccg ggtcgccaat ataaatgctt gatgagttaa tgaatgactt ccgtctggga 60

cttggttgca aataaagccg agctgcatct tagggagggg tggagacttt gcccctgttt 120

gtgccttgaa gccagcaggg ccttgccctac ggatacctcc acccaccctc ctgcccagca 180

agtggaggcc cgcagcccga gtgtcgccgc c atg gct tcg ccg cag ctc tgc 232  
Met Ala Ser Pro Gln Leu Cys  
1 5

cgc gcg ctg gtg tcg gcg caa tgg gtg gcg gag gcg ctg cgg gcc ccg 280  
Arg Ala Leu Val Ser Ala Gln Trp Val Ala Glu Ala Leu Arg Ala Pro  
10 15 20

cgc gct ggg cag cct ctg cag ctg ctg gac gcc tcc tgg tac ctg ccg 328  
Arg Ala Gly Gln Pro Leu Gln Leu Leu Asp Ala Ser Trp Tyr Leu Pro  
25 30 35

aag ctg ggg cgc gac gcg cga cgc gag ttc gag gag cgc cac atc ccg 376  
Lys Leu Gly Arg Asp Ala Arg Arg Glu Phe Glu Glu Arg His Ile Pro  
40 45 50 55

ggc gcc gct ttc ttc gac atc gac cag tgc agc gac cgc acc tcg ccc 424  
Gly Ala Ala Phe Phe Asp Ile Asp Gln Cys Ser Asp Arg Thr Ser Pro  
60 65 70

tac gac cac atg ctg ccc ggg gcc gag cat ttc gcg gag tac gca ggc 472  
Tyr Asp His Met Leu Pro Gly Ala Glu His Phe Ala Glu Tyr Ala Gly  
75 80 85

cgc ctg ggc gtg ggc gcg gcc acc cac gtc gtg atc tac gac gcc agc 520  
Arg Leu Gly Val Gly Ala Ala Thr His Val Val Ile Tyr Asp Ala Ser  
90 95 100

gac cag ggc ctc tac tcc gcc ccg cgc gtc tgg tgg atg ttc cgc gcc 568  
Asp Gln Gly Leu Tyr Ser Ala Pro Arg Val Trp Trp Met Phe Arg Ala  
105 110 115

ttc ggc cac cac gcc gtg tca ctg ctt gat ggc ggc ctc cgc cac tgg 616  
Phe Gly His His Ala Val Ser Leu Leu Asp Gly Gly Leu Arg His Trp  
120 125 130 135

ctg cgc cag aac ctc ccg ctc agc tcc ggc aag agc caa cct gct ccc 664  
Leu Arg Gln Asn Leu Pro Leu Ser Ser Gly Lys Ser Gln Pro Ala Pro  
140 145 150

gcc gag ttc cgc gct cag ctc gac ccc gcc ttc atc aag acc tac gag 712  
Ala Glu Phe Arg Ala Gln Leu Asp Pro Ala Phe Ile Lys Thr Tyr Glu  
155 160 165

gac atc aag gag aac ctg gaa tcc ccg cgc ttc cag gtg gtg gac tcc 760  
Asp Ile Lys Glu Asn Leu Glu Ser Arg Arg Phe Gln Val Val Asp Ser  
170 175 180

cga gcc act ggc agg ttc cgc ggc acc gag ccc gag ccc cga gac ggc 808  
Arg Ala Thr Gly Arg Phe Arg Gly Thr Glu Pro Glu Pro Arg Asp Gly  
185 190 195

att gaa cct ggc cac atc cca ggt acc gtg aac atc ccc ttc aca gac 856  
Ile Glu Pro Gly His Ile Pro Gly Thr Val Asn Ile Pro Phe Thr Asp  
200 205 210 215

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ttc ctg agc cag gag ggg ctg gag aag agc cct gag gag atc cgc cat      904
Phe Leu Ser Gln Glu Gly Leu Glu Lys Ser Pro Glu Glu Ile Arg His
                220                225                230

ctg ttc cag gag aag aaa gtg gac ctg tct aag cca ctg gtg gcc acg      952
Leu Phe Gln Glu Lys Lys Val Asp Leu Ser Lys Pro Leu Val Ala Thr
                235                240                245

tgt ggc tct ggc gtc aca gcc tgc cac gtg gca cta ggg gcc tac ctc      1000
Cys Gly Ser Gly Val Thr Ala Cys His Val Ala Leu Gly Ala Tyr Leu
                250                255                260

tgc ggc aag cca gac gtg ccc atc tac gat ggc tcc tgg gtg gag tgg      1048
Cys Gly Lys Pro Asp Val Pro Ile Tyr Asp Gly Ser Trp Val Glu Trp
                265                270                275

tac atg cgc gcc cgg ccc gag gat gtc atc tca gag ggc cgg ggg aag      1096
Tyr Met Arg Ala Arg Pro Glu Asp Val Ile Ser Glu Gly Arg Gly Lys
280                285                290                295

acc cac tgaagctggg caggacacag gcgagctcag gtgatgccgg ccaccagcaa      1152
Thr His

tgccctggcct ggtagctccg cttctgcttt caccaagaga gtgtttcttc actcaactca      1212

ggtggcattt ggggtgacat ctcaaaggcc aggaattccg ttgacttggt ggctgccagt      1272

aggggcgggg ggaaaggcgg aggcgagccc tggaggaggg aggccacaac tccgagctgc      1332

ccacctgggtg ctgagctggg gccccgcctc ctttctggtt tatttttgag gaaataaaat      1392

aaccaagtgc taaatcttgt aaaaaaaaaa aa                                  1424

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<210> 312  
 <211> 1631  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (91)..(1425)

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<400> 312
ccccccccga ggtctctgcg cagcccagcc cgccggtcca cgccgcgcac cgctccgagg      60

gccagcgcca cccgctccgc agccggcacc      atg cgc gag atc gtg cac atc      111
                                         Met Arg Glu Ile Val His Ile
                                         1                5

cag gcg ggc cag tgc ggc aac cag atc ggc gcc aag ttt tgg gag gtc      159
Gln Ala Gly Gln Cys Gly Asn Gln Ile Gly Ala Lys Phe Trp Glu Val
                10                15                20

atc agc gat gag cat ggg atc gac ccc aca ggc agt tac cat gga gac      207
Ile Ser Asp Glu His Gly Ile Asp Pro Thr Gly Ser Tyr His Gly Asp
                25                30                35

agt gac ttg cag ctg gag aga atc aac gtg tac tac aat gag gct gct      255
Ser Asp Leu Gln Leu Glu Arg Ile Asn Val Tyr Tyr Asn Glu Ala Ala
40                45                50                55

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ggt aac aaa tat gta cct cgg gcc atc ctg gtg gat ctg gag cct ggc Gly Asn Lys Tyr Val Pro Arg Ala Ile Leu Val Asp Leu Glu Pro Gly	303
60 65 70	
acc atg gac tct gtc agg tct gga ccc ttc ggc cag atc ttc aga cca Thr Met Asp Ser Val Arg Ser Gly Pro Phe Gly Gln Ile Phe Arg Pro	351
75 80 85	
gac aac ttc gtg ttc ggc cag agt gga gcc ggg aat aac tgg gcc aag Asp Asn Phe Val Phe Gly Gln Ser Gly Ala Gly Asn Asn Trp Ala Lys	399
90 95 100	
ggc cac tac aca gag gga gcc gag ctg gtc gac tcg gtc ctg gat gtg Gly His Tyr Thr Glu Gly Ala Glu Leu Val Asp Ser Val Leu Asp Val	447
105 110 115	
gtg agg aag gag tca gag agc tgt gac tgt ctc cag ggc ttc cag ctg Val Arg Lys Glu Ser Glu Ser Cys Asp Cys Leu Gln Gly Phe Gln Leu	495
120 125 130 135	
acc cac tct ctg ggg ggc ggc acg ggg tcc ggg atg ggc acc ctg ctc Thr His Ser Leu Gly Gly Gly Thr Gly Ser Gly Met Gly Thr Leu Leu	543
140 145 150	
atc agc aag atc cgg gaa gag tac cca gac cgc atc atg aac acc ttc Ile Ser Lys Ile Arg Glu Glu Tyr Pro Asp Arg Ile Met Asn Thr Phe	591
155 160 165	
agc gtc atg ccc tca ccc aag gtg tca gac acg gtg gtg gag ccc tac Ser Val Met Pro Ser Pro Lys Val Ser Asp Thr Val Val Glu Pro Tyr	639
170 175 180	
aac gcc acc ctc tct gtc cac cag ctg gtg gaa aac aca gat gaa acc Asn Ala Thr Leu Ser Val His Gln Leu Val Glu Asn Thr Asp Glu Thr	687
185 190 195	
tac tcc att gat aac gag gcc ctg tat gac atc tgc ttc cgc acc ctg Tyr Ser Ile Asp Asn Glu Ala Leu Tyr Asp Ile Cys Phe Arg Thr Leu	735
200 205 210 215	
aag ctg acc acc ccc acc tac ggg gac ctc aac cac ctg gtg tcg gcc Lys Leu Thr Thr Pro Thr Tyr Gly Asp Leu Asn His Leu Val Ser Ala	783
220 225 230	
acc atg agc ggg gtc acc acc tgc ctg cgc ttc ccg ggc cag ctg aac Thr Met Ser Gly Val Thr Thr Cys Leu Arg Phe Pro Gly Gln Leu Asn	831
235 240 245	
gca gac ctg cgc aag ctg gcg gtg aac atg gtg ccc ttc cct cgc ctg Ala Asp Leu Arg Lys Leu Ala Val Asn Met Val Pro Phe Pro Arg Leu	879
250 255 260	
cac ttc ttc atg ccc ggc ttc gcg ccc ctg acc agc cgg ggc agc cag His Phe Phe Met Pro Gly Phe Ala Pro Leu Thr Ser Arg Gly Ser Gln	927
265 270 275	
cag tac cgg gcg ctc acg gtg ccc gag ctc acc cag cag atg ttc gac Gln Tyr Arg Ala Leu Thr Val Pro Glu Leu Thr Gln Gln Met Phe Asp	975
280 285 290 295	
tcc aag aac atg atg gcc gcc tgc gac ccg cgc cac ggc cgc tac ctg Ser Lys Asn Met Met Ala Ala Cys Asp Pro Arg His Gly Arg Tyr Leu	1023
300 305 310	

acg gtg gct gcc atc ttc cgg ggc cgc atg tcc atg aag gag gtg gac 1071  
 Thr Val Ala Ala Ile Phe Arg Gly Arg Met Ser Met Lys Glu Val Asp  
 315 320 325  
 gag cag atg ctc aac gtg cag aac aag aac agc agc tac ttc gtg gag 1119  
 Glu Gln Met Leu Asn Val Gln Asn Lys Asn Ser Ser Tyr Phe Val Glu  
 330 335 340  
 tgg atc ccc aac aac gtg aag acg gcc gtg tgc gac atc ccg ccc cgc 1167  
 Trp Ile Pro Asn Asn Val Lys Thr Ala Val Cys Asp Ile Pro Pro Arg  
 345 350 355  
 ggc ctg aag atg tcg gcc acc ttc atc ggc aac agc acg gcc atc cag 1215  
 Gly Leu Lys Met Ser Ala Thr Phe Ile Gly Asn Ser Thr Ala Ile Gln  
 360 365 370 375  
 gag ctg ttc aag cgc atc tcc gag cag ttc acg gcc atg ttc cgg cgc 1263  
 Glu Leu Phe Lys Arg Ile Ser Glu Gln Phe Thr Ala Met Phe Arg Arg  
 380 385 390  
 aag gcc ttc ctg cac tgg tac acg ggc gag ggc atg gac gag atg gag 1311  
 Lys Ala Phe Leu His Trp Tyr Thr Gly Glu Gly Met Asp Glu Met Glu  
 395 400 405  
 ttc acc gag gcc gag agc aac atg aac gac ctg gtg tcc gag tac cag 1359  
 Phe Thr Glu Ala Glu Ser Asn Met Asn Asp Leu Val Ser Glu Tyr Gln  
 410 415 420  
 cag tac cag gac gcc acg gcc gac gaa caa ggg gag ttc gag gag gag 1407  
 Gln Tyr Gln Asp Ala Thr Ala Asp Glu Gln Gly Glu Phe Glu Glu Glu  
 425 430 435  
 gag ggc gag gac gag gct taaaaa cttctcagat caatcgtgca tccttagtga 1461  
 Glu Gly Glu Asp Glu Ala  
 440 445  
 acttctgttg tcctcaagca tgggtcttct acttgtaaac tatggtgctc agttttgcct 1521  
 ctgtagaaaa ttcacactgt tgatgtaatg atgtggaact cctctaaaaa ttacagtatt 1581  
 gtctgtgaag gtatctatac taataaaaaa gcatgtgtag aaaaaaaaaa 1631

<210> 313  
 <211> 1047  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (373)..(912)

<400> 313  
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 cgcgtgggcg gtttcgtggg ctttacttgg cccgcgctta gggccctcgc ggggggcttg 120  
 tgggtcctcc tccccctccc actgacaact gcccactg ctcttcccgc cccggtcaca 180  
 gtgaaaatgt agacgggggc gttgtccgta cgactgtgcg ccagggtcgc gggaggggag 240

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ccctccgcgt gagcgcccc ctgggaatat tgaacataat cacctctcat tccagactat      300
gttaggtctt aatggtggga ggacgcccga gtgctcggcc cgtttcaccc cgaggaggaa      360
ggacactggg tc      atg acg cca tca gag ggc gcc aga gca ggg acc gga      408
                    Met Thr Pro Ser Glu Gly Ala Arg Ala Gly Thr Gly
                    1          5          10

cgc gag ttg gag atg ttg gac tcg ctg ttg gcc ttg ggc ggc ctg gtg      456
Arg Glu Leu Glu Met Leu Asp Ser Leu Leu Ala Leu Gly Gly Leu Val
      15          20          25

ctg ctt cgg gat tcc gtg gag tgg gag ggg cgc agt ctc ttg aag gcg      504
Leu Leu Arg Asp Ser Val Glu Trp Glu Gly Arg Ser Leu Leu Lys Ala
      30          35          40

ctt gtc aag aaa tct gca ctg tgt ggg gag caa gtg cat atc ctg ggc      552
Leu Val Lys Lys Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly
      45          50          55          60

tgt gaa gtg agc gag gaa gag ttt cgt gaa ggt ttt gac tct gat atc      600
Cys Glu Val Ser Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile
      65          70          75

aac aat cgg ctg gtt tac cat gac ttc ttc aga gac cct ctc aac tgg      648
Asn Asn Arg Leu Val Tyr His Asp Phe Phe Arg Asp Pro Leu Asn Trp
      80          85          90

tca aaa act gag gag gcc ttt cct ggg ggg ccg ctg gga gcc ttg aga      696
Ser Lys Thr Glu Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg
      95          100          105

gcc atg tgc aag agg aca gat cct gtt cct gtc acc att gct ctc gat      744
Ala Met Cys Lys Arg Thr Asp Pro Val Pro Val Thr Ile Ala Leu Asp
      110          115          120

tca ctc agc tgg ctg cta ctt cgc ctt ccc tgc acc aca ctc tgc cag      792
Ser Leu Ser Trp Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln
      125          130          135          140

gtc ctg cat gct gtg agc cat cag gac tct tgt cct ggt gag acc cct      840
Val Leu His Ala Val Ser His Gln Asp Ser Cys Pro Gly Glu Thr Pro
      145          150          155

cct tca ttg ttt ccc ctc ata cat ctc cct ctg cca agg agt gtg ccc      888
Pro Ser Leu Phe Pro Leu Ile His Leu Pro Leu Pro Arg Ser Val Pro
      160          165          170

ctt ttc ctt tct acc cta gaa taa acatctgggt tctccagtca gacctttttt      942
Leu Phe Leu Ser Thr Leu Glu *
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&lt;222&gt; (110) .. (919)

&lt;400&gt; 314

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                               Met Gly
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cag aac gac ctg atg ggc acg gcc gag gac ttc gcc gac cag ttc ctc      163
Gln Asn Asp Leu Met Gly Thr Ala Glu Asp Phe Ala Asp Gln Phe Leu
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cgt gtc aca aag cag tac ctg ccc cac gtg gcg cgc ctc tgt ctg atc      211
Arg Val Thr Lys Gln Tyr Leu Pro His Val Ala Arg Leu Cys Leu Ile
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Ser Thr Phe Leu Glu Asp Gly Ile Arg Met Trp Phe Gln Trp Ser Glu
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Gln Arg Asp Tyr Ile Asp Thr Thr Trp Asn Cys Gly Tyr Leu Leu Ala
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Ser Ser Phe Val Phe Leu Asn Leu Leu Gly Gln Leu Thr Gly Cys Val
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Leu Val Leu Ser Arg Asn Phe Val Gln Tyr Ala Cys Phe Gly Leu Phe
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gga atc ata gct ctg cag acg att gcc tac agc att tta tgg gac ttg      451
Gly Ile Ile Ala Leu Gln Thr Ile Ala Tyr Ser Ile Leu Trp Asp Leu
      100                      105                      110

aag ttt ttg atg agg aac ctg gcc ctg gga gga ggc ctg ttg ctg ctc      499
Lys Phe Leu Met Arg Asn Leu Ala Leu Gly Gly Gly Leu Leu Leu Leu
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cta gca gaa tcc cgt tct gaa ggg aag agc atg ttt gcg ggc gtc ccc      547
Leu Ala Glu Ser Arg Ser Glu Gly Lys Ser Met Phe Ala Gly Val Pro
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acc atg cgt gag agc tcc ccc aaa cag tac atg cag ctc gga ggc agg      595
Thr Met Arg Glu Ser Ser Pro Lys Gln Tyr Met Gln Leu Gly Gly Arg
      150                      155                      160

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Val Leu Leu Val Leu Met Phe Met Thr Leu Leu His Phe Asp Ala Ser
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ttc ttt tct att gtc cag aac atc gtg ggc aca gct ctg atg att tta      691
Phe Phe Ser Ile Val Gln Asn Ile Val Gly Thr Ala Leu Met Ile Leu
      180                      185                      190

gtg gcc att ggt ttt aaa acc aag ctg gct gct ttg act ctt gtt gtg      739
Val Ala Ile Gly Phe Lys Thr Lys Leu Ala Ala Leu Thr Leu Val Val
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tgg ctc ttt gcc atc aac gta tat ttc aac gcc ttc tgg acc att cca      787

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Val	Tyr	Lys	Pro	Met	His	Asp	Phe	Leu	Lys	Tyr	Asp	Phe	Phe	Gln	Thr	
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Met	Ser	Val	Ile	Gly	Gly	Leu	Leu	Leu	Val	Val	Ala	Leu	Gly	Pro	Gly	
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Gly	Val	Ser	Met	Asp	Glu	Lys	Lys	Lys	Glu	Trp	*					
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 cagcgcaact ttatatgaat taatactcaa gataactttt attgcttggt ttggtaagta 420  
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                   Met Leu Gly Leu Gln Thr Gln Val Tyr Leu Met Leu  
                   1                  5                  10  
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 Asp Leu His Leu Leu Ser His Cys Val Thr Leu Ser Leu Arg Arg Val  
                   15                  20                  25  
 agg ttg tgg gtg tca aga cta caa agg caa gta aca cac gtg aga agc 625  
 Arg Leu Trp Val Ser Arg Leu Gln Arg Gln Val Thr His Val Arg Ser  
                   30                  35                  40  
 tca ggc cag aat cag aga gaa gga tgg tca aga gtt ttg gag atg agg 673  
 Ser Gly Gln Asn Gln Arg Glu Gly Trp Ser Arg Val Leu Glu Met Arg  
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                   Met Thr Thr Asn Ala Gly Pro Leu His Pro Tyr Trp Pro  
                   1                  5                  10  
 cag cac cta aga ctg gac aac ttt gta cct aat gac cgc ccc acc tgg 218  
 Gln His Leu Arg Leu Asp Asn Phe Val Pro Asn Asp Arg Pro Thr Trp  
                   15                  20                  25  
 cat ata ctg gct ggc ctc ttc tct gtc aca ggg gtc tta gtc gtg acc 266  
 His Ile Leu Ala Gly Leu Phe Ser Val Thr Gly Val Leu Val Val Thr  
                   30                  35                  40                  45  
 aca tgg ctg ttg tca ggt cgt gct gcg gtt gtc cca ttg ggg act tgg 314  
 Thr Trp Leu Leu Ser Gly Arg Ala Ala Val Val Pro Leu Gly Thr Trp  
                   50                  55                  60  
 cgg cga ctg tcc ctg tgc tgg ttt gca gtg tgt ggg ttc att cac ctg 362

Arg	Arg	Leu	Ser	Leu	Cys	Trp	Phe	Ala	Val	Cys	Gly	Phe	Ile	His	Leu	
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Val	Ile	Glu	Gly	Trp	Phe	Val	Leu	Tyr	Tyr	Glu	Asp	Leu	Leu	Gly	Asp	
		80					85					90				
caa	gcc	ttc	tta	tct	caa	ctc	tgg	aaa	gag	tat	gcc	aag	gga	gac	agc	458
Gln	Ala	Phe	Leu	Ser	Gln	Leu	Trp	Lys	Glu	Tyr	Ala	Lys	Gly	Asp	Ser	
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cga	tac	atc	ctg	ggt	gac	aac	ttc	aca	gtg	tgc	atg	gaa	acc	atc	aca	506
Arg	Tyr	Ile	Leu	Gly	Asp	Asn	Phe	Thr	Val	Cys	Met	Glu	Thr	Ile	Thr	
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gct	tgc	ctg	tgg	gga	cca	ctc	agc	ctg	tgg	gtg	gtg	atc	gcc	ttt	ctc	554
Ala	Cys	Leu	Trp	Gly	Pro	Leu	Ser	Leu	Trp	Val	Val	Ile	Ala	Phe	Leu	
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cgc	cag	cat	ccc	ctc	cgc	ttc	att	cta	cag	ctt	gtg	gtc	tct	gtg	ggc	602
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Gln	Ile	Tyr	Gly	Asp	Val	Leu	Tyr	Phe	Leu	Thr	Glu	His	Arg	Asp	Gly	
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Phe	Gln	His	Gly	Glu	Leu	Gly	His	Pro	Leu	Tyr	Phe	Trp	Phe	Tyr	Phe	
	175					180					185					
gtc	ttc	atg	aat	gcc	ctg	tgg	ctg	gtg	ctg	cct	gga	gtc	ctt	gtg	ctt	746
Val	Phe	Met	Asn	Ala	Leu	Trp	Leu	Val	Leu	Pro	Gly	Val	Leu	Val	Leu	
190					195					200					205	
gat	gct	gtg	aag	cac	ctc	act	cat	gcc	cag	agc	acg	ctg	gat	gcc	aag	794
Asp	Ala	Val	Lys	His	Leu	Thr	His	Ala	Gln	Ser	Thr	Leu	Asp	Ala	Lys	
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gcc	aca	aaa	gcc	aag	agc	aag	aag	aac	tga	g	gagtgggtgga	ccaggctcga				845
Ala	Thr	Lys	Ala	Lys	Ser	Lys	Lys	Asn	*							
			225					230								
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 atg tca tat tta gat tca gtt gca tca aag tta ttg caa atg gtg aaa 164  
 Met Ser Tyr Leu Asp Ser Val Ala Ser Lys Leu Leu Gln Met Val Lys  
 1 5 10 15  
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 Lys Leu Ser Gln Ser Phe Cys Ser Asn Phe Lys Tyr Leu Thr Lys Tyr  
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 tca aga aaa cag gtt tct gat gaa atc aaa aag tca aga aga act gtg 260  
 Ser Arg Lys Gln Val Ser Asp Glu Ile Lys Lys Ser Arg Arg Thr Val  
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 gaa tca aat cct ata ttt ttc aag aag aac aag aaa ata cag tga gga 308  
 Glu Ser Asn Pro Ile Phe Phe Lys Lys Asn Lys Lys Ile Gln \*  
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817

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 Met Ile Ile Lys Cys Lys Ile Leu Leu Phe Leu Leu Asp Ser  
 1 5 10  
 tgt tat atc atg att att gtg cta cag ttt att gtg cat aat atg aaa 1177  
 Cys Tyr Ile Met Ile Ile Val Leu Gln Phe Ile Val His Asn Met Lys  
 15 20 25 30  
 aac aac tat gac agc ctt cag tcg ggc cag ggt gaa gct gct tat acc 1225  
 Asn Asn Tyr Asp Ser Leu Gln Ser Gly Gln Gly Glu Ala Ala Tyr Thr  
 35 40 45  
 acc tct gcc gtc aga ggg aca tgt ggt gac agc agt ggt gtg gct gca 1273  
 Thr Ser Ala Val Arg Gly Thr Cys Gly Asp Ser Ser Gly Val Ala Ala  
 50 55 60  
 cag ggc gca cta gag aga gct cag cac ccc tgc tgc ccg cca gca gag 1321  
 Gln Gly Ala Leu Glu Arg Ala Gln His Pro Cys Cys Pro Pro Ala Glu  
 65 70 75  
 ccc gtg ctg agg gaa tgc cgc aca gat gct gat gca ctg ggt gaa att 1369  
 Pro Val Leu Arg Glu Cys Arg Thr Asp Ala Asp Ala Leu Gly Glu Ile  
 80 85 90  
 tct agt att gaa cgt aaa ggt gta cag tgt ctt gct gtt att tta tga 1417  
 Ser Ser Ile Glu Arg Lys Gly Val Gln Cys Leu Ala Val Ile Leu \*  
 95 100 105 110  
 tggaaactga ttttgaaacc aaaaatagct aactaacttt atttaaggaa aggatattaa 1477  
 tttgtactaa cagaggggtga aagctgttca catttgtcaa caaatctgc ttgctgcagt 1537  
 agtaacctca agtggttaaa acttgatttc ccgagaaaac taaaaccttt gtgcctaaaa 1597  
 ttgatgactt gagttcaagt gggatgagca agaagatgtg ttatcttggt gttcaacagt 1657  
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aaaa

1721

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<220>  
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<400> 321

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ttgggtctctg caagtggctc tcagcccctt cttcttttct gcctcacctt ccaattcggt      120
tgccgcgcgcc gtcccgccagc tgctgtttcc ggagttgccc cttcccatg ttccggggca      180
ggagtccgca aagcgaagat ccgcccgcgc gttcctcatc  atg tcc gaa ctg act      235
                                         Met Ser Glu Leu Thr
                                         1             5

aaa gag ctg atg gag ctg gtg tgg ggc acc aag agc agc ccc ggt ctc      283
Lys Glu Leu Met Glu Leu Val Trp Gly Thr Lys Ser Ser Pro Gly Leu
                        10             15             20

tcg gac acc att ttc tgc cgc tgg acg caa ggg ttt gtg ttt agt gaa      331
Ser Asp Thr Ile Phe Cys Arg Trp Thr Gln Gly Phe Val Phe Ser Glu
                        25             30             35

tca gag gga tct gca tta gaa cag ttt gaa ggt ggc ccc tgt gct gtt      379
Ser Glu Gly Ser Ala Leu Glu Gln Phe Glu Gly Gly Pro Cys Ala Val
                        40             45             50

att gca cct gtt cag gca ttt ctt ttg aag aag ctc ctg ttt tct tcg      427
Ile Ala Pro Val Gln Ala Phe Leu Leu Lys Lys Leu Leu Phe Ser Ser
                        55             60             65

gag aag tct tct tgg cgg gat tgt tca gag gaa gag cag aag gaa ctc      475
Glu Lys Ser Ser Trp Arg Asp Cys Ser Glu Glu Glu Gln Lys Glu Leu
                        70             75             80             85

ctt tgt cat acc ttg tgt gat att tta gaa agt gct tgt tgt gac cac      523
Leu Cys His Thr Leu Cys Asp Ile Leu Glu Ser Ala Cys Cys Asp His
                        90             95             100

tct gga tca tac tgc ttg gtt tca tgg tta aga gga aag aca act gag      571
Ser Gly Ser Tyr Cys Leu Val Ser Trp Leu Arg Gly Lys Thr Thr Glu
                        105             110             115

gaa act gct agt att tct ggg agt cct gca gag tct agt tgc caa gtg      619
Glu Thr Ala Ser Ile Ser Gly Ser Pro Ala Glu Ser Ser Cys Gln Val
                        120             125             130

gaa cat tct tct gcc ttg gct gtc gaa gag ctt ggc ttt gag cga ttt      667
Glu His Ser Ser Ala Leu Ala Val Glu Glu Leu Gly Phe Glu Arg Phe
                        135             140             145

cat gca tta att caa aaa aga tcg ttc aga agt tta cca gaa tta aaa      715
His Ala Leu Ile Gln Lys Arg Ser Phe Arg Ser Leu Pro Glu Leu Lys

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150	155	160	165	
gat gct gtc ttg gac cag tat tca atg tgg gga aat aaa ttt gga gta				763
Asp Ala Val Leu Asp Gln Tyr Ser Met Trp Gly Asn Lys Phe Gly Val				
	170	175	180	
ttg ctt ttt ctg tat tct gta tta ctg aca aag ggc att gaa aac ata				811
Leu Leu Phe Leu Tyr Ser Val Leu Leu Thr Lys Gly Ile Glu Asn Ile				
	185	190	195	
aaa aac gaa att gaa gat gca agt gaa ccc ttg ata gat cct gta tat				859
Lys Asn Glu Ile Glu Asp Ala Ser Glu Pro Leu Ile Asp Pro Val Tyr				
	200	205	210	
gga cat ggc agc caa agt tta att aat ctc ctg ctg acg gga cat gct				907
Gly His Gly Ser Gln Ser Leu Ile Asn Leu Leu Leu Thr Gly His Ala				
	215	220	225	
gtt tct aat gta tgg gat ggt gat aga gag tgc tca gga atg aaa ctt				955
Val Ser Asn Val Trp Asp Gly Asp Arg Glu Cys Ser Gly Met Lys Leu				
	230	235	240	245
ctt ggt ata cat gaa caa gca gca gta gga ttt tta aca cta atg gaa				1003
Leu Gly Ile His Glu Gln Ala Ala Val Gly Phe Leu Thr Leu Met Glu				
	250	255	260	
gct tta aga tac tgt aag gtt ggt tct tac ttg aaa tct cca aaa ttc				1051
Ala Leu Arg Tyr Cys Lys Val Gly Ser Tyr Leu Lys Ser Pro Lys Phe				
	265	270	275	
cct att tgg att gtt ggc agt gag act cac ctc acc gta ttt ttt gcc				1099
Pro Ile Trp Ile Val Gly Ser Glu Thr His Leu Thr Val Phe Phe Ala				
	280	285	290	
aag gat atg gct tta gtt gcc cct gaa gct cct tca gaa caa gcc aga				1147
Lys Asp Met Ala Leu Val Ala Pro Glu Ala Pro Ser Glu Gln Ala Arg				
	295	300	305	
aga gtt ttt caa acc tac gac cca gaa gat aat gga ttc ata ccc gat				1195
Arg Val Phe Gln Thr Tyr Asp Pro Glu Asp Asn Gly Phe Ile Pro Asp				
	310	315	320	325
tca ctt ctg gaa gat gtg atg aaa gca ttg gac ctt gtt tca gat cct				1243
Ser Leu Leu Glu Asp Val Met Lys Ala Leu Asp Leu Val Ser Asp Pro				
	330	335	340	
gaa tat ata aat ctc atg aag aat aaa tta gat cca gaa gga tta gga				1291
Glu Tyr Ile Asn Leu Met Lys Asn Lys Leu Asp Pro Glu Gly Leu Gly				
	345	350	355	
atc ata tta ttg ggc cca ttt ctt caa gaa ttt ttt cct gat cag ggc				1339
Ile Ile Leu Leu Gly Pro Phe Leu Gln Glu Phe Phe Pro Asp Gln Gly				
	360	365	370	
tcc agt ggt cca gaa tct ttt act gtc tac cac tac aat gga ttg aag				1387
Ser Ser Gly Pro Glu Ser Phe Thr Val Tyr His Tyr Asn Gly Leu Lys				
	375	380	385	
cag tca aat tat aat gaa aag gtc atg tac gta gaa ggg act gca gtt				1435
Gln Ser Asn Tyr Asn Glu Lys Val Met Tyr Val Glu Gly Thr Ala Val				
	390	395	400	405
gtg atg ggt ttt gaa gat ccc atg cta cag aca gat gac act cct att				1483
Val Met Gly Phe Glu Asp Pro Met Leu Gln Thr Asp Asp Thr Pro Ile				

	410	415	420	
aaa cgc tgt ctg caa acc aaa tgg cca tac att gag tta ctc tgg acc				1531
Lys Arg Cys Leu Gln Thr Lys Trp Pro Tyr Ile Glu Leu Leu Trp Thr				
	425	430	435	
aca gat cgc tct cct tca cta aat taa tttgt ctaagtattt ataaggaaga				1583
Thr Asp Arg Ser Pro Ser Leu Asn *				
	440	445		
tcttaataac agatgttgaa agaaggagtc aagactggca attggctgga ttaagctaaa				1643
cactggtatc actgattaac tgtaaataac aattaaaaac acattttcag tgttttaaaaa				1703
aaaaa				1708

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<220>  
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tctggcccg cgaagttaag caaccaagag gcgggcctaa gaccggaagc aggaaggagg	180
gcgcaggaag cagggcgccg cagcctgtcg tacggtcctt ctgtgggtct gtcggtgccg	240
agggcagg atg gag aag ctg cgg ctc ctg ggc ctc cgc tac cag gag tac	290
Met Glu Lys Leu Arg Leu Leu Gly Leu Arg Tyr Gln Glu Tyr	
1 5 10	
gtg act cgt cac ccg gcc gcc acg gcc cag ctg gag aca gca gtg cgg	338
Val Thr Arg His Pro Ala Ala Thr Ala Gln Leu Glu Thr Ala Val Arg	
15 20 25 30	
ggc ttc agt tac ctg ctg gca ggt cga ttc gcc gat tcg cac gag ctg	386
Gly Phe Ser Tyr Leu Leu Ala Gly Arg Phe Ala Asp Ser His Glu Leu	
35 40 45	
tca gag ctg gtg tac tct gcc tct aac ctg ctt gtg ctg ctc aat gac	434
Ser Glu Leu Val Tyr Ser Ala Ser Asn Leu Leu Val Leu Leu Asn Asp	
50 55 60	
ggg atc cta cgg aag gag ctt cgg aaa aag ttg cct gtg tcg ctg tcc	482
Gly Ile Leu Arg Lys Glu Leu Arg Lys Lys Leu Pro Val Ser Leu Ser	
65 70 75	
cag cag aag ctg ctg aca tgg ctg agc gtg ctg gag tgc gtg gag gtg	530
Gln Gln Lys Leu Leu Thr Trp Leu Ser Val Leu Glu Cys Val Glu Val	
80 85 90	
ttc atg gag atg gga gct gcc aag gtg tgg ggt gaa gtg ggc cgc tgg	578
Phe Met Glu Met Gly Ala Ala Lys Val Trp Gly Glu Val Gly Arg Trp	
95 100 105 110	

ctt gtc atc gcc ctc atc cag ctg gcc aag gct gta ctg cgg atg ctc Leu Val Ile Ala Leu Ile Gln Leu Ala Lys Ala Val Leu Arg Met Leu 115 120 125	626
ctg ctg ctc tgg ttc aag gct ggc ctc cag act tca ccc cct atc gtt Leu Leu Leu Trp Phe Lys Ala Gly Leu Gln Thr Ser Pro Pro Ile Val 130 135 140	674
cca ctg gac aga gag acc cag gca cag ccc ccg gat ggt gac cac agc Pro Leu Asp Arg Glu Thr Gln Ala Gln Pro Pro Asp Gly Asp His Ser 145 150 155	722
cct ggc aac cat gag cag tcc tac gtg ggg aag cgg tca aac cgg gtg Pro Gly Asn His Glu Gln Ser Tyr Val Gly Lys Arg Ser Asn Arg Val 160 165 170	770
gtg cga acc ctc cag aac acg ccg tcc ctg cac tcc agg cac tgg gga Val Arg Thr Leu Gln Asn Thr Pro Ser Leu His Ser Arg His Trp Gly 175 180 185 190	818
gct ccc cag cag cgg gag gga cgg cag cag cag cat cac gag gag ctg Ala Pro Gln Gln Arg Glu Gly Arg Gln Gln Gln His His Glu Glu Leu 195 200 205	866
agt gcg acc ccc acc ccc ctg ggg ctg cag gag acc atc gca gag ttt Ser Ala Thr Pro Thr Pro Leu Gly Leu Gln Glu Thr Ile Ala Glu Phe 210 215 220	914
ttg tac att gcc cgg ccg ctg ctg cac ttg ctc agc ctg ggc ctg tgg Leu Tyr Ile Ala Arg Pro Leu Leu His Leu Leu Ser Leu Gly Leu Trp 225 230 235	962
ggt cag agg tcg tgg aaa ccc tgg ctc ttg gct ggt gtt gtg gac gtg Gly Gln Arg Ser Trp Lys Pro Trp Leu Leu Ala Gly Val Val Asp Val 240 245 250	1010
acc agc ctg agc ctc ctg agt gac aga aag ggc ctg acc cgg agg gag Thr Ser Leu Ser Leu Leu Ser Asp Arg Lys Gly Leu Thr Arg Arg Glu 255 260 265 270	1058
cgg cgg gag ctg cgg cgc cgg acc atc ctg ctg ctc tac tac ctg ctg Arg Arg Glu Leu Arg Arg Arg Thr Ile Leu Leu Leu Tyr Tyr Leu Leu 275 280 285	1106
cgc tct cct ttc tac gac cgc ttc tcc gag gcc agg atc ctc ttc ctg Arg Ser Pro Phe Tyr Asp Arg Phe Ser Glu Ala Arg Ile Leu Phe Leu 290 295 300	1154
ctc cag ttg ctg gcc gac cac gtc cct ggc gtt ggc ctg gtc aca agg Leu Gln Leu Leu Ala Asp His Val Pro Gly Val Gly Leu Val Thr Arg 305 310 315	1202
ccg ctc atg gat tac ttg ccc acc tgg cag aaa atc tac ttc tac agt Pro Leu Met Asp Tyr Leu Pro Thr Trp Gln Lys Ile Tyr Phe Tyr Ser 320 325 330	1250
tgg ggc tga cagacct cccggaagga ggggtgtgggg aggggtgggg cagggagccc Trp Gly * 335	1306
ctcttcctta ataaaactga ctccggcagc gaaaaaaaaa a	1347

<400> 323

824

cgggtggtgct cctgaatgtg gctgacctgg gctgctgggt ccgttgacta gggatcatctt 1048  
 gatctctgca gtttgcctca gctaccagtt tctttaggca gctctttgtc ctccctctgc 1108  
 ccagattttg atgtagtcta attgacatcc ttctcttccc aacttttgtg tgatctttta 1168  
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 <212> DNA  
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 <222> (444) .. (602)

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 acggtagtgg aggagactgt gagagaggat gcctcctccc caggagcata tggcttecta 120  
 ttaactgaag aactgcaggt tgcaggtgtg tggcatgcac gaggagtctg gcgtctgctc 180  
 ccgttttgac taatagaacc taaaggagct taagaaatca ggtgaatgtg aatcagcttt 240  
 gcacacgtct tttaaattga ttatctttat gtttaggctc taaacaggat tactttatcg 300  
 gcgtcgctaa tagcagttca tttattaagt tgattatcaa taatccctga caaatgagtc 360  
 ataagacgat ggttttatcc attcatccag tgtgtgagga gcacatataa tgcctcacag 420  
 tgaaggcgca atggcaatga taa atg aga cag ctc ttg ctt tca aag gct 470  
 Met Arg Gln Leu Leu Leu Ser Lys Ala  
 1 5  
 ata ggg act ctc ggg aaa gca aac agg cat gtg gta gag aca agc acg 518  
 Ile Gly Thr Leu Gly Lys Ala Asn Arg His Val Val Glu Thr Ser Thr  
 10 15 20 25  
 agc agt gag gaa ata tgc tgc agg gga cgt aac tcc agg gag cct tcc 566  
 Ser Ser Glu Glu Ile Cys Cys Arg Gly Arg Asn Ser Arg Glu Pro Ser  
 30 35 40  
 cag agg agg caa tca gag ctg ggc atg gaa gga tga ccgg cagcaaggag 616  
 Gln Arg Arg Gln Ser Glu Leu Gly Met Glu Gly \*  
 45 50  
 gagacggtga acagccgact tcaagtcaga ggagc 651

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (125) .. (2272)



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gctgggggtg gagccggagg aggaaggcgg cggcgacgac gaggaagacg ccgaggcctg      120

ggcc atg gaa ctg gcg gac gtg ggg gcg gca gcc agc tcg cag gga gtt      169
  Met Glu Leu Ala Asp Val Gly Ala Ala Ala Ser Ser Gln Gly Val
    1             5             10             15

cat gat caa gtg ttg ccc aca cca aat gct tca tcc aga gtc ata gta      217
His Asp Gln Val Leu Pro Thr Pro Asn Ala Ser Ser Arg Val Ile Val
          20             25             30

cat gtg gat ctg gat tgc ttt tat gca caa gta gaa atg atc tca aat      265
His Val Asp Leu Asp Cys Phe Tyr Ala Gln Val Glu Met Ile Ser Asn
          35             40             45

cca gag cta aaa gac aaa cct tta ggg gtt caa cag aaa tat ttg gtg      313
Pro Glu Leu Lys Asp Lys Pro Leu Gly Val Gln Gln Lys Tyr Leu Val
          50             55             60

gtt acc tgc aac tat gaa gct agg aaa ctt gga gtt aag aaa ctt atg      361
Val Thr Cys Asn Tyr Glu Ala Arg Lys Leu Gly Val Lys Lys Leu Met
          65             70             75

aat gtc aga gat gca aaa gaa aag tgt cca cag ttg gta tta gtt aat      409
Asn Val Arg Asp Ala Lys Glu Lys Cys Pro Gln Leu Val Leu Val Asn
          80             85             90             95

gga gaa gac ctg acc cgc tac aga gaa atg tct tat aag gtt aca gaa      457
Gly Glu Asp Leu Thr Arg Tyr Arg Glu Met Ser Tyr Lys Val Thr Glu
          100             105             110

tta ctg gaa gaa ttt agt cca gtt gtt gag aga ctt gga ttt gat gaa      505
Leu Leu Glu Glu Phe Ser Pro Val Val Glu Arg Leu Gly Phe Asp Glu
          115             120             125

aat ttt gtg gat cta aca gaa atg gtt gag agg aga cta cag cag ctg      553
Asn Phe Val Asp Leu Thr Glu Met Val Glu Arg Arg Leu Gln Gln Leu
          130             135             140

caa agt gat gaa ctt tct gcg gtg act gtg tcg ggt cat gta tac aat      601
Gln Ser Asp Glu Leu Ser Ala Val Thr Val Ser Gly His Val Tyr Asn
          145             150             155

aat cag tct ata aac ctg ctt gac gtc ttg cac atc aga cta ctt gtt      649
Asn Gln Ser Ile Asn Leu Leu Asp Val Leu His Ile Arg Leu Leu Val
          160             165             170             175

gga tct cag att gca gca gag atg cgg gaa gcc atg tat aat cag ttg      697
Gly Ser Gln Ile Ala Ala Glu Met Arg Glu Ala Met Tyr Asn Gln Leu
          180             185             190

ggg ctc act ggc tgt gct gga gtg gct tct aat aaa ctg ttg gca aaa      745
Gly Leu Thr Gly Cys Ala Gly Val Ala Ser Asn Lys Leu Leu Ala Lys
          195             200             205

tta gtt tct ggt gtc ttt aaa cca aat caa caa aca gtc tta tta cct      793
Leu Val Ser Gly Val Phe Lys Pro Asn Gln Gln Thr Val Leu Leu Pro
          210             215             220

gaa agt tgt caa cat ctt att cat agt ttg aat cac ata aag gaa ata      841
Glu Ser Cys Gln His Leu Ile His Ser Leu Asn His Ile Lys Glu Ile

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225	230	235	
cct ggt att ggc tat aaa act gcc aaa tgt ctt gaa gca ctg ggt atc			889
Pro Gly Ile Gly Tyr Lys Thr Ala Lys Cys Leu Glu Ala Leu Gly Ile			
240	245	250	255
aat agt gtg cgt gat ctc caa acc ttt tca ccc aaa att tta gaa aaa			937
Asn Ser Val Arg Asp Leu Gln Thr Phe Ser Pro Lys Ile Leu Glu Lys			
	260	265	270
gaa tta gga att tca gtt gct cag cgt atc caa aag ctc agt ttt gga			985
Glu Leu Gly Ile Ser Val Ala Gln Arg Ile Gln Lys Leu Ser Phe Gly			
	275	280	285
gag gat aac tcc cct gtg ata ctc tca gga cca cct cag tcc ttt agt			1033
Glu Asp Asn Ser Pro Val Ile Leu Ser Gly Pro Pro Gln Ser Phe Ser			
	290	295	300
gaa gaa gat tca ttt aaa aaa tgt tca tct gaa gtt gaa gct aaa aat			1081
Glu Glu Asp Ser Phe Lys Lys Cys Ser Ser Glu Val Glu Ala Lys Asn			
	305	310	315
aag att gaa gaa cta ctt gct agt ctt tta aac aga gta tgc caa gat			1129
Lys Ile Glu Glu Leu Leu Ala Ser Leu Leu Asn Arg Val Cys Gln Asp			
	320	325	330
gga agg aag cct cat aca gtg aga tta ata atc cgt cgg tat tcc tct			1177
Gly Arg Lys Pro His Thr Val Arg Leu Ile Ile Arg Arg Tyr Ser Ser			
	340	345	350
gag aag cac tat ggt cgt gag agt cgt cag tgc cct att cct tca cat			1225
Glu Lys His Tyr Gly Arg Glu Ser Arg Gln Cys Pro Ile Pro Ser His			
	355	360	365
gta att cag aaa tta ggg aca gga aat tat gat gtg atg acc cca atg			1273
Val Ile Gln Lys Leu Gly Thr Gly Asn Tyr Asp Val Met Thr Pro Met			
	370	375	380
gtt gat ata ctt atg aaa ctt ttt cga aat atg gtg aat gtg aag atg			1321
Val Asp Ile Leu Met Lys Leu Phe Arg Asn Met Val Asn Val Lys Met			
	385	390	395
cca ttt cac ctt acc ctt cta agt gtg tgc ttc tgc aac ctt aaa gca			1369
Pro Phe His Leu Thr Leu Leu Ser Val Cys Phe Cys Asn Leu Lys Ala			
	400	405	410
cta aat act gct aag aaa ggg ctt att gat tat tat tta atg cca tca			1417
Leu Asn Thr Ala Lys Lys Gly Leu Ile Asp Tyr Tyr Leu Met Pro Ser			
	420	425	430
tta tca act act tca cgc tct ggc aag cac agt ttt aaa atg aaa gac			1465
Leu Ser Thr Thr Ser Arg Ser Gly Lys His Ser Phe Lys Met Lys Asp			
	435	440	445
act cat atg gaa gat ttt ccc aaa gac aaa gaa aca aac cgg gat ttc			1513
Thr His Met Glu Asp Phe Pro Lys Asp Lys Glu Thr Asn Arg Asp Phe			
	450	455	460
cta cca agt gga aga att gaa agt aca aga act agg gag tct cca cta			1561
Leu Pro Ser Gly Arg Ile Glu Ser Thr Arg Thr Arg Glu Ser Pro Leu			
	465	470	475
gat acc aca aat ttt tct aaa gaa aaa gac att aat gaa ttc cca ctc			1609
Asp Thr Thr Asn Phe Ser Lys Glu Lys Asp Ile Asn Glu Phe Pro Leu			

480	485	490	495	
tgt tca ctt cct gaa ggt gtt gac caa gaa gtc ttc aag cag ctt cca				1657
Cys Ser Leu Pro Glu Gly Val Asp Gln Glu Val Phe Lys Gln Leu Pro				
500		505	510	
gta gat att caa gaa gaa atc ctt tct gga aaa tct agg gaa aaa ttt				1705
Val Asp Ile Gln Glu Glu Ile Leu Ser Gly Lys Ser Arg Glu Lys Phe				
515		520	525	
caa ggg aaa gga agt gtg agt tgt cca tta cat gcc tct aga gga gta				1753
Gln Gly Lys Gly Ser Val Ser Cys Pro Leu His Ala Ser Arg Gly Val				
530		535	540	
tta tct ttc ttt tct aaa aaa caa atg caa gat att ccc ata aat cct				1801
Leu Ser Phe Phe Ser Lys Lys Gln Met Gln Asp Ile Pro Ile Asn Pro				
545		550	555	
aga gat cat tta tcc agt agc aaa cag gta tcc tct gta tct cct tgt				1849
Arg Asp His Leu Ser Ser Ser Lys Gln Val Ser Ser Val Ser Pro Cys				
560		565	570	575
gaa ccg gga aca tca ggc ttt aat agc agt agt tct tct tac atg tct				1897
Glu Pro Gly Thr Ser Gly Phe Asn Ser Ser Ser Ser Ser Tyr Met Ser				
580		585	590	
agc caa aag gat tat tca tat tat tta gat aat aga tta aaa gat gaa				1945
Ser Gln Lys Asp Tyr Ser Tyr Tyr Leu Asp Asn Arg Leu Lys Asp Glu				
595		600	605	
cga ata agt caa gga cct aaa gaa cct caa gga ttc cac ttt aca aat				1993
Arg Ile Ser Gln Gly Pro Lys Glu Pro Gln Gly Phe His Phe Thr Asn				
610		615	620	
tca aac cct gct gtg tct gct ttt cat tca ttt cca aac ttg cag agt				2041
Ser Asn Pro Ala Val Ser Ala Phe His Ser Phe Pro Asn Leu Gln Ser				
625		630	635	
gag caa ctt ttc tcc aga aac cac act aca gat agc cat aag caa aca				2089
Glu Gln Leu Phe Ser Arg Asn His Thr Thr Asp Ser His Lys Gln Thr				
640		645	650	655
gta gca aca gac tct cat gaa gga ctt aca gaa aat aga gag cca gat				2137
Val Ala Thr Asp Ser His Glu Gly Leu Thr Glu Asn Arg Glu Pro Asp				
660		665	670	
tct gtt gat gag aaa att act ttc cct tct gac att gat cct caa gtt				2185
Ser Val Asp Glu Lys Ile Thr Phe Pro Ser Asp Ile Asp Pro Gln Val				
675		680	685	
ttc tat gaa cta cca gaa gca gta caa aag gaa ctg ctg gca gag tgg				2233
Phe Tyr Glu Leu Pro Glu Ala Val Gln Lys Glu Leu Leu Ala Glu Trp				
690		695	700	
aag aga aca gga tca gat ttc cac att gga cat aaa taa gcatattcag				2282
Lys Arg Thr Gly Ser Asp Phe His Ile Gly His Lys *				
705		710	715	
caaaaaggctc tgaaaagcaa gggaatacca ttatttttcgg attagcgggtt tattaagctc				2342
ttctatatatta aacactaata gatattcaat aacggagtaa actgttccag ataaagcaag				2402
aatagttgca agaagtaa tctggcacia agcgtaaaaa tataacagaa gaaataatgt				2462

aaaatactat cttttatgtc taaagccatt ttatattact tttcaataaa aagaatatca 2522  
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 Met Ala Ala  
 1  
 gag act cgg aac gtg gcc gga gca gag gcc cca ccg ccc cag aag cgc 163  
 Glu Thr Arg Asn Val Ala Gly Ala Glu Ala Pro Pro Pro Gln Lys Arg  
 5 10 15  
 tac tac cgg caa cgt gct cac tcc aac ccc atg gcg gac cac acg ctg 211  
 Tyr Tyr Arg Gln Arg Ala His Ser Asn Pro Met Ala Asp His Thr Leu  
 20 25 30 35  
 cgc tac cct gtg aag cca gag gag atg gac tgg tct gag cta tac cca 259  
 Arg Tyr Pro Val Lys Pro Glu Glu Met Asp Trp Ser Glu Leu Tyr Pro  
 40 45 50  
 gag ttc ttc gct cca ctc act caa aat cag agc cac gat gac cca aag 307  
 Glu Phe Phe Ala Pro Leu Thr Gln Asn Gln Ser His Asp Asp Pro Lys  
 55 60 65  
 gat aag aaa gaa aag aga gct cag gcc caa gtg gag ttt gca gac ata 355  
 Asp Lys Lys Glu Lys Arg Ala Gln Ala Gln Val Glu Phe Ala Asp Ile  
 70 75 80  
 ggc tgt ggc tat ggt ggc ctg tta gtg gaa ctg tca ccg ctg ttc cca 403  
 Gly Cys Gly Tyr Gly Gly Leu Leu Val Glu Leu Ser Pro Leu Phe Pro  
 85 90 95  
 gac aca ctt att ctg ggt ctg gag atc cgg gtg aag gtc tca gac tat 451  
 Asp Thr Leu Ile Leu Gly Leu Glu Ile Arg Val Lys Val Ser Asp Tyr  
 100 105 110 115  
 gta caa gac cgg att cgg gcc cta cgc gca gct cct gca ggt ggc ttc 499  
 Val Gln Asp Arg Ile Arg Ala Leu Arg Ala Ala Pro Ala Gly Gly Phe  
 120 125 130  
 cag aac atc gcc tgt ctc cgt agc aat gcc atg aag cac ctt cct aac 547  
 Gln Asn Ile Ala Cys Leu Arg Ser Asn Ala Met Lys His Leu Pro Asn  
 135 140 145  
 ttc ttc tac aag ggc cag ctg aca aag atg ttc ttc ctc ttc ccc gac 595  
 Phe Phe Tyr Lys Gly Gln Leu Thr Lys Met Phe Phe Leu Phe Pro Asp  
 150 155 160

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cca cat ttc aag cgg aca aag cac aag tgg cga atc atc agt ccc acc      643
Pro His Phe Lys Arg Thr Lys His Lys Trp Arg Ile Ile Ser Pro Thr
      165                      170                      175

ctg cta gca gaa tat gcc tac gtg cta aga gtt ggg gtg agt tgg gat      691
Leu Leu Ala Glu Tyr Ala Tyr Val Leu Arg Val Gly Val Ser Trp Asp
      180                      185                      190                      195

cgg agg gat gat ggg ggg ctg gtg tat acc ata acc gat gtg ctg gag      739
Arg Arg Asp Asp Gly Gly Leu Val Tyr Thr Ile Thr Asp Val Leu Glu
      200                      205                      210

cta cac gac tgg atg tgc act cat ttc gaa gag cac cca ctg ttt gag      787
Leu His Asp Trp Met Cys Thr His Phe Glu Glu His Pro Leu Phe Glu
      215                      220                      225

cgt gtg cct ctg gag gac ctg agt gaa gac ccc gtt gtg gga cat cta      835
Arg Val Pro Leu Glu Asp Leu Ser Glu Asp Pro Val Val Gly His Leu
      230                      235                      240

ggc acc tca act gag gag ggg aag aaa gtt cta cgt aat gga ggg aag      883
Gly Thr Ser Thr Glu Glu Gly Lys Lys Val Leu Arg Asn Gly Gly Lys
      245                      250                      255

aat ttc cca gcc atc ttc cga aga ata caa gat ccc gtc ctc cag gca      931
Asn Phe Pro Ala Ile Phe Arg Arg Ile Gln Asp Pro Val Leu Gln Ala
      260                      265                      270                      275

gtg acc tcc caa acc agc ctg cct ggt cac tga ctgcttac tctaccttag      982
Val Thr Ser Gln Thr Ser Leu Pro Gly His *
      280                      285

ctggacctcg tctcccaggg attagagaaa agagcaggag tcctgggtct tcccagttga      1042

gactgctgga gctgagacac agtactctct taaagaaggt ggggagctgc ccagggcaga      1102

accactggt gttcatgact acccctggct cctctcacct tgtccctcca ctgccaacag      1162

aaaacaaagc agctgactga gatggtcaaa ggactttgga ccatagggga tctttggaag      1222

gctgtggggt cttgctcttc cttagcactc ctttctcctt gtgagatctc tcctcagctg      1282

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cggccgctct agagtatccc tcgagggggc caagcttacg cgtaccacgc tttcttgtag      1462

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 atg gcg agt cca cct agg ggc tgg ggc tgc gga gag ctg ctg ctg ccc 165  
 Met Ala Ser Pro Pro Arg Gly Trp Gly Cys Gly Glu Leu Leu Leu Pro  
 1 5 10 15  
 ttc atg ctc ctg ggg acg ctg tgc gag cca gga tcc ggg cag atc cgc 213  
 Phe Met Leu Leu Gly Thr Leu Cys Glu Pro Gly Ser Gly Gln Ile Arg  
 20 25 30  
 tac tcg atg ccg gag gag ctg gac aaa ggc tcc ttc gtc ggc aac ata 261  
 Tyr Ser Met Pro Glu Glu Leu Asp Lys Gly Ser Phe Val Gly Asn Ile  
 35 40 45  
 gcc aag gac ctt ggg ctg gag ccc cag gag ctg gcg gag cgc gga gtc 309  
 Ala Lys Asp Leu Gly Leu Glu Pro Gln Glu Leu Ala Glu Arg Gly Val  
 50 55 60  
 cgc atc gtc tcc aga ggt agg acg cag ctt ttt gcc ctg aac ccg cga 357  
 Arg Ile Val Ser Arg Gly Arg Thr Gln Leu Phe Ala Leu Asn Pro Arg  
 65 70 75 80  
 agc ggc agc ttg gtc acc gcg ggc agg ata gac cgg gag gag ctc tgc 405  
 Ser Gly Ser Leu Val Thr Ala Gly Arg Ile Asp Arg Glu Glu Leu Cys  
 85 90 95  
 gct cag agc cca ctg tgt gtg gtg aac ttt aac atc ttg gtt gag aac 453  
 Ala Gln Ser Pro Leu Cys Val Val Asn Phe Asn Ile Leu Val Glu Asn  
 100 105 110  
 aaa atg aaa att tat gga gta gaa gta gaa ata atc gat att aat gat 501  
 Lys Met Lys Ile Tyr Gly Val Glu Val Glu Ile Ile Asp Ile Asn Asp  
 115 120 125  
 aac ttc ccg cgt ttc cgg gat gaa gag tta aaa gta aaa gtt aat gaa 549  
 Asn Phe Pro Arg Phe Arg Asp Glu Glu Leu Lys Val Lys Val Asn Glu  
 130 135 140  
 aat gcg gct gca ggg aca cgg tta gtg ctt ccc ttc gcg cgg gat gcg 597  
 Asn Ala Ala Ala Gly Thr Arg Leu Val Leu Pro Phe Ala Arg Asp Ala  
 145 150 155 160  
 gat gtg ggt gtg aac tct ctc cgg agt tac cag ctc agc tcc aat ctg 645  
 Asp Val Gly Val Asn Ser Leu Arg Ser Tyr Gln Leu Ser Ser Asn Leu  
 165 170 175  
 cac ttc tct ctg gat gtg gta agc gga act gat gga caa aag tat ccg 693  
 His Phe Ser Leu Asp Val Val Ser Gly Thr Asp Gly Gln Lys Tyr Pro  
 180 185 190  
 gag ctg gtg ttg gaa cag ccc cta gac cgc gag aaa gag act gtt cac 741  
 Glu Leu Val Leu Glu Gln Pro Leu Asp Arg Glu Lys Glu Thr Val His  
 195 200 205  
 gac ctc ctc ctc aca gct tta gat ggc gga gac ccg gta ctc tcc ggc 789  
 Asp Leu Leu Leu Thr Ala Leu Asp Gly Gly Asp Pro Val Leu Ser Gly  
 210 215 220  
 acc acg cac atc cgt gtt acg gtc ctc gac gca aac gac aat gcg ccc 837  
 Thr Thr His Ile Arg Val Thr Val Leu Asp Ala Asn Asp Asn Ala Pro  
 225 230 235 240  
 ctg ttc acc cca tcc gag tac agc gtg agt gtt cca gag aac ata cct 885



Leu	Phe	Thr	Pro	Ser	Glu	Tyr	Ser	Val	Ser	Val	Pro	Glu	Asn	Ile	Pro	
				245					250					255		
gtg	ggc	act	cgg	ctg	ctc	atg	cta	acc	gcc	acg	gat	cca	gat	gag	gga	933
Val	Gly	Thr	Arg	Leu	Leu	Met	Leu	Thr	Ala	Thr	Asp	Pro	Asp	Glu	Gly	
			260					265					270			
ata	aac	ggg	aaa	ttg	acc	tac	tct	ttt	cgc	aat	gaa	gaa	gaa	aaa	att	981
Ile	Asn	Gly	Lys	Leu	Thr	Tyr	Ser	Phe	Arg	Asn	Glu	Glu	Glu	Lys	Ile	
		275					280					285				
tcg	gag	act	ttc	caa	ctt	gat	tcc	aac	ctg	ggg	gaa	atc	tca	act	cta	1029
Ser	Glu	Thr	Phe	Gln	Leu	Asp	Ser	Asn	Leu	Gly	Glu	Ile	Ser	Thr	Leu	
	290					295				300						
caa	tca	ctg	gac	tat	gaa	gaa	tcc	aga	ttc	tac	ctc	atg	gaa	gtg	gta	1077
Gln	Ser	Leu	Asp	Tyr	Glu	Glu	Ser	Arg	Phe	Tyr	Leu	Met	Glu	Val	Val	
305					310				315						320	
gct	cag	gat	gga	ggc	gct	ctt	ggt	gcc	agc	gct	aag	gtg	gtg	gtc	aca	1125
Ala	Gln	Asp	Gly	Gly	Ala	Leu	Val	Ala	Ser	Ala	Lys	Val	Val	Val	Thr	
			325					330						335		
gta	cag	gac	gtg	aat	gac	aat	gcc	ccc	gaa	gtg	atc	ctc	acc	tct	ctg	1173
Val	Gln	Asp	Val	Asn	Asp	Asn	Ala	Pro	Glu	Val	Ile	Leu	Thr	Ser	Leu	
			340				345						350			
acc	agt	tcg	atc	tct	gaa	gac	tgt	ctt	ccc	gga	act	gta	atc	gcg	ctg	1221
Thr	Ser	Ser	Ile	Ser	Glu	Asp	Cys	Leu	Pro	Gly	Thr	Val	Ile	Ala	Leu	
		355					360					365				
ttt	agc	gta	cat	gat	ggc	gat	tct	gga	gaa	aat	ggc	gag	att	gca	tgc	1269
Phe	Ser	Val	His	Asp	Gly	Asp	Ser	Gly	Glu	Asn	Gly	Glu	Ile	Ala	Cys	
	370					375					380					
tct	att	cct	agg	aat	ttg	cct	ttt	aaa	ttg	gag	aag	tca	gtt	gat	aat	1317
Ser	Ile	Pro	Arg	Asn	Leu	Pro	Phe	Lys	Leu	Glu	Lys	Ser	Val	Asp	Asn	
385					390					395					400	
tac	tat	cac	cta	tta	aca	act	agg	gac	ctg	gac	aga	gaa	gag	act	tca	1365
Tyr	Tyr	His	Leu	Leu	Thr	Thr	Arg	Asp	Leu	Asp	Arg	Glu	Glu	Thr	Ser	
				405					410					415		
gat	tat	aat	atc	act	tta	acc	gtc	atg	gac	cat	gga	acc	ccg	ccc	ctc	1413
Asp	Tyr	Asn	Ile	Thr	Leu	Thr	Val	Met	Asp	His	Gly	Thr	Pro	Pro	Leu	
			420				425						430			
tct	aca	gaa	agc	cac	atc	ccc	ttg	aaa	gta	gca	gac	gtt	aat	gac	aac	1461
Ser	Thr	Glu	Ser	His	Ile	Pro	Leu	Lys	Val	Ala	Asp	Val	Asn	Asp	Asn	
		435					440					445				
cca	ccc	aat	ttc	cct	caa	gcc	tcc	tac	tcc	acc	tct	gtc	aca	gaa	aac	1509
Pro	Pro	Asn	Phe	Pro	Gln	Ala	Ser	Tyr	Ser	Thr	Ser	Val	Thr	Glu	Asn	
		450				455						460				
aat	ccc	aga	ggc	gtc	tct	atc	ttc	tct	gtg	aca	gcc	cat	gac	ccc	gac	1557
Asn	Pro	Arg	Gly	Val	Ser	Ile	Phe	Ser	Val	Thr	Ala	His	Asp	Pro	Asp	
465					470				475						480	
agc	ggc	gac	aac	gct	cga	gtc	acc	tac	tcc	ctg	gct	gaa	gac	aca	ttt	1605
Ser	Gly	Asp	Asn	Ala	Arg	Val	Thr	Tyr	Ser	Leu	Ala	Glu	Asp	Thr	Phe	
				485					490					495		
cag	ggg	gcg	ccc	ttg	tcc	tcc	tat	gta	tcc	att	aac	tct	gac	acc	ggc	1653

Gln Gly Ala	Pro Leu Ser Ser Tyr Val Ser Ile Asn Ser Asp Thr Gly	
500	505	510
gtc ctg tat gct ctg aga tcc ttc gac tat gag cag ttg aga gac cta		1701
Val Leu Tyr Ala Leu Arg Ser Phe Asp Tyr Glu Gln Leu Arg Asp Leu		
515	520	525
cag ttg tgg gtg aca gcc agc gac agt ggg aac cct cca ctt agc agc		1749
Gln Leu Trp Val Thr Ala Ser Asp Ser Gly Asn Pro Pro Leu Ser Ser		
530	535	540
aac gtg tcg ctg agc ctg ttt gtg ctg gac cag aac gac aat acg cct		1797
Asn Val Ser Leu Ser Leu Phe Val Leu Asp Gln Asn Asp Asn Thr Pro		
545	550	560
gag atc ctg tac ccc gcc ctc ccc aca gac ggt tcc acg ggc gtg gag		1845
Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp Gly Ser Thr Gly Val Glu		
565	570	575
ctg gcg cct cgc tcc gca gaa cct ggc tac ctg gtg acc aag gtg gta		1893
Leu Ala Pro Arg Ser Ala Glu Pro Gly Tyr Leu Val Thr Lys Val Val		
580	585	590
gcg gtg gac aaa gat tca ggc cag aac gcc tgg ctg tcc tac cgc ctg		1941
Ala Val Asp Lys Asp Ser Gly Gln Asn Ala Trp Leu Ser Tyr Arg Leu		
595	600	605
ctt aag gcc agc gag cca gga ctc ttt gcg gtt ggg ctg cac acg ggc		1989
Leu Lys Ala Ser Glu Pro Gly Leu Phe Ala Val Gly Leu His Thr Gly		
610	615	620
gag gtg cgc aca gcg cga gcc ctg ctg gac aga gac gcg ctc aag cag		2037
Glu Val Arg Thr Ala Arg Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln		
625	630	640
agc ctc gtg gtg gcc gtc gaa gac cat ggc cag ccc cct ctg tca gcc		2085
Ser Leu Val Val Ala Val Glu Asp His Gly Gln Pro Pro Leu Ser Ala		
645	650	655
acc ttc acg gtc acc gtt gcc gtg gcc gac agg atc cct gac atc ctg		2133
Thr Phe Thr Val Thr Val Ala Val Ala Asp Arg Ile Pro Asp Ile Leu		
660	665	670
gct gac cta ggc agt atc aag acc ccc att gac cct gag gat ctg gac		2181
Ala Asp Leu Gly Ser Ile Lys Thr Pro Ile Asp Pro Glu Asp Leu Asp		
675	680	685
ctc aca ctc tat ctt gtg gtg gca gtg gct gca gtc tcc tgc gtc ttc		2229
Leu Thr Leu Tyr Leu Val Val Ala Val Ala Val Ser Cys Val Phe		
690	695	700
ctg gcc ttc gtc atc gtg ctg ctg gtg ctc aga ctg agg cgc tgg cac		2277
Leu Ala Phe Val Ile Val Leu Leu Val Leu Arg Leu Arg Arg Trp His		
705	710	720
aag tca cgc ctg ctt cag gct gaa ggc agc agg ttg gcg ggt gtg ccc		2325
Lys Ser Arg Leu Leu Gln Ala Glu Gly Ser Arg Leu Ala Gly Val Pro		
725	730	735
gcc tcg cac ttt gtg ggc gtg gat ggg gtt cgg gct ttc ctg cag acc		2373
Ala Ser His Phe Val Gly Val Asp Gly Val Arg Ala Phe Leu Gln Thr		
740	745	750
tat tcc cac gag gtc tcc ctc acc gcg gac tcg agg aag agt cac ctg		2421

Tyr	Ser	His	Glu	Val	Ser	Leu	Thr	Ala	Asp	Ser	Arg	Lys	Ser	His	Leu		
		755					760					765					
atc	ttt	ccc	cag	ccc	aac	tac	gca	gac	acg	ctc	ctt	agt	gaa	gag	agc	2469	
Ile	Phe	Pro	Gln	Pro	Asn	Tyr	Ala	Asp	Thr	Leu	Leu	Ser	Glu	Glu	Ser		
	770					775					780						
tgt	gag	aaa	agc	gag	cct	ctt	ctg	atg	tct	gat	aag	gta	gat	gca	aac	2517	
Cys	Glu	Lys	Ser	Glu	Pro	Leu	Leu	Met	Ser	Asp	Lys	Val	Asp	Ala	Asn		
	785				790					795					800		
aaa	gaa	gaa	cgg	cga	gtt	cag	caa	gcc	ccg	ccc	aac	acg	gac	tgg	cgt	2565	
Lys	Glu	Glu	Arg	Arg	Val	Gln	Gln	Ala	Pro	Pro	Asn	Thr	Asp	Trp	Arg		
				805					810					815			
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Phe	Ser	Gln	Ala	Gln	Arg	Pro	Gly	Thr	Ser	Gly	Ser	Gln	Asn	Gly	Asp		
			820				825						830				
gac	acc	ggc	acc	tgg	ccc	aac	aac	cag	ttt	gac	aca	gag	atg	ctg	caa	2661	
Asp	Thr	Gly	Thr	Trp	Pro	Asn	Asn	Gln	Phe	Asp	Thr	Glu	Met	Leu	Gln		
		835					840					845					
gcc	atg	atc	ttg	gcg	tcc	gcc	agt	gaa	gct	gct	gat	ggg	agc	tcc	acc	2709	
Ala	Met	Ile	Leu	Ala	Ser	Ala	Ser	Glu	Ala	Ala	Asp	Gly	Ser	Ser	Thr		
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ctg	gga	ggg	ggt	gcc	ggc	acc	atg	gga	ttg	agc	gcc	cgc	tac	gga	ccc	2757	
Leu	Gly	Gly	Gly	Ala	Gly	Thr	Met	Gly	Leu	Ser	Ala	Arg	Tyr	Gly	Pro		
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cag	ttc	acc	ctg	cag	cac	gtg	ccc	gac	tac	cgc	cag	aat	gtc	tac	atc	2805	
Gln	Phe	Thr	Leu	Gln	His	Val	Pro	Asp	Tyr	Arg	Gln	Asn	Val	Tyr	Ile		
				885				890					895				
cca	ggc	agc	aat	gcc	aca	ctg	acc	aac	gca	gct	ggc	aag	cgg	gat	ggc	2853	
Pro	Gly	Ser	Asn	Ala	Thr	Leu	Thr	Asn	Ala	Ala	Gly	Lys	Arg	Asp	Gly		
			900					905					910				
aag	gcc	cca	gca	ggt	ggc	aat	ggc	aac	aag	aag	aag	tcg	ggc	aag	aag	2901	
Lys	Ala	Pro	Ala	Gly	Gly	Asn	Gly	Asn	Lys	Lys	Lys	Ser	Gly	Lys	Lys		
	915					920						925					
gag	aag	aag	taa													2913	
Glu	Lys	Lys	*														
	930																

&lt;210&gt; 328

&lt;211&gt; 1347

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;222&gt; (167)..(1291)

&lt;220&gt;

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&lt;223&gt; n = a,t,c or g

&lt;400&gt; 328

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aacctttccc caagctgaag ctgcagggta ttgaggtacc agccag  atg tct tcc      175
                                     Met Ser Ser
                                     1

cac aaa gga tct gtg gtg gca cag ggg aat ggg gct cct gcc agt aac      223
His Lys Gly Ser Val Val Ala Gln Gly Asn Gly Ala Pro Ala Ser Asn
      5                      10                      15

agg gaa gct gac acg gtg gaa ctg gct gaa ctg gga ccc ctg cta gaa      271
Arg Glu Ala Asp Thr Val Glu Leu Ala Glu Leu Gly Pro Leu Leu Glu
      20                      25                      30                      35

gag aag ggc aaa cgg gta atc gcc aac cca ccc aaa gct gaa gaa gag      319
Glu Lys Gly Lys Arg Val Ile Ala Asn Pro Pro Lys Ala Glu Glu Glu
                        40                      45                      50

caa aca tgc cca gtg ccc cag gaa gaa gag gag gag gtg cgg gta ctg      367
Gln Thr Cys Pro Val Pro Gln Glu Glu Glu Glu Glu Val Arg Val Leu
                        55                      60                      65

aca ctt ccc ctg caa gcc cac cac gcc atg gag aag atg gaa gag ttt      415
Thr Leu Pro Leu Gln Ala His His Ala Met Glu Lys Met Glu Glu Phe
      70                      75                      80

gtg tac aag gtc tgg gag gga cgt tgg agg gtc atc cca tat gat gtg      463
Val Tyr Lys Val Trp Glu Gly Arg Trp Arg Val Ile Pro Tyr Asp Val
      85                      90                      95

ctc cct gac tgg cta aag gac aac gac tat ctg cta cat ggt cat aga      511
Leu Pro Asp Trp Leu Lys Asp Asn Asp Tyr Leu Leu His Gly His Arg
      100                      105                      110                      115

cct ccc atg ccc tcc ttt cgg gct tgc ttc aag agc atc ttc cgc att      559
Pro Pro Met Pro Ser Phe Arg Ala Cys Phe Lys Ser Ile Phe Arg Ile
                        120                      125                      130

cat aca gaa act ggc aac atc tgg acc cat ctg ctt ggt ttc gtg ctg      607
His Thr Glu Thr Gly Asn Ile Trp Thr His Leu Leu Gly Phe Val Leu
                        135                      140                      145

ttt ctc ttt ttg gga atc ttg acc atg ctc aga cca aat atg tac ttc      655
Phe Leu Phe Leu Gly Ile Leu Thr Met Leu Arg Pro Asn Met Tyr Phe
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atg gcc cct cta cag gag aag gtg gtt ttt ggg atg ttc ttt ttg ggt      703
Met Ala Pro Leu Gln Glu Lys Val Val Phe Gly Met Phe Phe Leu Gly
      165                      170                      175

gca gtg ctc tgc ctc agc ttc tcc tgg ctc ttt cac acc gtc tat tgt      751
Ala Val Leu Cys Leu Ser Phe Ser Trp Leu Phe His Thr Val Tyr Cys
      180                      185                      190                      195

cat tca gag aaa gtc tct cgg act ttt tcc aaa ctg gac tat tca ggg      799
His Ser Glu Lys Val Ser Arg Thr Phe Ser Lys Leu Asp Tyr Ser Gly
                        200                      205                      210

att gct ctt cta att atg ggg agc ttt gtc ccc tgg ctc tat tat tcc      847
Ile Ala Leu Leu Ile Met Gly Ser Phe Val Pro Trp Leu Tyr Tyr Ser

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215	220	225	
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Phe Tyr Cys Ser Pro Gln Pro Arg Leu Ile Tyr Leu Ser Ile Val Cys			
230	235	240	
gtc ctg ggc att tct gcc atc att gtg gcg cag tgg gac cgg ttt gcc			943
Val Leu Gly Ile Ser Ala Ile Ile Val Ala Gln Trp Asp Arg Phe Ala			
245	250	255	
act cct aag cac cgg cag aca aga gca ggc gtg ttc ctg gga ctt ggc			991
Thr Pro Lys His Arg Gln Thr Arg Ala Gly Val Phe Leu Gly Leu Gly			
260	265	270	275
ttg agt ggc gtc gtg ccc acc atg cac ttt act atc gct gag ggc ttt			1039
Leu Ser Gly Val Val Pro Thr Met His Phe Thr Ile Ala Glu Gly Phe			
280	285	290	
gtc aag gcc acc aca gtg ggc cag atg ggc tgg ttc ttc ctc atg gct			1087
Val Lys Ala Thr Thr Val Gly Gln Met Gly Trp Phe Phe Leu Met Ala			
295	300	305	
gtg atg tac atc act gga gct ggc ctt tat gct gct cga att cct gag			1135
Val Met Tyr Ile Thr Gly Ala Gly Leu Tyr Ala Ala Arg Ile Pro Glu			
310	315	320	
cgc ttc ttt cct gga aaa ttt gac ata tgg ttc cag tct cat cag att			1183
Arg Phe Phe Pro Gly Lys Phe Asp Ile Trp Phe Gln Ser His Gln Ile			
325	330	335	
ttc cat gtc ctg gtg gtg gca gca gcc ttt gtc cac ttc tat gga gtc			1231
Phe His Val Leu Val Val Ala Ala Ala Phe Val His Phe Tyr Gly Val			
340	345	350	355
tcc aac ctt cag gaa ttc cgt tac ggc cta gaa ggc ggc tgt act gat			1279
Ser Asn Leu Gln Glu Phe Arg Tyr Gly Leu Glu Gly Gly Cys Thr Asp			
360	365	370	
gac acc ctt ctc tga gccttccac ctgcggggtg gaggaggaac ttccaagtg			1334
Asp Thr Leu Leu			
375			
ctttttaaaaa taa			1347

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (66)..(539)

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Met Asn Gln Glu Lys Leu Ala Lys Leu Gln Ala Gln Val Arg	
1 5 10	
ata ggg ggc aag ggt aca gct cgc aga aag aag aag gtg gta cat aga	155

Ile	Gly	Gly	Lys	Gly	Thr	Ala	Arg	Arg	Lys	Lys	Lys	Val	Val	His	Arg	
15					20				25					30		
aca	gcc	aca	gct	gat	gac	aaa	aag	ctt	cag	agt	tct	cta	aaa	aaa	ctg	203
Thr	Ala	Thr	Ala	Asp	Asp	Lys	Lys	Leu	Gln	Ser	Ser	Leu	Lys	Lys	Leu	
			35					40					45			
gct	gtg	aat	aat	ata	gct	ggt	att	gaa	gag	gtg	aac	atg	att	aaa	gat	251
Ala	Val	Asn	Asn	Ile	Ala	Gly	Ile	Glu	Glu	Val	Asn	Met	Ile	Lys	Asp	
		50					55					60				
gat	ggg	aca	gtt	att	cat	ttc	aac	aat	ccc	aaa	gtc	caa	gct	tcc	ctt	299
Asp	Gly	Thr	Val	Ile	His	Phe	Asn	Asn	Pro	Lys	Val	Gln	Ala	Ser	Leu	
		65				70					75					
tct	gct	aat	acc	ttt	gca	att	act	ggt	cat	gca	gaa	gcc	aaa	cca	atc	347
Ser	Ala	Asn	Thr	Phe	Ala	Ile	Thr	Gly	His	Ala	Glu	Ala	Lys	Pro	Ile	
	80				85				90							
aca	gaa	atg	ctt	cct	gga	ata	tta	agt	cag	ctt	ggt	gct	gac	agt	tta	395
Thr	Glu	Met	Leu	Pro	Gly	Ile	Leu	Ser	Gln	Leu	Gly	Ala	Asp	Ser	Leu	
	95			100				105						110		
aca	agc	ctt	agg	aag	tta	gct	gaa	cag	ttc	cca	cgg	caa	gtc	ttg	gac	443
Thr	Ser	Leu	Arg	Lys	Leu	Ala	Glu	Gln	Phe	Pro	Arg	Gln	Val	Leu	Asp	
			115					120					125			
agt	aaa	gca	cca	aaa	cca	gaa	gac	att	gat	gag	gaa	gat	gat	gat	gtt	491
Ser	Lys	Ala	Pro	Lys	Pro	Glu	Asp	Ile	Asp	Glu	Glu	Asp	Asp	Asp	Val	
		130					135					140				
cca	gat	ctt	gta	gaa	aat	ttt	gat	gag	gca	tca	aag	aat	gaa	gct	aac	539
Pro	Asp	Leu	Val	Glu	Asn	Phe	Asp	Glu	Ala	Ser	Lys	Asn	Glu	Ala	Asn	
	145				150						155					
taaaagtttg	gttttttgga	gctggcatgg	actagattta	acaaatcagc	tatgtggttc											599
caaagtttta	cagacatgga	gaacatcacc	tggtactagt	tcagtaatat	aaatattttg											659
tatattaata	atgctgtttg	ttcagcattt	ttcggtcatt	tgattttgca	ttttgcactt											719
cctcccagga	tatttttttg	gtcaaaatat	gaagtattgg	tgcaagtttg	gggtgttttg											779
gtttttgatt	cctgggtttt	ttgttttttg	tttgggggat	ttttggtgta	tgtatgttta											839
tgtatgtgtg	tgggtatgtg	tgtatacagt	ggagagcaaa	ttggaaaaca	gttctattta											899
tcctcctccc	tccccagtag	aaataaaaaa	aa													931

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 tccgagcgcc gggctccggg cgccctgccc tgcgcctggg gcagcagcct ttgctgggtct 180  
 tgggggcgcc ccccgcttcc cgccccgggg gtccgcggcc ggcaggacc atg ctg 235  
 Met Leu  
 1  
 ctg aaa gag tac cgg atc tgc atg ccg ctc acc gta gac gag tac aaa 283  
 Leu Lys Glu Tyr Arg Ile Cys Met Pro Leu Thr Val Asp Glu Tyr Lys  
 5 10 15  
 att gga cag ctg tac atg atc agc aaa cac agc cat gaa cag agt gac 331  
 Ile Gly Gln Leu Tyr Met Ile Ser Lys His Ser His Glu Gln Ser Asp  
 20 25 30  
 cgg gga gaa ggg gtg gag gtc gtc cag aat gag ccc ttt gag gac cct 379  
 Arg Gly Glu Gly Val Glu Val Val Gln Asn Glu Pro Phe Glu Asp Pro  
 35 40 45 50  
 cac cat ggc aat ggg cag ttc acc gag aag cgg gtg tat ctc aac agc 427  
 His His Gly Asn Gly Gln Phe Thr Glu Lys Arg Val Tyr Leu Asn Ser  
 55 60 65  
 aaa ctg cct agt tgg gct aga gct gtt gtc ccc aaa ata ttt tat gtg 475  
 Lys Leu Pro Ser Trp Ala Arg Ala Val Val Pro Lys Ile Phe Tyr Val  
 70 75 80  
 aca gag aag gct tgg aac tat tat ccc tac aca att aca gaa tac aca 523  
 Thr Glu Lys Ala Trp Asn Tyr Tyr Pro Tyr Thr Ile Thr Glu Tyr Thr  
 85 90 95  
 tgt tcc ttt ctg ccg aaa ttc tcc att cat ata gaa acc aag tat gag 571  
 Cys Ser Phe Leu Pro Lys Phe Ser Ile His Ile Glu Thr Lys Tyr Glu  
 100 105 110  
 gac aac aaa gga agc aat gac acc att ttc gac aat gaa gcc aaa gac 619  
 Asp Asn Lys Gly Ser Asn Asp Thr Ile Phe Asp Asn Glu Ala Lys Asp  
 115 120 125 130  
 gtg gag aga gaa gtt tgc ttt att gat att gcc tgc gat gaa att cca 667  
 Val Glu Arg Glu Val Cys Phe Ile Asp Ile Ala Cys Asp Glu Ile Pro  
 135 140 145  
 gag cgc tac tac aaa gaa tct gag gat cct aag cac ttc aag tca gag 715  
 Glu Arg Tyr Tyr Lys Glu Ser Glu Asp Pro Lys His Phe Lys Ser Glu  
 150 155 160  
 aag aca gga cgg gga cag ttg agg gaa ggc tgg aga gat agt cat cag 763  
 Lys Thr Gly Arg Gly Gln Leu Arg Glu Gly Trp Arg Asp Ser His Gln  
 165 170 175  
 cct atc atg tgc tcc tac aag ctg gtg act gtg aag ttt gag gtc tgg 811  
 Pro Ile Met Cys Ser Tyr Lys Leu Val Thr Val Lys Phe Glu Val Trp  
 180 185 190  
 ggg ctt cag acc aga gtg gaa caa ttt gta cac aag gtg gtc cga gac 859  
 Gly Leu Gln Thr Arg Val Glu Gln Phe Val His Lys Val Val Arg Asp  
 195 200 205 210  
 att ctg ctg att gga cat aga cag gct ttt gca tgg gtt gat gag tgg 907  
 Ile Leu Leu Ile Gly His Arg Gln Ala Phe Ala Trp Val Asp Glu Trp  
 215 220 225

tat gat atg aca atg gat gat gtt cgg gaa tac gag aaa aac atg cat 955  
 Tyr Asp Met Thr Met Asp Asp Val Arg Glu Tyr Glu Lys Asn Met His  
                   230                  235                  240

gaa caa acc aac ata aaa gtt tgc aat cag cat tcc tcc cct gtg gat 1003  
 Glu Gln Thr Asn Ile Lys Val Cys Asn Gln His Ser Ser Pro Val Asp  
                   245                  250                  255

gac ata gag agt cat gcc caa aca agt aca tga caatggat gaagtccgag 1054  
 Asp Ile Glu Ser His Ala Gln Thr Ser Thr \*  
                   260                  265

aatttgaacg agccactcag gaagccacca acaagaaaat cggcattttc ccacctgcaa 1114

tttctatctc cagcatcccc ctgctgcctt cttccgtccg cagtgcgcct tctagtgtc 1174

catccacccc tctctccaca gacgcacccg aatttctgtc cgttcccaaa gatcggcccc 1234

ggaaaaagtc tgccccagaa actctcacac ttccagaccc tgagaaaaaa gccaccctga 1294

atttaccggg catgcactct tcagataagc catgtcggcc caaatctgag taactttata 1354

taaatatctc atgggggtttt atattttcaa aaaaaaaaaa 1394

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 <212> DNA  
 <213> Homo sapiens

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 <222> (301) .. (615)

<400> 331

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gcgtccgcgg acgcgtgggg tgccggcggg agagctggct tggggcgctg gcacctctc 120

ttacagcttt actcctgcc a gcttgggaaa aggccggaga aggtgaaatt ctgtgtgtc 180

cctccggcga gagactttgt cagctcccgc acagtaacat cctgaataaa gtcaaaactc 240

aaccaacagg tggaagtcca agaatccgag tggaggctca ccgaggcgaa ggggcccaacc 300

atg gga aag gag agt gga tgg gac tca ggc agg gct gct gta gca gct 348  
 Met Gly Lys Glu Ser Gly Trp Asp Ser Gly Arg Ala Ala Val Ala Ala  
           1                  5                  10                  15

gtg gtc gga gga gtt gtg gct gtg ggg act gtg ctc gtg gcg ctc agt 396  
 Val Val Gly Gly Val Val Ala Val Gly Thr Val Leu Val Ala Leu Ser  
                   20                  25                  30

gcc atg ggc ttc acc tca gta gga atc gcc gca tcc tcc ata gca gcc 444  
 Ala Met Gly Phe Thr Ser Val Gly Ile Ala Ala Ser Ser Ile Ala Ala  
                   35                  40                  45

aag atg atg tct aca gca gcc att gcc aac ggg ggc gga gtt gct gct 492  
 Lys Met Met Ser Thr Ala Ala Ile Ala Asn Gly Gly Gly Val Ala Ala  
           50                  55                  60

ggc agt ctg gtg gct att ctg cag tca gtg ggg gca gct gga ctc tct 540

Gly Ser Leu Val Ala Ile Leu Gln Ser Val Gly Ala Ala Gly Leu Ser  
65 70 75 80

gtg aca tct aaa gtt atc ggg ggc ttt gct ggg aca gct ctt ggg gcc 588  
Val Thr Ser Lys Val Ile Gly Gly Phe Ala Gly Thr Ala Leu Gly Ala  
85 90 95

tgg ctg ggt tca ccc cct tcc agc tga acacc acactgaggc agggagttgg 640  
Trp Leu Gly Ser Pro Pro Ser Ser \*

100 105

ctctcttggt ggagatgact ttctctgggcc tctggatgac aatcttccaa aggacaagtc 700

tcctactccc aaaactatattt aaggaagcat gaaaaataaa gatgctgggtt atcttctcct 760

aaaaaaaaaa aa 772

<210> 332  
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<212> DNA  
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<220>  
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<222> (336) .. (716)

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gcccctggaa agggttccaa gtccttttagt acccgacgct gtctgggaat tccgggcggt 180  
tcggctcctt ggtcgcagag gcaggaggcg tgcgtggcag gagggttcgg gttatatact 240  
cctaggtcct gggacagaat agttacgacc tctgggacag gaactcttct ctcttttgtt 300  
aataaacttc caactccctc ctcagaccgc accgc atg tct gtc atg gac ctc 353  
Met Ser Val Met Asp Leu  
1 5

gcc aat act tgc tcc agc ttt cag tcg gac ctg gat ttc tgt tca gat 401  
Ala Asn Thr Cys Ser Ser Phe Gln Ser Asp Leu Asp Phe Cys Ser Asp  
10 15 20

tgc ggc tcg gtc ctg cct ctg ccc ggg gct cag gat acg gtc acc tgt 449  
Cys Gly Ser Val Leu Pro Leu Pro Gly Ala Gln Asp Thr Val Thr Cys  
25 30 35

att cgc tgt ggc ttc aac atc aac gtt cgg gac ttt gag ggg aag gtt 497  
Ile Arg Cys Gly Phe Asn Ile Asn Val Arg Asp Phe Glu Gly Lys Val  
40 45 50

gtg aag act tcg gtt gtg ttc cac caa ctg ggg aca gcc atg cct atg 545  
Val Lys Thr Ser Val Val Phe His Gln Leu Gly Thr Ala Met Pro Met  
55 60 65 70

tcg gtg gag gaa ggg cct gag tgc cag gga cct gtg gtt gac agg cgc 593  
Ser Val Glu Glu Gly Pro Glu Cys Gln Gly Pro Val Val Asp Arg Arg  
75 80 85

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tgc cct cga tgt ggt cat gaa gga atg gca tac cac acc aga cag atg      641
Cys Pro Arg Cys Gly His Glu Gly Met Ala Tyr His Thr Arg Gln Met
          90                      95                      100

cgt tca gcc gat gaa ggg caa act gtc ttc tac acc tgt acc aac tgc      689
Arg Ser Ala Asp Glu Gly Gln Thr Val Phe Tyr Thr Cys Thr Asn Cys
          105                      110                      115

aag ttc cag gag aag gaa gac tct tga ccttt ttcctgggca actctacagt      741
Lys Phe Gln Glu Lys Glu Asp Ser *
          120                      125

ccctccctcc tttcgggaagg tgaaggatac tgggttttta gatgccttgt ccatcctgtc      801

tggttgcaat gttttgctcc cagaagagaa tcagatcatc atgtggggat taccattgtt      861

cctggagtac tcctaccctt agttgaattt ccttattaaa gttatatattt tctataaaaa      921
aaaaaaaaaa                                                                931

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<210> 333
<211> 2043
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (189)..(1571)

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<220>
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<222> (1)...(2043)
<223> n = a,t,c or g

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<400> 333
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aagggctcgc cgtccttctc cgtttctcgc tgcttcggga cgcgctctct gcggctctgt      120
gagcgccctt gagcgccggc agcggccgcg gggggatctt caggttatct tatgatgagg      180
cttttgct atg gct aat gat ccc ttg gaa ggc ttc cat gaa gta aac ctt      230
Met Ala Asn Asp Pro Leu Glu Gly Phe His Glu Val Asn Leu
          1                      5                      10

gct tca cct act tct ccg gac ctt ctt ggt gtg tat gaa tca gga act      278
Ala Ser Pro Thr Ser Pro Asp Leu Leu Gly Val Tyr Glu Ser Gly Thr
          15                      20                      25                      30

caa gag cag act acc tca cca agt gtc atc tac cgg cca cac cct tca      326
Gln Glu Gln Thr Thr Ser Pro Ser Val Ile Tyr Arg Pro His Pro Ser
          35                      40                      45

gct tta tcc tct gta cct atc cag gca aat gca tta gat gtt tct gaa      374
Ala Leu Ser Ser Val Pro Ile Gln Ala Asn Ala Leu Asp Val Ser Glu
          50                      55                      60

ctt cct aca caa ccc gtg tat tca tcc ccc aga cgt tta aat tgt gcg      422
Leu Pro Thr Gln Pro Val Tyr Ser Ser Pro Arg Arg Leu Asn Cys Ala
          65                      70                      75

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gaa ata tct agt atc agc ttt cat gtt aca gac cca gcc cct tgc tct	470
Glu Ile Ser Ser Ile Ser Phe His Val Thr Asp Pro Ala Pro Cys Ser	
80 85 90	
acc tct gga gtc aca gct gga tta act aaa tta act aca aga aag gac	518
Thr Ser Gly Val Thr Ala Gly Leu Thr Lys Leu Thr Thr Arg Lys Asp	
95 100 105 110	
aac tat aat gca gag aga gag ttt tta cag ggt gct act ata aca gag	566
Asn Tyr Asn Ala Glu Arg Glu Phe Leu Gln Gly Ala Thr Ile Thr Glu	
115 120 125	
gct tgc gat ggc agt gat gat att ttt ggg ttg agt act gat agt ctg	614
Ala Cys Asp Gly Ser Asp Asp Ile Phe Gly Leu Ser Thr Asp Ser Leu	
130 135 140	
tct cgt tta cga agc cca tct gtt ttg gaa gtt aga gaa aag ggc tat	662
Ser Arg Leu Arg Ser Pro Ser Val Leu Glu Val Arg Glu Lys Gly Tyr	
145 150 155	
gaa cga tta aaa gaa gaa ctc gca aaa gct cag agg gaa ctg aag tta	710
Glu Arg Leu Lys Glu Glu Leu Ala Lys Ala Gln Arg Glu Leu Lys Leu	
160 165 170	
aaa gat gaa gaa tgt gag agg ctt tca aaa gtg cga gat caa ctt gga	758
Lys Asp Glu Glu Cys Glu Arg Leu Ser Lys Val Arg Asp Gln Leu Gly	
175 180 185 190	
cag gaa ttg gaa gaa ctc aca gct agt cta ttt gag gaa gct cat aaa	806
Gln Glu Leu Glu Glu Leu Thr Ala Ser Leu Phe Glu Glu Ala His Lys	
195 200 205	
atg gtg aga gaa gca aat atc aag cag gca aca gca gaa aaa cag cta	854
Met Val Arg Glu Ala Asn Ile Lys Gln Ala Thr Ala Glu Lys Gln Leu	
210 215 220	
aaa gaa gca caa gga aaa att gat gta ctt caa gct gaa gta gct gca	902
Lys Glu Ala Gln Gly Lys Ile Asp Val Leu Gln Ala Glu Val Ala Ala	
225 230 235	
ttg aag aca ctt gta ttg tcc agt tct cca aca tca cct acg cag gag	950
Leu Lys Thr Leu Val Leu Ser Ser Ser Pro Thr Ser Pro Thr Gln Glu	
240 245 250	
cct ttg cca ggt gga aag aca cct ttt aaa aag ggg cat aca aga aat	998
Pro Leu Pro Gly Gly Lys Thr Pro Phe Lys Lys Gly His Thr Arg Asn	
255 260 265 270	
aaa agc aca agc agt gct atg agt ggc agt cat cat gac ctc agt gtg	1046
Lys Ser Thr Ser Ser Ala Met Ser Gly Ser His His Asp Leu Ser Val	
275 280 285	
ata cag cca att gta aaa gac tgc aaa gag gct gac tta tcc ttg tat	1094
Ile Gln Pro Ile Val Lys Asp Cys Lys Glu Ala Asp Leu Ser Leu Tyr	
290 295 300	
aat gaa ttc cga ttg tgg aag gat gag ccc aca atg gac agg acg tgt	1142
Asn Glu Phe Arg Leu Trp Lys Asp Glu Pro Thr Met Asp Arg Thr Cys	
305 310 315	
cct ttc tta gac aaa atc tac cag gaa gat atc ttt cca tgt tta aca	1190
Pro Phe Leu Asp Lys Ile Tyr Gln Glu Asp Ile Phe Pro Cys Leu Thr	
320 325 330	

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ttc tca aaa agt gag ttg gct tca gct gtt ctg gag gct gtg gaa aac      1238
Phe Ser Lys Ser Glu Leu Ala Ser Ala Val Leu Glu Ala Val Glu Asn
335                      340                      345                      350

aat act cta agc att gaa cca gtg gga tta caa cct atc cgg ttt gtg      1286
Asn Thr Leu Ser Ile Glu Pro Val Gly Leu Gln Pro Ile Arg Phe Val
                      355                      360                      365

aaa gct tct gca gtt gaa tgc gga gga cca aaa aaa tgt gct ctc act      1334
Lys Ala Ser Ala Val Glu Cys Gly Gly Pro Lys Lys Cys Ala Leu Thr
                      370                      375                      380

ggc cag agt aag tcc tgt aaa cac aga att aaa tta ggg gac tca agc      1382
Gly Gln Ser Lys Ser Cys Lys His Arg Ile Lys Leu Gly Asp Ser Ser
                      385                      390                      395

aac tat tat tat att tct cct ttt tgc aga tac agg atc act tct gta      1430
Asn Tyr Tyr Tyr Ile Ser Pro Phe Cys Arg Tyr Arg Ile Thr Ser Val
                      400                      405                      410

tgt aac ttt ttt aca tac att cga tac att cag cag gga ctc gtg aaa      1478
Cys Asn Phe Phe Thr Tyr Ile Arg Tyr Ile Gln Gln Gly Leu Val Lys
415                      420                      425                      430

cag cag gat gtt gat cag atg ttt tgg gag gtt atg cag ttg aga aaa      1526
Gln Gln Asp Val Asp Gln Met Phe Trp Glu Val Met Gln Leu Arg Lys
                      435                      440                      445

gag atg tca ttg gca aag ctg ggt tat ttc aaa gag gaa ctc tga tgc      1574
Glu Met Ser Leu Ala Lys Leu Gly Tyr Phe Lys Glu Glu Leu *
                      450                      455                      460

tctgcgtggg accatgcctg aactccccga ataactgaaa aatggctgaa tatttttatg 1634
gttacttgat atttatttcc aaggagtgag cctaagactt tttcccctt ttgcaaattg 1694
ctctaagaag taccatgatt tcttttaaac tgatctatgc tgtgtttgct tattcttttag 1754
ttgaacacac tatgaagaat tccaggtgta ctagtgaatg taatttatag ttgccaaaaa 1814
aaagcgcgcg gctgaattta gtagtagagc gacctggaat ccgacggtac tgcagcgtac 1874
actttctata ggagtcgata gagctgcgaa catgtcaagt gttctggtga atgtacgcgc 1934
natcaccaca tcgagcgaca taatgtagct ggggctagag ggcacccata tgctgccatg 1994
cgctcatcgg actgcggcac gcatagacgc acgcggaagc gtcgatggc 2043

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<210> 334
<211> 797
<212> DNA
<213> Homo sapiens

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<220>
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<222> (94)..(666)

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<220>
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<223> n = a,t,c or g

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&lt;400&gt; 334

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aattcccggg tcgacccacg cgtccggcag agc atg gcg gcg ggc gag ctt gag      114
                               Met Ala Ala Gly Glu Leu Glu
                               1                               5

ggt ggc aaa ccc ctg agc ggg ctg ctg aat gcg ctg gcc cag gac act      162
Gly Gly Lys Pro Leu Ser Gly Leu Leu Asn Ala Leu Ala Gln Asp Thr
                               10                               15                               20

ttc cac ggg tac ccc ggc atc aca gag gag ctg cta cgg agc cag cta      210
Phe His Gly Tyr Pro Gly Ile Thr Glu Glu Leu Leu Arg Ser Gln Leu
                               25                               30                               35

tat cca gag gtg cca ccc gag gag ttc cgc ccc ttt ctg gca aag atg      258
Tyr Pro Glu Val Pro Pro Glu Glu Phe Arg Pro Phe Leu Ala Lys Met
                               40                               45                               50                               55

agg ggg att ctt aag tct att gcg tct gca gac atg gat ttc aac cag      306
Arg Gly Ile Leu Lys Ser Ile Ala Ser Ala Asp Met Asp Phe Asn Gln
                               60                               65                               70

ctg gag gca ttc ttg act gct caa acc aaa aag caa ggt ggg atc aca      354
Leu Glu Ala Phe Leu Thr Ala Gln Thr Lys Lys Gln Gly Gly Ile Thr
                               75                               80                               85

tct gac caa gct gct gtc att tcc aaa ttc tgg aag agc cac aag aca      402
Ser Asp Gln Ala Ala Val Ile Ser Lys Phe Trp Lys Ser His Lys Thr
                               90                               95                               100

aaa atc cgt gag agc ctc atg aac cag agc cgc tgg aat agc ggg ctt      450
Lys Ile Arg Glu Ser Leu Met Asn Gln Ser Arg Trp Asn Ser Gly Leu
                               105                               110                               115

cgg ggc ctg agc tgg aga gtt gat ggc aag tct cag tca agg cac tca      498
Arg Gly Leu Ser Trp Arg Val Asp Gly Lys Ser Gln Ser Arg His Ser
                               120                               125                               130                               135

gct caa ata cac aca cct gtt gcc att ata gag ctg gaa tta ggc aaa      546
Ala Gln Ile His Thr Pro Val Ala Ile Ile Glu Leu Glu Leu Gly Lys
                               140                               145                               150

tat gga cag gaa tct gaa ttt ctg tgt ttg gaa ttt gat gag gtc aaa      594
Tyr Gly Gln Glu Ser Glu Phe Leu Cys Leu Glu Phe Asp Glu Val Lys
                               155                               160                               165

gtc aac caa att ctg aag acg ctg tca gag gta gaa gaa agt atc agc      642
Val Asn Gln Ile Leu Lys Thr Leu Ser Glu Val Glu Glu Ser Ile Ser
                               170                               175                               180

aca ctg atc agc cag cct aac tga agatgatgta tgaaggagtt ggagttgttg      696
Thr Leu Ile Ser Gln Pro Asn *
                               185                               190

aaaccaaggt gtccatgatc cctccccact gaccttttct aagaaaattc ttgtgccgc      756

attggtatta aatcctcgca ttcagtctta aaaaaaaaaa a      797

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&lt;210&gt; 335

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 <212> DNA  
 <213> Homo sapiens

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 <222> (76)..(408)

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 gcttagttag gagct atg gct aaa cat cat cct gat ttg atc ttt tgc cgc 111  
                   Met Ala Lys His His Pro Asp Leu Ile Phe Cys Arg  
                   1                  5                  10  
 aag cag gct ggt gtt gcc atc gga aga ctg tgt gaa aaa tgt gat ggc 159  
 Lys Gln Ala Gly Val Ala Ile Gly Arg Leu Cys Glu Lys Cys Asp Gly  
                   15                  20                  25  
 aag tgt gtg att tgt gac tcc tat gtg cgt ccc tgc act ctg gtg cgc 207  
 Lys Cys Val Ile Cys Asp Ser Tyr Val Arg Pro Cys Thr Leu Val Arg  
                   30                  35                  40  
 ata tgt gat gag tgt aac tat gga tct tac cag ggg cgc tgt gtg atc 255  
 Ile Cys Asp Glu Cys Asn Tyr Gly Ser Tyr Gln Gly Arg Cys Val Ile  
                   45                  50                  55                  60  
 tgt gga gga cct ggg gtc tct gat gcc tat tat tgt aag gag tgc acc 303  
 Cys Gly Gly Pro Gly Val Ser Asp Ala Tyr Tyr Cys Lys Glu Cys Thr  
                   65                  70                  75  
 atc cag gag aag gac aga gat ggc tgc cca aag att gtc aat ctg ggc 351  
 Ile Gln Glu Lys Asp Arg Asp Gly Cys Pro Lys Ile Val Asn Leu Gly  
                   80                  85                  90  
 agc tct aag aca gac ctc ttc tat gaa cgc aaa aaa tac ggc ttc aag 399  
 Ser Ser Lys Thr Asp Leu Phe Tyr Glu Arg Lys Lys Tyr Gly Phe Lys  
                   95                  100                  105  
 aag agg tga ttggtgg gtggcccctt cctcccccca acatcagtct gctgcagctg 455  
 Lys Arg \*  
                   110  
 ccagaaaaca tgcctactac taccagcaga aaaggagcag agcccagagc atcaccagga 515  
 gtgcctgcta gtgtactggc agcttgccac cccctcctct cccttcaccc agacacgtgg 575  
 tagggatgga aaaggattct tcacagagca ctctggcaca ccatatcgga gaaaacttga 635  
 tagattagtt aatgggtttt cttgaattcg agaagcatag atctgttctc catattggta 695  
 tgttctccct caaccaagat cttctaaaaa gaaataatat tttagtcttc tgcttgagga 755  
 actgactgtg aagcgacgcc cagtgaaaaa catgttcttg cagcagctct ggtggcagct 815  
 gtccttgagg aacctttggg gtgtgggtggg aagctatcag aacaagaaat gtaggcattt 875  
 cccgtttttt tggggggggg gggggggggg gccagggctc tgccctcttg aaaggcattt 935

acttggtttaa cacttgtcca gctacagtgg ggtacagtag ctggctattc acaggcatca 995  
 tcatagccca ctagtctcat attattttcc ttttgagaaa ttggaaactc tttctgttgc 1055  
 tattatatta ataaagttgg tgtttatattt ctggtaaaaa aaaaaaa 1102

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 <212> DNA  
 <213> Homo sapiens

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 <222> (125)..(502)

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 cgac atg aaa ctg ctt acc cac aat ctg ctg agc tgc cat gtg cgg ggg 169  
 Met Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly  
 1 5 10 15  
 gtg ggg tcc cgt ggc ttc ccc ctg cgc ctc cag gcc acc gag gtc cgt 217  
 Val Gly Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg  
 20 25 30  
 atc tgc cct gtg gaa ttc aac ccc aac ttc gtg gcg cgt atg ata cct 265  
 Ile Cys Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro  
 35 40 45  
 aaa gtg gag tgg tgc gcg ttc ctg gag gcg gcc gat aac ttg cgt ctg 313  
 Lys Val Glu Trp Ser Ala Phe Leu Glu Ala Ala Asp Asn Leu Arg Leu  
 50 55 60  
 atc cag gtg ccg aaa ggg ccg gtt gag gga tat gag gag aat gag gag 361  
 Ile Gln Val Pro Lys Gly Pro Val Glu Gly Tyr Glu Glu Asn Glu Glu  
 65 70 75  
 ttt ctg agg acc atg cac cac ctg ctg ctg gag gtg gaa gtg ata gag 409  
 Phe Leu Arg Thr Met His His Leu Leu Leu Glu Val Glu Val Ile Glu  
 80 85 90 95  
 ggc acc ctg cag tgc ccg gaa tct gga cgt atg ttc ccc atc agc cgc 457  
 Gly Thr Leu Gln Cys Pro Glu Ser Gly Arg Met Phe Pro Ile Ser Arg  
 100 105 110  
 ggg atc ccc aac atg ctg ctg agt gaa gag gaa act gag agt tga ttg 505  
 Gly Ile Pro Asn Met Leu Leu Ser Glu Glu Glu Thr Glu Ser \*  
 115 120 125  
 tgccaggcgc ccagtttttc ttgttatgac tgtgtatttt tgttgatcta taccctgttt 565  
 ccgaattctg ccgtgtgtat cccaaccct tgaccaatg acaccaaaca cagtgttttt 625  
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 ttcacgggag ccctagagag gacaccggga cacccagaag ccgggaa atg gat tca 176  
 Met Asp Ser  
 1  
 gtg gcc ttt gag gat gtg gct gtc agc ttc acc cag gag gag tgg gct 224  
 Val Ala Phe Glu Asp Val Ala Val Ser Phe Thr Gln Glu Glu Trp Ala  
 5 10 15  
 ttg ctg gat cct tcc cag aag aat ctc tac agg gat gtg atg cag gaa 272  
 Leu Leu Asp Pro Ser Gln Lys Asn Leu Tyr Arg Asp Val Met Gln Glu  
 20 25 30 35  
 acc ttc aag aac ctg acc tct gta gga aaa aca tgg aaa gtt cag aac 320  
 Thr Phe Lys Asn Leu Thr Ser Val Gly Lys Thr Trp Lys Val Gln Asn  
 40 45 50  
 att gaa gat gag tac aaa aat ccc agg aga aat cta agt ctt atg aga 368  
 Ile Glu Asp Glu Tyr Lys Asn Pro Arg Arg Asn Leu Ser Leu Met Arg  
 55 60 65  
 gag aaa ctc tgt gaa agt aaa gaa agt cat cac tgt gga gaa agc ttc 416  
 Glu Lys Leu Cys Glu Ser Lys Glu Ser His His Cys Gly Glu Ser Phe  
 70 75 80  
 aac cag att gca gat gac atg ctg aac agg aaa act ctt cct gga ata 464  
 Asn Gln Ile Ala Asp Asp Met Leu Asn Arg Lys Thr Leu Pro Gly Ile  
 85 90 95  
 aca cca tgt gaa agc agt gtg tgt gga gaa gtt ggc acg ggt cat tca 512  
 Thr Pro Cys Glu Ser Ser Val Cys Gly Glu Val Gly Thr Gly His Ser  
 100 105 110 115  
 tct ctt aat acg cat atc aga gct gac act gga cac aag tca tct gag 560  
 Ser Leu Asn Thr His Ile Arg Ala Asp Thr Gly His Lys Ser Ser Glu  
 120 125 130  
 tat cag gaa tat gga gag aat cca tat aga aat aag gaa tgt aag aaa 608  
 Tyr Gln Glu Tyr Gly Glu Asn Pro Tyr Arg Asn Lys Glu Cys Lys Lys  
 135 140 145  
 gcc ttc agt tat ctt gac tcc ttt caa tca cat gat aaa gct tgc act 656  
 Ala Phe Ser Tyr Leu Asp Ser Phe Gln Ser His Asp Lys Ala Cys Thr  
 150 155 160  
 aaa gag aaa ccc tat gat ggt aaa gaa tgt aca gaa acc ttc att tcc 704

Lys	Glu	Lys	Pro	Tyr	Asp	Gly	Lys	Glu	Cys	Thr	Glu	Thr	Phe	Ile	Ser		
165						170					175						
cat	tca	tgc	att	caa	aga	cac	agg	gta	atg	cac	agt	gga	gat	gga	cct		752
His	Ser	Cys	Ile	Gln	Arg	His	Arg	Val	Met	His	Ser	Gly	Asp	Gly	Pro		
180					185					190					195		
tat	aaa	tgt	aag	ttt	tgt	ggg	aaa	gcc	ttc	tat	ttt	ctc	aat	tta	tgt		800
Tyr	Lys	Cys	Lys	Phe	Cys	Gly	Lys	Ala	Phe	Tyr	Phe	Leu	Asn	Leu	Cys		
				200				205						210			
ctt	atc	cat	gaa	cga	att	cac	act	ggt	gtg	aaa	cca	tat	aag	tgt	aaa		848
Leu	Ile	His	Glu	Arg	Ile	His	Thr	Gly	Val	Lys	Pro	Tyr	Lys	Cys	Lys		
			215					220					225				
caa	tgt	ggt	aag	gcc	ttt	act	cgt	tcc	act	acc	ctt	cca	gta	cat	gaa		896
Gln	Cys	Gly	Lys	Ala	Phe	Thr	Arg	Ser	Thr	Thr	Leu	Pro	Val	His	Glu		
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aga	act	cac	aca	gga	gtg	aat	gcc	gat	gaa	tgt	aaa	gaa	tgt	ggg	aat		944
Arg	Thr	His	Thr	Gly	Val	Asn	Ala	Asp	Glu	Cys	Lys	Glu	Cys	Gly	Asn		
		245				250					255						
gca	ttc	agt	ttt	cct	agt	gaa	att	cgt	aga	cat	aaa	agg	tct	cac	act		992
Ala	Phe	Ser	Phe	Pro	Ser	Glu	Ile	Arg	Arg	His	Lys	Arg	Ser	His	Thr		
260					265					270					275		
gga	gaa	aaa	ccc	tat	gag	tgt	aag	caa	tgt	ggg	aaa	gtc	ttc	att	tct		1040
Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Gln	Cys	Gly	Lys	Val	Phe	Ile	Ser		
				280				285						290			
ttc	agt	tcc	att	cag	tat	cat	aag	atg	act	cac	act	gga	gag	aaa	ccc		1088
Phe	Ser	Ser	Ile	Gln	Tyr	His	Lys	Met	Thr	His	Thr	Gly	Glu	Lys	Pro		
			295					300					305				
tat	gaa	tgt	aag	cag	tgt	ggg	aaa	gcc	ttt	aga	tgt	ggc	tca	cac	ctt		1136
Tyr	Glu	Cys	Lys	Gln	Cys	Gly	Lys	Ala	Phe	Arg	Cys	Gly	Ser	His	Leu		
		310					315					320					
caa	aag	cat	gga	agg	act	cac	act	gga	gag	aaa	ccc	tat	gaa	tgt	agg		1184
Gln	Lys	His	Gly	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Arg		
		325				330					335						
caa	tgt	ggt	aaa	gcc	ttc	aga	tgt	acc	tcg	gac	ctt	caa	agg	cat	gaa		1232
Gln	Cys	Gly	Lys	Ala	Phe	Arg	Cys	Thr	Ser	Asp	Leu	Gln	Arg	His	Glu		
340				345						350					355		
aag	aca	cac	act	gag	gat	aaa	ccc	tat	gga	tgt	aag	cag	tgt	ggg	aaa		1280
Lys	Thr	His	Thr	Glu	Asp	Lys	Pro	Tyr	Gly	Cys	Lys	Gln	Cys	Gly	Lys		
				360				365					370				
ggc	ttt	aga	tgt	gct	tca	caa	ctt	caa	att	cat	gaa	agg	acg	cac	agt		1328
Gly	Phe	Arg	Cys	Ala	Ser	Gln	Leu	Gln	Ile	His	Glu	Arg	Thr	His	Ser		
			375				380						385				
gga	gag	aaa	ccc	cat	gaa	tgt	aag	gaa	tgt	gga	aaa	gta	ttc	aag	tat		1376
Gly	Glu	Lys	Pro	His	Glu	Cys	Lys	Glu	Cys	Gly	Lys	Val	Phe	Lys	Tyr		
		390					395					400					
ttt	tct	tcc	ttg	cgt	ata	cat	gaa	agg	acg	cac	act	gga	gag	aag	ccc		1424
Phe	Ser	Ser	Leu	Arg	Ile	His	Glu	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro		
		405				410					415						
cat	gaa	tgt	aag	caa	tgt	gga	aaa	gca	ttc	agg	tat	ttc	tct	tcc	ttg		1472

His	Glu	Cys	Lys	Gln	Cys	Gly	Lys	Ala	Phe	Arg	Tyr	Phe	Ser	Ser	Leu	
420					425					430					435	
cat	ata	cat	gaa	agg	aca	cac	act	gga	gat	aag	cca	tat	gag	tgt	aag	1520
His	Ile	His	Glu	Arg	Thr	His	Thr	Gly	Asp	Lys	Pro	Tyr	Glu	Cys	Lys	
				440					445					450		
gta	tgt	ggc	aaa	gcc	ttc	act	tgt	tcc	agt	tcc	att	cga	tat	cat	gaa	1568
Val	Cys	Gly	Lys	Ala	Phe	Thr	Cys	Ser	Ser	Ser	Ile	Arg	Tyr	His	Glu	
			455					460					465			
agg	act	cac	act	gga	gag	aaa	ccc	tat	gaa	tgt	aag	cac	tgt	ggg	aag	1616
Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	His	Cys	Gly	Lys	
		470					475					480				
gcc	ttt	att	tcc	aat	tac	att	cga	tat	cat	gaa	agg	act	cac	act	gga	1664
Ala	Phe	Ile	Ser	Asn	Tyr	Ile	Arg	Tyr	His	Glu	Arg	Thr	His	Thr	Gly	
	485					490					495					
gag	aaa	ccc	tat	caa	tgc	aag	caa	tgt	ggc	aaa	gcc	ttt	att	cgt	gcc	1712
Glu	Lys	Pro	Tyr	Gln	Cys	Lys	Gln	Cys	Gly	Lys	Ala	Phe	Ile	Arg	Ala	
500				505					510					515		
agt	tca	tgt	cga	gaa	cat	gaa	aga	act	cat	acc	att	aat	aga	tga	gaa	1760
Ser	Ser	Cys	Arg	Glu	His	Glu	Arg	Thr	His	Thr	Ile	Asn	Arg	*		
			520					525				530				
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gaaaagagag	tggtgaaaga	acctctggat	aactgctttt	tgaattgaga	agagagactt											1880
gcgataggac	aataaaatct	agaagaactt	ggatgggttc	gtaatacaat	tcacctatag											1940
ccaatcttgc	atgagatttc	aaaggcacag	aaaaggaagg	catcagtcac	atattagagg											2000
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tcgcccgcgc	gtcccagcgc	ccccagccct	cccgcgaggg	cgccccggga	cggaaggatc	180
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ctccgcgcgc	gcctgggccc	atg gcc aat tac atc cac gtc cct ccc ggc tcc	292			
		Met Ala Asn Tyr Ile His Val Pro Pro Gly Ser				
		1 5 10				
ccg gag gtg ccc aag ctg aac gtc acc gtt cag gat cag gaggagcacc	341					
Pro Glu Val Pro Lys Leu Asn Val Thr Val Gln Asp Gln						
	15 20					
gctgccggga	gggggcccctg	agcctcctgc	aacacctgcg	gcctcactgg	gacccccagg	401
aggtgaccct	gcagctcttc	acagatggaa	tcacaaataa	acttattggc	tggtacgtgg	461
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tcgatcgaga	tgaggaagta	aagagttttc	gagtgttgca	ggctcatggg	tgtgcaccac	581
aactctactg	taccttcaat	aatggactat	gctatgaatt	tatacaagga	gaagcactgg	641
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acctggcata	tgatattgga	aatcatttca	atgaatttgc	aggtgtgagt	gatgtagact	1061
atagtctgta	tccagataga	gaactacaga	gtcagtggct	gcgtgcttac	cttgaagcct	1121
acaaagaatt	taagggtctt	gggactgaag	ttactgaaaa	ggaggtagaa	atactcttca	1181
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<212> DNA
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851

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ggg aac aag tgt gac atg gaa gac gag cgg gtc atc tca act gag cga 626

ggg caa cat tta gga gaa cag ctt ggg ttt gag ttt ttt gaa aca agt 674

gcc aag gac aac att aat gtc aag cag aca ttt gag cgc ctt gtg gat 722

atc atc tgc gac aaa atg tca gag agt ttg gag act gat cct gcc atc 770

act gct gca aag cag aac acg aga ctc aag gaa act cct cct cca ccg 818

cag ccc aac tgt gcc tgc tag tgt ccc cgt gca cac agg cag ctc cag 866

ggg gct ctg gtt gcc aac aaa cag cat ttg taa atg gtc tat tag cct 914

tca ttt ata ctg cct aac aat tat ttg aag gaa taa att gat gtc aat 962

ggc tcg tac gca ttc aat tct tgg gag ctt tcc tgt tta ata tgt ggc 1010

aaa tat gtg atc tta aat tta taa gga cta tcc at tgatg ttggagccgg 41

ttagcgaacc ccaagagtgc agagtgtgga gcgtggagcg ccgggactgt gcacgcttga 101

ccggaagccc agaccagtgc ggtcctagcc agagagaaag gacatttgcc aacaatgaga 161

cacgaagcgc ccatgcagat ggcctctgcc caagatgcca ggtacggcca gaaagactcc 221

tctgatcaga actttgacta catgttcaaa ttactcatca tcggcaatag cagtgtgggg 281

aaaacatctt ttctattccg ttatgcagat gactccttta catctgcatt cgtcagcaca 341

gttgggatcg atttcaaagt aaaaactgta ttcaaaaatg aaaagagaat caagcttcag 401

atttgggaca cagcaggcca ggaaagatac aggactatca ccacagccta ttatcgtgga 461

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aacaagtgtg acatggaaga cgagcgggtc atctcaactg agcgagggtca acatttagga 641
gaacagcttg ggtttgagtt ttttgaaaca agtgccaagg acaacattaa tgtcaagcag 701
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<210> 340
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<212> DNA
<213> Homo sapiens

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<220>
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<222> (3)..(4139)

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      1             5             10             15

cta att cat ctc tcc agc aaa gga cac atc tct cca gca aag gac acc 95
Leu Ile His Leu Ser Ser Lys Gly His Ile Ser Pro Ala Lys Asp Thr
      20             25             30

tct ctc cag caa agg aca cct gca gag atg tcc cca gtc ctt cac ttc 143
Ser Leu Gln Gln Arg Thr Pro Ala Glu Met Ser Pro Val Leu His Phe
      35             40             45

tat gtt cgt ccc tct ggc cat gag ggg gca gcc tct gga cac act cgg 191
Tyr Val Arg Pro Ser Gly His Glu Gly Ala Ala Ser Gly His Thr Arg
      50             55             60

agg aaa ctg caa ggg aaa ctg cca gag ctg cag ggc gtc gag act gaa 239
Arg Lys Leu Gln Gly Lys Leu Pro Glu Leu Gln Gly Val Glu Thr Glu
      65             70             75

ctg tgc tac aac gtg aac tgg aca gct gag gcc ctc ccc agt gct gag 287
Leu Cys Tyr Asn Val Asn Trp Thr Ala Glu Ala Leu Pro Ser Ala Glu
      80             85             90             95

gag aca aag aag ctg atg tgg ctg ttt ggt tgc ccc tta ctg ctg gat 335
Glu Thr Lys Lys Leu Met Trp Leu Phe Gly Cys Pro Leu Leu Leu Asp
      100            105            110

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gat gtt gct cgg gag tcc tgg ctc ctt cct ggc tcc aat gac ctg ctg	383
Asp Val Ala Arg Glu Ser Trp Leu Leu Pro Gly Ser Asn Asp Leu Leu	
115 120 125	
ctg gag gtc ggg ccc agg ctg aac ttc tcc acc cca aca tcc acc aac	431
Leu Glu Val Gly Pro Arg Leu Asn Phe Ser Thr Pro Thr Ser Thr Asn	
130 135 140	
atc gtg tca gtg tgc cgc gcc act ggg ctg ggg cct gtg gat cgt gtg	479
Ile Val Ser Val Cys Arg Ala Thr Gly Leu Gly Pro Val Asp Arg Val	
145 150 155	
gag acc acc cgg cgc tac cgg ctc tcg ttt gcc cac ccc ccg tca gct	527
Glu Thr Thr Arg Arg Tyr Arg Leu Ser Phe Ala His Pro Pro Ser Ala	
160 165 170 175	
gag gtg gaa gcc att gct ctg gct acc ctg cac gac cgg atg aca gag	575
Glu Val Glu Ala Ile Ala Leu Ala Thr Leu His Asp Arg Met Thr Glu	
180 185 190	
cag cac ttc ccc cat ccc atc cag agt ttc tcc cct gag agc atg ccg	623
Gln His Phe Pro His Pro Ile Gln Ser Phe Ser Pro Glu Ser Met Pro	
195 200 205	
gaa ccc ctc aat ggc cct atc aat ata ctg ggt gag ggc cgg ctt gcg	671
Glu Pro Leu Asn Gly Pro Ile Asn Ile Leu Gly Glu Gly Arg Leu Ala	
210 215 220	
ctg gag aag gcc aac cag gag ctt ggt ctg gct tta gac tct tgg gac	719
Leu Glu Lys Ala Asn Gln Glu Leu Gly Leu Ala Leu Asp Ser Trp Asp	
225 230 235	
cta gac ttc tac acc aag cgc ttc cag gag cta cag cgg aac ccg agc	767
Leu Asp Phe Tyr Thr Lys Arg Phe Gln Glu Leu Gln Arg Asn Pro Ser	
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act gtg gag gcc ttt gac ttg gcg cag tcc aat agc gag cac agc cga	815
Thr Val Glu Ala Phe Asp Leu Ala Gln Ser Asn Ser Glu His Ser Arg	
260 265 270	
cac tgg ttc ttc aag ggc cag ctc cac gtg gat ggg cag aag ctg gtg	863
His Trp Phe Phe Lys Gly Gln Leu His Val Asp Gly Gln Lys Leu Val	
275 280 285	
cac tca ctg ttt gag tcc atc atg agc acc cag gaa tcc tcg aac ccc	911
His Ser Leu Phe Glu Ser Ile Met Ser Thr Gln Glu Ser Ser Asn Pro	
290 295 300	
aac aac gtc ctc aaa ttc tgt gat aac agc agt gca atc cag gga aag	959
Asn Asn Val Leu Lys Phe Cys Asp Asn Ser Ser Ala Ile Gln Gly Lys	
305 310 315	
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Glu Val Arg Phe Leu Arg Pro Glu Asp Pro Thr Arg Pro Ser Arg Phe	
320 325 330 335	
cag caa cag caa ggg ctg aga cat gtt gtc ttc aca gca gag act cac	1055
Gln Gln Gln Gln Gly Leu Arg His Val Val Phe Thr Ala Glu Thr His	
340 345 350	
aac ttt ccc aca gga gta tgc ccc ttt agt ggt gca acc act ggc aca	1103
Asn Phe Pro Thr Gly Val Cys Pro Phe Ser Gly Ala Thr Thr Gly Thr	
355 360 365	

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gcc cgg ccc ctg gag gtt gcc att gaa gcc agt aat gga gct tct gac Ala Arg Pro Leu Glu Val Ala Ile Glu Ala Ser Asn Gly Ala Ser Asp 420 425 430	1295
tat ggc aac aag ttt ggg gaa cca gtg ctg gct ggc ttc gcc cgc tcc Tyr Gly Asn Lys Phe Gly Glu Pro Val Leu Ala Gly Phe Ala Arg Ser 435 440 445	1343
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atc atg ttt agt ggg ggc att ggg tcc atg gaa gct gac cac ata agc Ile Met Phe Ser Gly Gly Ile Gly Ser Met Glu Ala Asp His Ile Ser 465 470 475	1439
aag gag gcc cca gag cca ggc atg gaa gtt gta aag gtt gga ggt ccc Lys Glu Ala Pro Glu Pro Gly Met Glu Val Val Lys Val Gly Gly Pro 480 485 490 495	1487
gtc tac agg att gga gtt gga ggt gga gct gct tca tct gtg cag gtg Val Tyr Arg Ile Gly Val Gly Gly Gly Ala Ala Ser Ser Val Gln Val 500 505 510	1535
cag gga gat aac acc agt gac ctg gac ttt ggg gct gtg cag cga gga Gln Gly Asp Asn Thr Ser Asp Leu Asp Phe Gly Ala Val Gln Arg Gly 515 520 525	1583
gac ccg gag atg gaa cag aag atg aac cgt gtg atc agg gct tgt gtg Asp Pro Glu Met Glu Gln Lys Met Asn Arg Val Ile Arg Ala Cys Val 530 535 540	1631
gag gcc ccc aag gga aac ccc atc tgc agc ctt cat gat cag ggc gct Glu Ala Pro Lys Gly Asn Pro Ile Cys Ser Leu His Asp Gln Gly Ala 545 550 555	1679
ggt ggc aat ggc aat gtc cta aaa gag ctg agt gac cca gct gga gcc Gly Gly Asn Gly Asn Val Leu Lys Glu Leu Ser Asp Pro Ala Gly Ala 560 565 570 575	1727
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ctg gtg gac gat cgg gag tgt cct gtc aga aga aat ggc cag ggg gat Leu Val Asp Asp Arg Glu Cys Pro Val Arg Arg Asn Gly Gln Gly Asp 640 645 650 655	1967
gcc ccc ccg aca ccc ccg cca acc cct gtg gac ctg gag ctc gaa tgg Ala Pro Pro Thr Pro Pro Pro Thr Pro Val Asp Leu Glu Leu Glu Trp 660 665 670	2015
gtg ctg ggc aag atg cct cgg aag gag ttc ttc ctg cag agg aag ccc Val Leu Gly Lys Met Pro Arg Lys Glu Phe Phe Leu Gln Arg Lys Pro 675 680 685	2063
ccc atg ctg cag cct ctg gcc ttg ccc cca ggg ctg agc gtg cac cag Pro Met Leu Gln Pro Leu Ala Leu Pro Pro Gly Leu Ser Val His Gln 690 695 700	2111
gct ctg gag agg gtt ctg agg ctg ccc gcc gtg gcc agc aag cgc tac Ala Leu Glu Arg Val Leu Arg Leu Pro Ala Val Ala Ser Lys Arg Tyr 705 710 715	2159
ctc acc aat aag gtg gac cgc tcc gtg gga ggc ctg gtg gcc cag cag Leu Thr Asn Lys Val Asp Arg Ser Val Gly Gly Leu Val Ala Gln Gln 720 725 730 735	2207
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<213> Homo sapiens

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<222> (197) .. (748)

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<223> n = a,t,c or g

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attccagtgg gccgcttggc ggtgtcgttg cggtaccagg tccgcgtgag gggttcgggg 180

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860

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 cccagtcctcg cgggcgtgga gcgccggagg acccgccctc gggctc atg gcg gcc 175  
 Met Ala Ala  
 1  
 ccg gtc cgc ctg ggc cgg aag cgc ccg ctg cct gcc tgt ccc aac ccg 223  
 Pro Val Arg Leu Gly Arg Lys Arg Pro Leu Pro Ala Cys Pro Asn Pro  
 5 10 15  
 ctc ttc gtt cgc tgg ctg acc gag tgg cgg gac gag gcg acc cgc agc 271  
 Leu Phe Val Arg Trp Leu Thr Glu Trp Arg Asp Glu Ala Thr Arg Ser  
 20 25 30 35  
 agg cac cgc acg cgc ttc gta ttt cag aag gcg ctg cgt tcc ctc cga 319  
 Arg His Arg Thr Arg Phe Val Phe Gln Lys Ala Leu Arg Ser Leu Arg  
 40 45 50  
 cgg tac cca ctg ccg ctg cgc agc ggg aag gaa gct aag atc cta cag 367  
 Arg Tyr Pro Leu Pro Leu Arg Ser Gly Lys Glu Ala Lys Ile Leu Gln  
 55 60 65  
 cac ttc gga gac ggg ctc tgc cgg atg ctg gac gag cgg ctg cag cgg 415  
 His Phe Gly Asp Gly Leu Cys Arg Met Leu Asp Glu Arg Leu Gln Arg  
 70 75 80  
 cac cga aca tcg ggc ggt gac cat gcc ccg gac tca cca tct gga gag 463  
 His Arg Thr Ser Gly Gly Asp His Ala Pro Asp Ser Pro Ser Gly Glu  
 85 90 95  
 aac agt cca gcc ccg cag ggg cga ctt gcg gaa gtc cag gac tct tcc 511  
 Asn Ser Pro Ala Pro Gln Gly Arg Leu Ala Glu Val Gln Asp Ser Ser  
 100 105 110 115  
 atg cca gtt cct gcc cag ccc aaa gcg gga ggc tct ggc agc tac tgg 559  
 Met Pro Val Pro Ala Gln Pro Lys Ala Gly Gly Ser Gly Ser Tyr Trp  
 120 125 130  
 cca gct cgg cac tca gga gcc cga gtg ata ctg ctg gtg ctc tac cgg 607  
 Pro Ala Arg His Ser Gly Ala Arg Val Ile Leu Leu Val Leu Tyr Arg  
 135 140 145  
 gag cac ctg aat cct aat ggt cac cac ttc tta acc aag gag gag ctg 655  
 Glu His Leu Asn Pro Asn Gly His His Phe Leu Thr Lys Glu Glu Leu  
 150 155 160  
 ctg cag agg tgt gct cag aag tcc ccc agg gta gcc cct ggg agt gcc 703



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Pro	Pro	Trp	Pro	Ala	Leu	Arg	Ser	Leu	Leu	His	Arg	Asn	Leu	Val	Leu	
180					185					190					195	
agg	aca	cac	cag	cca	gcc	agg	tac	tca	ttg	acc	cca	gag	ggc	ctg	gag	799
Arg	Thr	His	Gln	Pro	Ala	Arg	Tyr	Ser	Leu	Thr	Pro	Glu	Gly	Leu	Glu	
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Leu	Ala	Gln	Lys	Leu	Ala	Glu	Ser	Glu	Gly	Leu	Ser	Leu	Leu	Asn	Val	
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ggc	atc	ggg	ccc	aag	gag	ccc	cct	ggg	gag	gag	aca	gca	gtg	cca	gga	895
Gly	Ile	Gly	Pro	Lys	Glu	Pro	Pro	Gly	Glu	Glu	Thr	Ala	Val	Pro	Gly	
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gca	gct	tca	gca	gag	ctt	gcc	agt	gaa	gca	ggg	gtc	cag	cag	cag	cca	943
Ala	Ala	Ser	Ala	Glu	Leu	Ala	Ser	Glu	Ala	Gly	Val	Gln	Gln	Gln	Pro	
		245				250					255					
ctg	gag	ctg	agg	cct	gga	gag	tac	agg	gtg	ctg	ttg	tgt	gtg	gac	att	991
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Gly	Glu	Thr	Arg	Gly	Gly	Gly	His	Arg	Pro	Glu	Leu	Leu	Arg	Glu	Leu	
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Gln	Arg	Leu	His	Val	Thr	His	Thr	Val	Arg	Lys	Leu	His	Val	Gly	Asp	
			295					300					305			
ttt	gtg	tgg	gtg	gct	cag	gag	acc	aat	cct	aga	gac	cca	gca	aac	cct	1135
Phe	Val	Trp	Val	Ala	Gln	Glu	Thr	Asn	Pro	Arg	Asp	Pro	Ala	Asn	Pro	
		310					315					320				
ggg	gag	ttg	gta	ctg	gat	cac	att	gtg	gag	cgc	aag	cga	ctg	gat	gac	1183
Gly	Glu	Leu	Val	Leu	Asp	His	Ile	Val	Glu	Arg	Lys	Arg	Leu	Asp	Asp	
		325				330					335					
ctt	tgc	agc	agc	atc	atc	gac	ggc	cgc	ttc	cgg	gag	cag	aag	ttc	cga	1231
Leu	Cys	Ser	Ser	Ile	Ile	Asp	Gly	Arg	Phe	Arg	Glu	Gln	Lys	Phe	Arg	
340					345					350					355	
ctg	aag	cgc	tgt	ggt	ctg	gag	cgc	cgg	gta	tac	ctg	gtg	gaa	gag	cat	1279
Leu	Lys	Arg	Cys	Gly	Leu	Glu	Arg	Arg	Val	Tyr	Leu	Val	Glu	Glu	His	
				360					365					370		
ggt	tcc	gtc	cac	aac	ctc	agc	ctt	cct	gag	agc	aca	ctg	ctg	cag	gct	1327
Gly	Ser	Val	His	Asn	Leu	Ser	Leu	Pro	Glu	Ser	Thr	Leu	Leu	Gln	Ala	
				375				380						385		
gtc	acc	aac	act	cag	gtc	att	gat	ggc	ttt	ttt	gtg	aag	cgc	aca	gca	1375
Val	Thr	Asn	Thr	Gln	Val	Ile	Asp	Gly	Phe	Phe	Val	Lys	Arg	Thr	Ala	
		390					395					400				
gac	att	aag	gag	tca	gcc	gcc	tac	ctg	gcc	ctc	ttg	act	cgg	ggc	ctg	1423
Asp	Ile	Lys	Glu	Ser	Ala	Ala	Tyr	Leu	Ala	Leu	Leu	Thr	Arg	Gly	Leu	
		405				410					415					
cag	aga	ctc	tac	cag	ggc	cac	acc	cta	cgc	agc	cgc	ccc	tgg	gga	acc	1471

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<210> 343
<211> 2013
<212> DNA
<213> Homo sapiens
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<220>
<221> misc_feature
<222> (1)...(2013)
<223> n = a,t,c or g
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cggcctgctc	actcctcagc	tgcaggagcc	agacgtgtgg	agtcccagca	gaggccaacc		120
tgtgtctctt	catctccctg	ggaaaggtgc	ccccgaggtg	aaagag	atg gcc tgg		175
					Met Ala Trp		
					1		
tgg aaa tcc tgg att gaa cag gag ggt gtc aca gtg aag agc agc tcc							223
Trp Lys Ser Trp Ile Glu Gln Glu Gly Val Thr Val Lys Ser Ser Ser							
	5				10		
						15	
cac ttc aac cca gac cct gat gca gag acc ctc tac aaa gcc atg aag							271
His Phe Asn Pro Asp Pro Asp Ala Glu Thr Leu Tyr Lys Ala Met Lys							
20					25		
						30	
							35
ggg atc ggg acc aac gag cag gct atc atc gat gtg ctc acc aag aga							319
Gly Ile Gly Thr Asn Glu Gln Ala Ile Ile Asp Val Leu Thr Lys Arg							
			40			45	
							50
agc aac acg cag cgg cag cag atc gcc aag tcc ttc aag gct cag ttc							367
Ser Asn Thr Gln Arg Gln Gln Ile Ala Lys Ser Phe Lys Ala Gln Phe							
			55			60	
							65
ggc aag gac ctc act gag acc ttg aag tct gag ctc agt ggc aag ttt							415
Gly Lys Asp Leu Thr Glu Thr Leu Lys Ser Glu Leu Ser Gly Lys Phe							
		70				75	
							80
gag agg ctc att gtg gcc ctt atg tac ccg cca tac aga tac gaa gcc							463
Glu Arg Leu Ile Val Ala Leu Met Tyr Pro Pro Tyr Arg Tyr Glu Ala							
	85					90	
							95
aag gag ctg cat gac gcc atg aag ggc tta gga acc aag gag ggt gtc							511
Lys Glu Leu His Asp Ala Met Lys Gly Leu Gly Thr Lys Glu Gly Val							
100					105		
						110	
							115
atc att gag atc ctg gcc tct cgg acc aag aac cag ctg cgg gag ata							559
Ile Ile Glu Ile Leu Ala Ser Arg Thr Lys Asn Gln Leu Arg Glu Ile							
			120				
						125	
							130
atg aag gcg tat gag gaa gac tat ggg tcc agc ctg gag gag gac atc							607
Met Lys Ala Tyr Glu Glu Asp Tyr Gly Ser Ser Leu Glu Glu Asp Ile							
			135				
						140	
							145
caa gca gac aca agt ggc tac ctg gag agg atc ctg gtg tgc ctc ctg							655
Gln Ala Asp Thr Ser Gly Tyr Leu Glu Arg Ile Leu Val Cys Leu Leu							
			150				
						155	
							160
cag ggc agc agg gat gat gtg agc agc ttt gtg gac ccg gca ctg gcc							703
Gln Gly Ser Arg Asp Asp Val Ser Ser Phe Val Asp Pro Ala Leu Ala							
						170	
							175
ctc caa gac gca cag gat ctg tat gcg gca ggc gag aag att cgt ggg							751
Leu Gln Asp Ala Gln Asp Leu Tyr Ala Ala Gly Glu Lys Ile Arg Gly							
180					185		
						190	
							195
act gat gag atg aaa ttc atc acc atc ctg tgc acg cgc agt gcc act							799
Thr Asp Glu Met Lys Phe Ile Thr Ile Leu Cys Thr Arg Ser Ala Thr							
			200				
						205	
							210
cac ctg ctg aga gtg ttt gaa gag tat gag aaa att gcc aac aag agc							847
His Leu Leu Arg Val Phe Glu Glu Tyr Glu Lys Ile Ala Asn Lys Ser							
			215				
						220	
							225

att gag gac agc atc aag agt gag acc cat ggc tca ctg gag gag gcc 895  
 Ile Glu Asp Ser Ile Lys Ser Glu Thr His Gly Ser Leu Glu Glu Ala  
 230 235 240

atg ctc act gtg gtg aaa tgc acc caa aac ctc cac agc tac ttt gca 943  
 Met Leu Thr Val Val Lys Cys Thr Gln Asn Leu His Ser Tyr Phe Ala  
 245 250 255

gag aga ctc tac tat gcc atg aag gga gca ggg acg cgt gat ggg acc 991  
 Glu Arg Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Arg Asp Gly Thr  
 260 265 270 275

ctg ata aga aac atc gtt tca agg agc gag att gac tta aat ctt atc 1039  
 Leu Ile Arg Asn Ile Val Ser Arg Ser Glu Ile Asp Leu Asn Leu Ile  
 280 285 290

aaa tgt cac ttc aag aag atg tac ggc aag acc ctc agc agc atg atc 1087  
 Lys Cys His Phe Lys Lys Met Tyr Gly Lys Thr Leu Ser Ser Met Ile  
 295 300 305

atg gaa gac acc agc ggc gac tac aag aac gcc ctg ctg agc ctg gtg 1135  
 Met Glu Asp Thr Ser Gly Asp Tyr Lys Asn Ala Leu Leu Ser Leu Val  
 310 315 320

ggc agc gac ccc tga ggcacagaag aacaagagca aagaccatga agccagagtc 1190  
 Gly Ser Asp Pro \*  
 325

tccaggactc ctcaactcaac ctccggccatg gacgcagggtt ggggtgtgagg ggggtcccag 1250

cctttcggtc ttctatttcc ctatttccag tgctttccag ccgggtttct gacccagagg 1310

gtggaaccgg cctggactcc tcttcccaac ttcttccagg tcatttccca gtgtgagcac 1370

aatgccaaacc ttagtgtttc tccagccaga cagatgcctc agcatgaagg gcttggggac 1430

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cacagggttat acagacccca gcccattcc catctactga aacagggtct ccacaagagg 1550

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acacgaatcc atcccaaccg agatgccatt aacattcatc taaaaatggt aggctctaaa 1730

tggacgaaaa attctctcgc catcttaata acaaaataaa ctacaaattc ctgacccaag 1790

gacactgtgt tataagaggc gtgggtccc ctggtggctg accaggtcag ctgccctggc 1850

cttgcacccc tctgcatgca gcacagaagg gtgtgaccat gccctcagca ccactcttgt 1910

cccactgaa cggcaactga gactgggtac ctggagattc tgaagtgcct ttgctgtggt 1970

tttcaaaata ataaagattt gtattcaact caaaaaaaaaaaa aaa 2013

&lt;210&gt; 344

&lt;211&gt; 864

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (57) .. (836)

&lt;400&gt; 344

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atg gcg gcg tcg agg ctg gag cta aac ctg gtg cgg ctg cta tcc cgc	104
Met Ala Ala Ser Arg Leu Glu Leu Asn Leu Val Arg Leu Leu Ser Arg	
1 5 10 15	
tgc gag gcg atg gca gcg gag aaa cgg gac ccg gac gag tgg cgc ctg	152
Cys Glu Ala Met Ala Ala Glu Lys Arg Asp Pro Asp Glu Trp Arg Leu	
20 25 30	
gag aag tac gtg gga gcc cta gag gac atg ttg cag gcc ctg aag gtc	200
Glu Lys Tyr Val Gly Ala Leu Glu Asp Met Leu Gln Ala Leu Lys Val	
35 40 45	
cac gcg agc aaa ccg gcc tct gag gtg atc aat gaa tat tcc tgg aag	248
His Ala Ser Lys Pro Ala Ser Glu Val Ile Asn Glu Tyr Ser Trp Lys	
50 55 60	
gtg gat ttt ctg aag ggg atg ctg caa gcc gag aag ctg acc tcc tcc	296
Val Asp Phe Leu Lys Gly Met Leu Gln Ala Glu Lys Leu Thr Ser Ser	
65 70 75 80	
tca gag aaa gca ctg gcc aac cag ttc ctg gcc cct ggc cgt gtg cca	344
Ser Glu Lys Ala Leu Ala Asn Gln Phe Leu Ala Pro Gly Arg Val Pro	
85 90 95	
acc aca gcc aga gag cga gtg ccc gcc aca aag acg gtg cat ctg cag	392
Thr Thr Ala Arg Glu Arg Val Pro Ala Thr Lys Thr Val His Leu Gln	
100 105 110	
tca cgg gcg cgg tac acc agc gag atg cgg agt gag cta cta ggc acg	440
Ser Arg Ala Arg Tyr Thr Ser Glu Met Arg Ser Glu Leu Leu Gly Thr	
115 120 125	
gac tct gca gag cct gag atg gac gta agg aag aga act gga gtg gca	488
Asp Ser Ala Glu Pro Glu Met Asp Val Arg Lys Arg Thr Gly Val Ala	
130 135 140	
ggg tcc cag cca gtg agt gag aag cag tcg gca gct gag cta gac ctc	536
Gly Ser Gln Pro Val Ser Glu Lys Gln Ser Ala Ala Glu Leu Asp Leu	
145 150 155 160	
gtc ctg cag cga cat cag aac ctc cag gaa aag ctg gcg gaa gag atg	584
Val Leu Gln Arg His Gln Asn Leu Gln Glu Lys Leu Ala Glu Glu Met	
165 170 175	
cta gga ctg gcc cgg agc ctc aag acc aat acc ctg gcc gcc cag agt	632
Leu Gly Leu Ala Arg Ser Leu Lys Thr Asn Thr Leu Ala Ala Gln Ser	
180 185 190	
gtc atc aag aag gac aac cag acc ctg tca cac tca ctg aaa atg gcg	680
Val Ile Lys Lys Asp Asn Gln Thr Leu Ser His Ser Leu Lys Met Ala	
195 200 205	
gac cag aac ctg gag aaa ctg aag acg gag tca gag cgt ctg gag cag	728
Asp Gln Asn Leu Glu Lys Leu Lys Thr Glu Ser Glu Arg Leu Glu Gln	
210 215 220	
cac acg cag aag tca gtc aac tgg ctg ctc tgg gcc atg ctc att atc	776

His Thr Gln Lys Ser Val Asn Trp Leu Leu Trp Ala Met Leu Ile Ile  
 225 230 235 240  
 gtc tgc ttc atc ttc att agc atg atc ctc ttc att cga atc atg cct 824  
 Val Cys Phe Ile Phe Ile Ser Met Ile Leu Phe Ile Arg Ile Met Pro  
 245 250 255  
 aaa ctc aaa taa agacccccgc ccacctaataa aaaaaaaaaa 864  
 Lys Leu Lys \*  
 260

<210> 345  
 <211> 827  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (217)..(618)

<220>  
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 <222> (1)...(827)  
 <223> n = a,t,c or g

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 gggttcttag gcctttggct tggactgag acttacacca tcagcttccc tggctcctgag 120  
 acttttggac ttggattgag ccacgctact ggcaccccag gatctccagc ttgcagacag 180  
 cctgtcgtgg gacttcacag cctccataat tataga atg gca atg gtc tct gcg 234  
 Met Ala Met Val Ser Ala  
 1 5  
 atg tcc tgg gtc ctg tat ttg tgg ata agt gct tgt gca atg cta ctc 282  
 Met Ser Trp Val Leu Tyr Leu Trp Ile Ser Ala Cys Ala Met Leu Leu  
 10 15 20  
 tgc cat gga tcc ctt cag cac act ttc cag cag cat cac ctg cac aga 330  
 Cys His Gly Ser Leu Gln His Thr Phe Gln Gln His His Leu His Arg  
 25 30 35  
 cca gaa gga ggg acg tgt gaa gtg ata gca gca cac cga tgt tgt aac 378  
 Pro Glu Gly Gly Thr Cys Glu Val Ile Ala Ala His Arg Cys Cys Asn  
 40 45 50  
 aag aat cgc att gag gag cgg tca caa aca gta aag tgt tcc tgt cta 426  
 Lys Asn Arg Ile Glu Glu Arg Ser Gln Thr Val Lys Cys Ser Cys Leu  
 55 60 65 70  
 cct gga aaa gtg gct gga aca aca aga aac cgg cct tct tgc gtc gat 474  
 Pro Gly Lys Val Ala Gly Thr Thr Arg Asn Arg Pro Ser Cys Val Asp  
 75 80 85  
 gcc tcc ata gtg att ggg aaa tgg tgg tgt gag atg gag cct tgc cta 522  
 Ala Ser Ile Val Ile Gly Lys Trp Trp Cys Glu Met Glu Pro Cys Leu  
 90 95 100



gaa gga gaa gaa tgt aag aca ctc cct gac aat tct gga tgg atg tgc 570  
 Glu Gly Glu Glu Cys Lys Thr Leu Pro Asp Asn Ser Gly Trp Met Cys  
           105                          110                          115

gca aca ggc aac aaa att aag acc acg aga att cac cca aga acc taa 618  
 Ala Thr Gly Asn Lys Ile Lys Thr Thr Arg Ile His Pro Arg Thr \*  
           120                          125                          130

cagaagcatt tgtggtagta aagggaaaac caaccctttg gaaaatacat tttggganc 678  
 tcaaaacatc tcacatatat acaagccaaa tgggatttct tacttncact ttgactggct 738  
 accngataat cacagtnctg ttacttgtgt ntaacgaaaa taccctacag tggaggaaga 798  
 cacaggcggt tttgggcaac accatnggg 827

<210> 346  
 <211> 1541  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (420) .. (989)

<400> 346  
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 atctttcact ccctggcctg ctaagagtta ctactcagg caatccctgc tccaccagag 180  
 gagactgtcc aattgccaaag caaccactg ctggccaatc acagagcttg gaggtgatgt 240  
 catggcaaga gcgagcagtg gtgctgatgt tgagagaagc ccagggtacc actaattgag 300  
 ggagtgagga agagagcagc tcgcttctaa ctggactgca cgttggtgac agcgtcccaa 360  
 gctggtgaca gaccactct gtaactttca gctagattca gccaccagat cccagaaac 419  
 atg acc ctt gct gcc tac aaa gag aag atg aag gag ctc ccg ctg gtg 467  
 Met Thr Leu Ala Ala Tyr Lys Glu Lys Met Lys Glu Leu Pro Leu Val  
           1                          5                          10                          15  
 tcc ttg ttc tgc tcc tgc ttc ctg gcc gat ccc ctg aat aag tcg tcc 515  
 Ser Leu Phe Cys Ser Cys Phe Leu Ala Asp Pro Leu Asn Lys Ser Ser  
                           20                          25                          30  
 tac aaa tat gaa gca gac acg gtg gac ctg aat tgg tgc gtc att tcc 563  
 Tyr Lys Tyr Glu Ala Asp Thr Val Asp Leu Asn Trp Cys Val Ile Ser  
           35                          40                          45  
 gac atg gaa gtc atc gag ctg aac aaa tgc acc tcg ggc caa tcc ttt 611  
 Asp Met Glu Val Ile Glu Leu Asn Lys Cys Thr Ser Gly Gln Ser Phe  
           50                          55                          60  
 gaa gtc atc ctg aag cca ccc tcc ttt gat ggg gtt ccc gag ttc aac 659  
 Glu Val Ile Leu Lys Pro Pro Ser Phe Asp Gly Val Pro Glu Phe Asn  
           65                          70                          75                          80  
 gcc tcc ctg cca agg cgg cga gac cca tcc ctg gaa gag atc cag aag 707  
 Ala Ser Leu Pro Arg Arg Arg Asp Pro Ser Leu Glu Glu Ile Gln Lys

	85	90	95	
aaa cta gaa gcg gct gag gag cga agg aag tac cag gaa gcg gag ctc				755
Lys Leu Glu Ala Ala Glu Glu Arg Arg Lys Tyr Gln Glu Ala Glu Leu				
	100	105	110	
ctg aaa cac cta gca gag aaa cgg gaa cat gag aga gag gtg atc caa				803
Leu Lys His Leu Ala Glu Lys Arg Glu His Glu Arg Glu Val Ile Gln				
	115	120	125	
aag gcc att gag gaa aac aac aac ttc atc aag atg gct aag gaa aaa				851
Lys Ala Ile Glu Glu Asn Asn Asn Phe Ile Lys Met Ala Lys Glu Lys				
	130	135	140	
ctg gcc cag aag atg gaa tcc aac aag gag aac agg gag gcc cac ctc				899
Leu Ala Gln Lys Met Glu Ser Asn Lys Glu Asn Arg Glu Ala His Leu				
	145	150	155	160
gcc gcc atg ttg gaa cgg ctg caa gag aag gac aag cac gcc gag gag				947
Ala Ala Met Leu Glu Arg Leu Gln Glu Lys Asp Lys His Ala Glu Glu				
	165	170	175	
gtg cgg aaa aac aag gag ctg aag gaa gag gcc tcc agg taa agcctag				996
Val Arg Lys Asn Lys Glu Leu Lys Glu Glu Ala Ser Arg *				
	180	185	190	
aggccaaaga actttccagg tcagccggac agctccagca gctccacgtt ccaggcagcc				1056
tcgcccgcgc gctgcgctcc cagcactggg gtttgggggg aggggggtgg ccaaggggcg				1116
tttcctctgc ttttggtggt tgtacatggt aagaattgac cagtgaagcc atcctatttg				1176
tttcggggga acaatgacgg ggtgggagag gggagaggag agagtgtggg aaagggagat				1236
ggagaagaac tcaaggacat tgcaaccctg cccggcgcag atctgatttt cacatctcta				1296
cctggacatt gagcctccag gcaccatggt gaggagagat gaaaaccagg gcggtagaac				1356
ttcaggggtga aggacagagt cctgggtggg gcagcggctg cagggcgcac cagagaaccc				1416
agccagaggg ggtgtgagta ccagtgggtgt tgcttccacc ctgcagcagg tgggatgagg				1476
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aaaaa				1541

<210> 347  
 <211> 1220  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (39) .. (998)

<220>  
 <221> misc\_feature  
 <222> (1) ... (1220)  
 <223> n = a,t,c or g

<400> 347

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atc tat tcg atg atg aag ata ccc cac caa acc caa aaa aag aga tct Ile Tyr Ser Met Met Lys Ile Pro His Gln Thr Gln Lys Lys Arg Ser 10 15 20		101
ctc gag gat ccg aat tcg cgg ccg cgt cga cgc ggt gtc ctg agc cga Leu Glu Asp Pro Asn Ser Arg Pro Arg Arg Gly Val Leu Ser Arg 25 30 35		149
tta cag cta ggt agt gga gcg ccg ctg ctt acc tgg gtg cag gag aca Leu Gln Leu Gly Ser Gly Ala Pro Leu Leu Thr Trp Val Gln Glu Thr 40 45 50		197
gcc gga gtc gct ggg gga gct ccg cgc cgc cgg acg ccc gtg acc atg Ala Gly Val Ala Gly Gly Ala Pro Arg Arg Arg Thr Pro Val Thr Met 55 60 65		245
tgg agg ctg ctg gct cgc gct agt gcg ccg ctc ctg cgg gtg ccc ttg Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro Leu 70 75 80 85		293
tca gat tcc tgg gca ctc ctc ccc gcc agt gct ggc gta aag aca ctg Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr Leu 90 95 100		341
ctc cca gta cca agt ttt gaa gat gtt tcc att cct gaa aaa ccc aag Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro Glu Lys Pro Lys 105 110 115		389
ctt aga ttt att gaa agg gca cca ctt gtg cca aaa gta aga aga gaa Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys Val Arg Arg Glu 120 125 130		437
cct aaa aat tta agt gac ata cgg gga cct tcc act gaa gct acg gag Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr Glu Ala Thr Glu 135 140 145		485
ttt aca gaa ggc aat ttt gca atc ttg gca ttg ggt ggt ggc tac ctg Phe Thr Glu Gly Asn Phe Ala Ile Leu Ala Leu Gly Gly Gly Tyr Leu 150 155 160 165		533
cat tgg ggc cac ttt gaa atg atg cgc ctg aca atc aac cgc tct atg His Trp Gly His Phe Glu Met Met Arg Leu Thr Ile Asn Arg Ser Met 170 175 180		581
gac ccc aag aac atg ttt gcc ata tgg cga gta cca gcc cct ttc aag Asp Pro Lys Asn Met Phe Ala Ile Trp Arg Val Pro Ala Pro Phe Lys 185 190 195		629
ccc atc act cgc aaa agt gtt ggg cat cgc atg ggg gga ggc aaa ggt Pro Ile Thr Arg Lys Ser Val Gly His Arg Met Gly Gly Gly Lys Gly 200 205 210		677
gct att gac cac tac gtg aca cct gtg aag gct ggc cgc ctt gtt gta Ala Ile Asp His Tyr Val Thr Pro Val Lys Ala Gly Arg Leu Val Val 215 220 225		725
gag atg ggt ggg cgt tgt gaa ttt gaa gaa gtg caa ggt ttc ctt gac Glu Met Gly Gly Arg Cys Glu Phe Glu Glu Val Gln Gly Phe Leu Asp 230 235 240 245		773

cag gtt gcc cac aag ttg ccc ttc gca gca aag gct gtg agc cgc ggg 821  
 Gln Val Ala His Lys Leu Pro Phe Ala Ala Lys Ala Val Ser Arg Gly  
 250 255 260  
 act cta gag aag atg cga aaa gat caa gag gaa aga gaa cgt aac aac 869  
 Thr Leu Glu Lys Met Arg Lys Asp Gln Glu Glu Arg Glu Arg Asn Asn  
 265 270 275  
 cag aac ccc tgg aca ttt gag cga ata gcc act gcc aac atg ctg ggc 917  
 Gln Asn Pro Trp Thr Phe Glu Arg Ile Ala Thr Ala Asn Met Leu Gly  
 280 285 290  
 ata cgg aaa gta ctg agc cca tat gac ttg acc cac aag ggg aaa tac 965  
 Ile Arg Lys Val Leu Ser Pro Tyr Asp Leu Thr His Lys Gly Lys Tyr  
 295 300 305  
 tgg ggc aag ttc tac atg ccc aaa cgt gtg tag tgagtgtgta ggagataact 1016  
 Trp Gly Lys Phe Tyr Met Pro Lys Arg Val \*  
 310 315 320  
 gtatataggc tactgaaaga aggattctgc atttctattc ccctcagcct acccactgaa 1076  
 gtctttgggt agctcttaag ccataactaa ggagcagcat ttgagtagat ttctgaaaaa 1136  
 caatgttatt tgttgattta aaaagaaaac tgtattttta ttaaataaaa tttaaaccatc 1196  
 acttcaggat ataaaaaaaaaaaa 1220

<210> 348  
 <211> 2159  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (3) .. (1868)

<400> 348  
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 Arg Asn Arg Ser Gly Ile Pro Gly Ser Thr His Ala Ser Gly Gly  
 1 5 10 15  
 tcc ggg agc gcg gcg gag acg atg cct gag atc aga gtc acg ccc ttg 95  
 Ser Gly Ser Ala Ala Glu Thr Met Pro Glu Ile Arg Val Thr Pro Leu  
 20 25 30  
 ggg gcc ggc cag gac gtg ggc cga agc tgc atc ctg gtc tcc att gcg 143  
 Gly Ala Gly Gln Asp Val Gly Arg Ser Cys Ile Leu Val Ser Ile Ala  
 35 40 45  
 ggc aag aat gtc atg ctg gac tgt gga atg cac atg ggc ttc aat gac 191  
 Gly Lys Asn Val Met Leu Asp Cys Gly Met His Met Gly Phe Asn Asp  
 50 55 60  
 gac cga cgc ttc cct gac ttc tcc tac atc acc cag aac ggc cgc cta 239  
 Asp Arg Arg Phe Pro Asp Phe Ser Tyr Ile Thr Gln Asn Gly Arg Leu  
 65 70 75  
 aca gac ttc ctg gac tgt gtg atc att agc cac ttc cac ctg gac cac 287  
 Thr Asp Phe Leu Asp Cys Val Ile Ile Ser His Phe His Leu Asp His  
 80 85 90 95

tgc ggg gca ctc ccc tac ttc agc gag atg gtg ggc tac gac ggc ccc Cys Gly Ala Leu Pro Tyr Phe Ser Glu Met Val Gly Tyr Asp Gly Pro	335
100 105 110	
atc tac atg act cac ccc acc cag gcc atc tgc ccc atc ttg ctg gag Ile Tyr Met Thr His Pro Thr Gln Ala Ile Cys Pro Ile Leu Leu Glu	383
115 120 125	
gac tac cgc aag atc gcc gta gac aag aag ggc gag gcc aac ttc ttc Asp Tyr Arg Lys Ile Ala Val Asp Lys Lys Gly Glu Ala Asn Phe Phe	431
130 135 140	
acc tcc cag atg atc aaa gac tgc atg aag aag gtg gtg gct gtc cac Thr Ser Gln Met Ile Lys Asp Cys Met Lys Lys Val Val Ala Val His	479
145 150 155	
ctc cac cag acg gtc cag gta gat gat gag ctg gag atc aag gcc tac Leu His Gln Thr Val Gln Val Asp Asp Glu Leu Glu Ile Lys Ala Tyr	527
160 165 170 175	
tat gca ggc cac gtg ctg ggg gca gcc atg ttc cag att aaa gtg ggc Tyr Ala Gly His Val Leu Gly Ala Ala Met Phe Gln Ile Lys Val Gly	575
180 185 190	
tca gag tct gtg gtc tac acg ggt gat tat aac atg acc cca gac cga Ser Glu Ser Val Val Tyr Thr Gly Asp Tyr Asn Met Thr Pro Asp Arg	623
195 200 205	
cac tta gga gct gcc tgg att gac aag tgc cgc ccc aac ctg ctc atc His Leu Gly Ala Ala Trp Ile Asp Lys Cys Arg Pro Asn Leu Leu Ile	671
210 215 220	
aca gag tcc acg tac gcc acg acc atc cgt gac tcc aag cgc tgc cgg Thr Glu Ser Thr Tyr Ala Thr Thr Ile Arg Asp Ser Lys Arg Cys Arg	719
225 230 235	
gag cga gac ttc ctg aag aaa gtc cac gag acc gtg gag cgt ggt ggg Glu Arg Asp Phe Leu Lys Lys Val His Glu Thr Val Glu Arg Gly Gly	767
240 245 250 255	
aag gtg ctg ata cct gtg ttc gcg ctg ggc cgc gcc cag gag ctc tgc Lys Val Leu Ile Pro Val Phe Ala Leu Gly Arg Ala Gln Glu Leu Cys	815
260 265 270	
atc ctc ctg gag acc ttc tgg gag cgc atg aac ctg aag gtg ccc atc Ile Leu Leu Glu Thr Phe Trp Glu Arg Met Asn Leu Lys Val Pro Ile	863
275 280 285	
tac ttc tcc acg ggg ctg acc gag aag gcc aac cac tac tac aag ctg Tyr Phe Ser Thr Gly Leu Thr Glu Lys Ala Asn His Tyr Tyr Lys Leu	911
290 295 300	
ttc atc ccc tgg acc aac cag aag atc cgc aag act ttc gtg cag agg Phe Ile Pro Trp Thr Asn Gln Lys Ile Arg Lys Thr Phe Val Gln Arg	959
305 310 315	
aac atg ttt gag ttc aag cac atc aag gcc ttc gac cgg gct ttt gct Asn Met Phe Glu Phe Lys His Ile Lys Ala Phe Asp Arg Ala Phe Ala	1007
320 325 330 335	
gac aac cca gga ccg atg gtt gtg ttt gcc acg cca gga atg ctg cac Asp Asn Pro Gly Pro Met Val Val Phe Ala Thr Pro Gly Met Leu His	1055
340 345 350	

gct ggg cag tcc ctg cag atc ttc cgg aaa tgg gcc gga aac gaa aag Ala Gly Gln Ser Leu Gln Ile Phe Arg Lys Trp Ala Gly Asn Glu Lys 355 360 365	1103
aac atg gtc atc atg ccc ggc tac tgc gtg cag ggc acc gtc ggc cac Asn Met Val Ile Met Pro Gly Tyr Cys Val Gln Gly Thr Val Gly His 370 375 380	1151
aag atc ctc agc ggg cag cgg aag ctc gag atg gag ggg cgg cag gtg Lys Ile Leu Ser Gly Gln Arg Lys Leu Glu Met Glu Gly Arg Gln Val 385 390 395	1199
ctg gag gtc aag atg cag gtg gag tac atg tca ttc agc gca cac gcg Leu Glu Val Lys Met Gln Val Glu Tyr Met Ser Phe Ser Ala His Ala 400 405 410 415	1247
gac gcc aag ggc atc atg cag ctg gtg ggc cag gca gag ccg gag agc Asp Ala Lys Gly Ile Met Gln Leu Val Gly Gln Ala Glu Pro Glu Ser 420 425 430	1295
gtg ctg ctg gtg cat ggc gag gcc aag aag atg gag ttc ctg aag cag Val Leu Leu Val His Gly Glu Ala Lys Lys Met Glu Phe Leu Lys Gln 435 440 445	1343
aag atc gag cag gag ctc cgg gtc aac tgc tac atg ccg gcc aat ggc Lys Ile Glu Gln Glu Leu Arg Val Asn Cys Tyr Met Pro Ala Asn Gly 450 455 460	1391
gag acg gtg acg ctg ccc aca agc ccc agc atc ccc gta ggc atc tcg Glu Thr Val Thr Leu Pro Thr Ser Pro Ser Ile Pro Val Gly Ile Ser 465 470 475	1439
ctg ggg ctg ctg aag cgg gag atg gcg cag ggg ctg ctc cct gag gcc Leu Gly Leu Leu Lys Arg Glu Met Ala Gln Gly Leu Leu Pro Glu Ala 480 485 490 495	1487
aag aag cct cgg ctc ctg cac ggc acc ctg atc atg aag gac agc aac Lys Lys Pro Arg Leu Leu His Gly Thr Leu Ile Met Lys Asp Ser Asn 500 505 510	1535
ttc cgg ctg gtg tcc tca gag caa gcc ctc aaa gag ctg ggt ctg gct Phe Arg Leu Val Ser Ser Glu Gln Ala Leu Lys Glu Leu Gly Leu Ala 515 520 525	1583
gag cac cag ctg cgc ttc acc tgc cgc gtg cac ctg cat gac aca cgc Glu His Gln Leu Arg Phe Thr Cys Arg Val His Leu His Asp Thr Arg 530 535 540	1631
aag gag cag gag acg gca ttg cgc gtc tac agc cac ctc aag agc gtc Lys Glu Gln Glu Thr Ala Leu Arg Val Tyr Ser His Leu Lys Ser Val 545 550 555	1679
ctg aag gac cac tgt gtg cag cac ctc ccg gac ggc tct gtg act gtg Leu Lys Asp His Cys Val Gln His Leu Pro Asp Gly Ser Val Thr Val 560 565 570 575	1727
gag tcc gtc ctc ctc cag gcc gcc gcc cct tct gag gac cca ggc acc Glu Ser Val Leu Leu Gln Ala Ala Ala Pro Ser Glu Asp Pro Gly Thr 580 585 590	1775
aag gtg ctg ctg gtc tcc tgg acc tac cag gac gag gag ctg ggg agc Lys Val Leu Leu Val Ser Trp Thr Tyr Gln Asp Glu Glu Leu Gly Ser 595 600 605	1823



ttc ctc aca tct ctg ctg aag aag ggc ctc ccc cag gcc ccc agc tga 1871  
 Phe Leu Thr Ser Leu Leu Lys Lys Gly Leu Pro Gln Ala Pro Ser  
           610                          615                          620

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tta ggc ttc gct tcc tac ggg gcg cac ggc gcc caa ttc cca gat gcc 96  
 Leu Gly Phe Ala Ser Tyr Gly Ala His Gly Ala Gln Phe Pro Asp Ala  
                           20                          25                          30

tac ggg aag gag ctg ttt gac aag gcc aac aaa cac cac ttc tta cac 144  
 Tyr Gly Lys Glu Leu Phe Asp Lys Ala Asn Lys His His Phe Leu His  
                           35                          40                          45

agc ctg gcc ctg tta ggg gtg ccc cat tgc aga aag cca ctc tgg gct 192  
 Ser Leu Ala Leu Leu Gly Val Pro His Cys Arg Lys Pro Leu Trp Ala  
                           50                          55                          60

ggg tta ttg cta gct tcc gga acg acc tta ttc tgc acc agc ttt tac 240  
 Gly Leu Leu Leu Ala Ser Gly Thr Thr Leu Phe Cys Thr Ser Phe Tyr  
   65                          70                          75                          80

tac cag gct ctg agt gga gac ccc agc atc cag act ttg gcc cct gcg 288  
 Tyr Gln Ala Leu Ser Gly Asp Pro Ser Ile Gln Thr Leu Ala Pro Ala  
                           85                          90                          95

gga ggg acc ctg cta ctc ttg ggc tgg ctt gcc ttg gct ctt tga gct 336  
 Gly Gly Thr Leu Leu Leu Leu Gly Trp Leu Ala Leu Ala Leu \*  
                           100                          105                          110

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 agaggattaa aaaggaaagg caaataaaaa aaaaaaaa 434

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gcc ggg aaa atg gag gct gtg att gag aag gaa tgc agc gcg ctc gga      95
Ala Gly Lys Met Glu Ala Val Ile Glu Lys Glu Cys Ser Ala Leu Gly
              20              25              30

ggc ctc ttc cag acc atc atc agc gac atg aag ggg agc tat cca gtt      143
Gly Leu Phe Gln Thr Ile Ile Ser Asp Met Lys Gly Ser Tyr Pro Val
              35              40              45

tgg gaa gat ttc ata aac aaa gca gga aag ctg cag tcc cag ctt cgg      191
Trp Glu Asp Phe Ile Asn Lys Ala Gly Lys Leu Gln Ser Gln Leu Arg
              50              55              60

aca aca gta gta gca gca gct gcc ttc ttg gac gcc ttt cag aaa gtg      239
Thr Thr Val Val Ala Ala Ala Ala Phe Leu Asp Ala Phe Gln Lys Val
              65              70              75

gct gac atg gcc acc aac aca cgt ggt ggg acc agg gag att gga tct      287
Ala Asp Met Ala Thr Asn Thr Arg Gly Gly Thr Arg Glu Ile Gly Ser
      80              85              90              95

gct ctc acc agg atg tgc atg agg cac aga agc att gaa gcc aag ctg      335
Ala Leu Thr Arg Met Cys Met Arg His Arg Ser Ile Glu Ala Lys Leu
              100              105              110

agg cag ttt tcg agc gct tta att gat tgt ctg ata aac cca ctt caa      383
Arg Gln Phe Ser Ser Ala Leu Ile Asp Cys Leu Ile Asn Pro Leu Gln
              115              120              125

gaa cag atg gaa gaa tgg aag aaa gtg gcc aac cag ctg gat aaa gac      431
Glu Gln Met Glu Glu Trp Lys Lys Val Ala Asn Gln Leu Asp Lys Asp
              130              135              140

cac gca aaa gaa tat aag aaa gcc cgc caa gag ata aaa aag aag tcc      479
His Ala Lys Glu Tyr Lys Lys Ala Arg Gln Glu Ile Lys Lys Lys Ser
              145              150              155

tcg gat acg ctg aaa ctg cag aag aaa gca aaa aaa ggg aga ggt gat      527
Ser Asp Thr Leu Lys Leu Gln Lys Lys Ala Lys Lys Gly Arg Gly Asp
      160              165              170              175

atc cag cct cag ttg gac agt gct ctc caa gat gtc aat gat aag tat      575
Ile Gln Pro Gln Leu Asp Ser Ala Leu Gln Asp Val Asn Asp Lys Tyr
              180              185              190

ctc tta ttg gaa gaa aca gaa aag cag gct gtc cgg aag gct ttg att      623
Leu Leu Leu Glu Glu Thr Glu Lys Gln Ala Val Arg Lys Ala Leu Ile
              195              200              205

gaa gaa cgt ggc cga ttc tgt acc ttc atc tct atg ctg cgg cca gtg      671
Glu Glu Arg Gly Arg Phe Cys Thr Phe Ile Ser Met Leu Arg Pro Val
              210              215              220

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att gaa gaa gaa atc tca atg cta ggg gaa ata acc cac ctt cag acc      719
Ile Glu Glu Glu Ile Ser Met Leu Gly Glu Ile Thr His Leu Gln Thr
    225                      230                      235

atc tcg gaa gat cta aaa agc ctg acc atg gac cct cac aaa ctg ccc      767
Ile Ser Glu Asp Leu Lys Ser Leu Thr Met Asp Pro His Lys Leu Pro
    240                      245                      250                      255

tcc tca agt gaa cag gtg att ctg gac ttg aaa ggt tct gat tac agc      815
Ser Ser Ser Glu Gln Val Ile Leu Asp Leu Lys Gly Ser Asp Tyr Ser
                      260                      265                      270

tgg tcg tat cag acg cca ccc tct tcc ccc agc acc acc atg tcc aga      863
Trp Ser Tyr Gln Thr Pro Pro Ser Ser Pro Ser Thr Thr Met Ser Arg
                      275                      280                      285

aag tcc agt gtc tgc agc agc ctg aac agt gtc aac agc agt gac tcc      911
Lys Ser Ser Val Cys Ser Ser Leu Asn Ser Val Asn Ser Ser Asp Ser
                      290                      295                      300

cgg tcc agc ggc tcc cac tcg cat tcc ccc agc tca cat tac cgc tac      959
Arg Ser Ser Gly Ser His Ser His Ser Pro Ser Ser His Tyr Arg Tyr
    305                      310                      315

cgc agc tcc aac ctg gcc cag cag gct cct gtg agg ctg tcc agc gtg      1007
Arg Ser Ser Asn Leu Ala Gln Gln Ala Pro Val Arg Leu Ser Ser Val
    320                      325                      330                      335

tcc tcc cat gac tca gga ttc ata tcc cag gat gcc ttc cag tcc aag      1055
Ser Ser His Asp Ser Gly Phe Ile Ser Gln Asp Ala Phe Gln Ser Lys
                      340                      345                      350

tca cca tcc ccc atg ccg cca gag gcc ccc aac cag cgc cgc aaa gag      1103
Ser Pro Ser Pro Met Pro Pro Glu Ala Pro Asn Gln Arg Arg Lys Glu
                      355                      360                      365

aag cga gaa ccg gac ccc aac ggg gga gga ccc act acc gcc agc ggc      1151
Lys Arg Glu Pro Asp Pro Asn Gly Gly Gly Pro Thr Thr Ala Ser Gly
                      370                      375                      380

cca cct gca gca gct gag gag gct cag aga cca cgg agc atg a          1194
Pro Pro Ala Ala Ala Glu Glu Ala Gln Arg Pro Arg Ser Met
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Met Asn Leu Glu Gly Leu Glu Met Val Ala Val Leu Val Val Leu Ala
    1                      5                      10                      15

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ctg ttt gtc aag gtc ctg gag cag ttt ggc ctc ttt gag cct gtc tcc      96

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Leu	Phe	Val	Lys	Val	Leu	Glu	Gln	Phe	Gly	Leu	Phe	Glu	Pro	Val	Ser	
			20					25					30			
ttg	gaa	ggc	cac	cct	cca	ggg	ccc	act	aaa	aaa	gcg	ctg	aag	cag	cga	144
Leu	Glu	Gly	His	Pro	Pro	Gly	Pro	Thr	Lys	Lys	Ala	Leu	Lys	Gln	Arg	
		35					40					45				
ttc	ctc	aag	ctg	ctg	ccg	tgc	tgc	ggg	ccc	caa	gcc	ctg	ccc	tca	gtc	192
Phe	Leu	Lys	Leu	Leu	Pro	Cys	Cys	Gly	Pro	Gln	Ala	Leu	Pro	Ser	Val	
	50					55					60					
agt	gaa	agc	aag	tgc	ctc	tca	tgt	gct	tcc	ggg	ggc	ggg	gct	cga	tgt	240
Ser	Glu	Ser	Lys	Cys	Leu	Ser	Cys	Ala	Ser	Gly	Gly	Gly	Ala	Arg	Cys	
65					70					75					80	
gtg	cac	agc	gtg	gac	gat	gaa	ttt	gaa	ttg	tcc	acc	gtg	tgt	cac	cgg	288
Val	His	Ser	Val	Asp	Asp	Glu	Phe	Glu	Leu	Ser	Thr	Val	Cys	His	Arg	
				85				90						95		
cct	gag	ggt	ctg	gag	cag	ctg	cag	gag	caa	acc	aaa	ttc	acg	cgc	aag	336
Pro	Glu	Gly	Leu	Glu	Gln	Leu	Gln	Glu	Gln	Thr	Lys	Phe	Thr	Arg	Lys	
			100					105					110			
gag	ttg	cag	gtc	ctg	tac	cgg	ggc	ttc	aag	aac	gaa	tgt	ccc	agc	gga	384
Glu	Leu	Gln	Val	Leu	Tyr	Arg	Gly	Phe	Lys	Asn	Glu	Cys	Pro	Ser	Gly	
		115					120					125				
att	gtc	aat	gag	gag	aac	ttc	aag	cag	att	tac	tcc	cag	ttc	ttt	cct	432
Ile	Val	Asn	Glu	Glu	Asn	Phe	Lys	Gln	Ile	Tyr	Ser	Gln	Phe	Phe	Pro	
	130					135					140					
caa	gga	gac	tcc	agc	acc	tat	gcc	act	ttt	ctc	ttc	aat	gcc	ttt	gac	480
Gln	Gly	Asp	Ser	Ser	Thr	Tyr	Ala	Thr	Phe	Leu	Phe	Asn	Ala	Phe	Asp	
145					150					155					160	
acc	aac	cat	gat	ggc	tcg	gtc	agt	ttt	gag	gac	ttt	gtg	gct	ggt	ttg	528
Thr	Asn	His	Asp	Gly	Ser	Val	Ser	Phe	Glu	Asp	Phe	Val	Ala	Gly	Leu	
				165					170					175		
tcc	gtg	att	ctt	cgg	gga	act	gta	gat	gac	agg	ctt	aat	tgg	gcc	ttc	576
Ser	Val	Ile	Leu	Arg	Gly	Thr	Val	Asp	Asp	Arg	Leu	Asn	Trp	Ala	Phe	
			180					185					190			
aac	ctg	tat	gac	ctt	aac	aag	gac	ggc	tgc	atc	acc	aag	gag	gaa	atg	624
Asn	Leu	Tyr	Asp	Leu	Asn	Lys	Asp	Gly	Cys	Ile	Thr	Lys	Glu	Glu	Met	
		195					200					205				
ctt	gac	atc	atg	aag	tcc	atc	tat	gac	atg	atg	ggc	aag	tac	acg	tac	672
Leu	Asp	Ile	Met	Lys	Ser	Ile	Tyr	Asp	Met	Met	Gly	Lys	Tyr	Thr	Tyr	
	210					215					220					
cct	gca	ctc	cgg	gag	gag	gcc	cca	agg	gaa	cac	gtg	gag	agc	ttc	ttc	720
Pro	Ala	Leu	Arg	Glu	Glu	Ala	Pro	Arg	Glu	His	Val	Glu	Ser	Phe	Phe	
225					230					235					240	
cag	aag	atg	gac	aga	aac	aag	gat	ggt	gtg	gtg	acc	att	gag	gaa	ttc	768
Gln	Lys	Met	Asp	Arg	Asn	Lys	Asp	Gly	Val	Val	Thr	Ile	Glu	Glu	Phe	
				245				250						255		
att	gag	tct	tgt	caa	aag	gat	gag	aac	atc	atg	agg	tcc	atg	cag	ctc	816
Ile	Glu	Ser	Cys	Gln	Lys	Asp	Glu	Asn	Ile	Met	Arg	Ser	Met	Gln	Leu	
			260					265						270		
ttt	gac	aat	gtc	atc	tag	cccca	ggagaggggg	tcagtgtttc	ctgggggggac							870

Phe Asp Asn Val Ile \*

275

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 Met Ile Trp  
 1  
 tac aca gag aag ggg cac cta acc aag act agg gac ttc aag aag tta 165  
 Tyr Thr Glu Lys Gly His Leu Thr Lys Thr Arg Asp Phe Lys Lys Leu  
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 Arg Lys Leu Ser Gly Ser Gly Asp Ser Trp Ala Arg Ala Pro Thr His  
 20 25 30 35  
 cac aca att cag aca aga gct ttg tgg ccc tgt gca aga aag gac ctc 261  
 His Thr Ile Gln Thr Arg Ala Leu Trp Pro Cys Ala Arg Lys Asp Leu  
 40 45 50  
 att att ctt ttt acc tta cag aat gtt gct gag gca cag tgc atc gcc 309  
 Ile Ile Leu Phe Thr Leu Gln Asn Val Ala Glu Ala Gln Cys Ile Ala

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Asn Gln Val Gln Leu Phe Tyr Ala Thr Asp Arg Lys Glu Thr Tyr Gly			
70	75	80	
tta gtg gag acc ttt aac ctc aga cca aat gag ttc aaa tat atg tct			405
Leu Val Glu Thr Phe Asn Leu Arg Pro Asn Glu Phe Lys Tyr Met Ser			
85	90	95	
gtc atc gct gaa ttg gag caa agc gga ctt gga gca gaa ctg aaa tgt			453
Val Ile Ala Glu Leu Glu Gln Ser Gly Leu Gly Ala Glu Leu Lys Cys			
100	105	110	115
gcc cag aac caa aat aag act tag aactgtacag gttggccctt cacctagttg			507
Ala Gln Asn Gln Asn Lys Thr *			
120			
actcagccct cgatagtcta gagcccaccc cctcctcagg aactcaagag ctcagcattt			567
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245 250 255	
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Met Ser Pro Val Thr Thr Pro Thr Asp Glu Asp Val Gly His Arg Ile
      580                      585                      590                      595

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Lys His Val Ala Gly Ser Thr Gln Thr Arg His Ile Pro Glu Asp Thr
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ccc aac ggt ttc cac ctg cag agc gtg tcc aag ctg ctg ctg gtt atc      2227
Pro Asn Gly Phe His Leu Gln Ser Val Ser Lys Leu Leu Leu Val Ile
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Ser Cys Val Ile Cys Phe Ser Leu Val Leu Leu Val Ile Leu Asn Met
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Met Leu Phe Tyr Lys Leu Trp Met Leu Glu Tyr Thr Thr Gln Thr Leu
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act gcc tgg cag ggt cta agg ctc caa gaa agg tta ccc cag tct cag      2371
Thr Ala Trp Gln Gly Leu Arg Leu Gln Glu Arg Leu Pro Gln Ser Gln
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Asp Gln Met Lys Asp Ser Leu Ile Asn Leu Gln Asn Gly Ile Arg Ser
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ctg acc agt gat gac gag gac tac gtg ccc cct gac gac gac ttc aac	1075
Leu Thr Ser Asp Asp Glu Asp Tyr Val Pro Pro Asp Asp Asp Phe Asn	
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Thr Met Gly Tyr Cys Glu Glu Ile Pro Val Glu Glu Asn Glu Val Asn	
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Asp Ser Ser Ser Lys Ser Ser Ile Glu Thr Lys Pro Asp Ala Ser Pro	
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Gln Leu Pro Lys Lys Ser Ile Thr Asn Ser Thr Leu Thr Ser Thr Gly	
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Ser Ser Glu Ala Pro Val Ser Phe Asp Gly Leu Pro Leu Glu Glu Glu	
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Ala Leu Glu Gly Asp Gly Ser Leu Glu Lys Glu Leu Ala Ile Asp Asn	
310 315 320	
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Ile Met Gly Glu Lys Ile Glu Met Ile Ala Pro Val Asn Ser Pro Ser	
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Leu Asp Phe Asn Asp Asn Glu Asp Ile Pro Thr Glu Leu Ser Asp Ser	
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Ser Asp Thr His Asp Glu Gly Glu Val Gln Ala Phe Tyr Glu Asp Leu	
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Tyr Thr Leu Thr Arg Val Ala Arg Asn Lys Ser Arg Leu Arg Val Ser	
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Thr Glu Leu Arg Tyr Arg Lys Gln Pro Trp Gly Leu Val Lys Thr Phe	
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Ile Glu Lys Asn Phe Trp Ser Gly Leu Glu Asp Tyr Phe Arg His Leu	
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Lys His Val Ala Gly Ser Thr Gln Thr Arg His Ile Pro Glu Asp Thr	
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ccc aac ggt ttc cac ctg cag agc gtg tcc aag ctg ctg ctg gtt atc	2227
Pro Asn Gly Phe His Leu Gln Ser Val Ser Lys Leu Leu Leu Val Ile	
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Ser Cys Val Leu Val Leu Leu Val Ile Leu Asn Met Met Leu Phe Tyr	
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Lys Leu Trp Met Leu Glu Tyr Thr Thr Gln Thr Leu Thr Ala Trp Gln	
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Gly Leu Arg Leu Gln Glu Arg Leu Pro Gln Ser Gln Thr Glu Trp Ala	
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Gln Leu Leu Glu Ser Gln Gln Lys Tyr His Asp Thr Glu Leu Gln Lys	
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695 700 705	
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 Ser Glu Ser Glu Glu Lys Arg Asn Arg Tyr His \*  
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 Thr Glu Arg Asp Gly Leu Ala Pro Glu Lys Thr Ser Pro Asp Arg Asp  
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 aag aaa aaa gag cag tca gaa gta tct gtt tct cct aga gct tca aaa 271  
 Lys Lys Lys Glu Gln Ser Glu Val Ser Val Ser Pro Arg Ala Ser Lys  
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 cat cat tat tca aga tca cga tca agg tca aga gaa aga aaa cga aag 319  
 His His Tyr Ser Arg Ser Arg Ser Arg Ser Arg Glu Arg Lys Arg Lys  
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 Gly Arg Arg His Glu Ser Lys Asp Lys Ser Ser Lys Lys His Lys Ser  
 70 75 80 85  
 gag gaa cat aat gac aaa gaa cat tct tct gat aaa gga aga gag cga 463  
 Glu Glu His Asn Asp Lys Glu His Ser Ser Asp Lys Gly Arg Glu Arg  
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Pro Met Lys Phe Ala Glu Gln Glu Lys Lys Arg Lys Met Leu Trp Gln	
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375 380 385	
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390 395 400 405	

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Leu Asp Leu Glu Ala Gly Pro Ser Ser Gly Lys Leu Cys Pro Arg Ala				
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Arg Arg Trp Gln Pro Leu Pro Ser *				
	125	130		
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 <222> (95) .. (781)

caagctggct agcgtttaaa cttaagcttg gtaccgagct cggatccact agtccagtgt				60
ggtggaattc ggtcggcagc acagagctct ggag				
		atg aag acc ctg ttc ctg		112
		Met Lys Thr Leu Phe Leu		
		1	5	
ggt gtc acg ctc ggc ctg gcc gct gcc ctg tcc ttc acc ctg gag gag				160
Gly Val Thr Leu Gly Leu Ala Ala Ala Leu Ser Phe Thr Leu Glu Glu				
	10	15	20	
gag gat atc aca ggg acc tgg tac gtg aag gcc atg gtg gtc gat aag				208
Glu Asp Ile Thr Gly Thr Trp Tyr Val Lys Ala Met Val Val Asp Lys				
	25	30	35	
gac ttt ccg gag gac agg agg ccc agg aag gtg tcc cca gtg aag gtg				256
Asp Phe Pro Glu Asp Arg Arg Pro Arg Lys Val Ser Pro Val Lys Val				
	40	45	50	
aca gcc ctg ggc ggt ggg aac ttg gaa gcc acg ttc acc ttc atg agg				304
Thr Ala Leu Gly Gly Gly Asn Leu Glu Ala Thr Phe Thr Phe Met Arg				
	55	60	65	70
gag gat cgg tgc atc cag aag aaa atc ctg atg cgg aag acg gag gag				352
Glu Asp Arg Cys Ile Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu				
	75	80	85	
cct ggc aaa ttc agc gcc tat ggg ggc agg aag ctc ata tac ctg cag				400
Pro Gly Lys Phe Ser Ala Tyr Gly Gly Arg Lys Leu Ile Tyr Leu Gln				
	90	95	100	
gag ctg ccc ggg acg gac gac tac gtc ttt tac tgc aaa gac cag cgc				448



Glu	Leu	Pro	Gly	Thr	Asp	Asp	Tyr	Val	Phe	Tyr	Cys	Lys	Asp	Gln	Arg	
	105						110					115				
cgt	ggg	ggc	ctg	cgc	tac	atg	gga	aag	ctt	gtg	gca	tct	gct	ccc	tgc	496
Arg	Gly	Gly	Leu	Arg	Tyr	Met	Gly	Lys	Leu	Val	Ala	Ser	Ala	Pro	Cys	
	120					125					130					
agg	gcc	gtg	ccg	ctg	tcc	cca	cgt	cgg	ctc	acc	tgg	cca	cct	cac	ctg	544
Arg	Ala	Val	Pro	Leu	Ser	Pro	Arg	Arg	Leu	Thr	Trp	Pro	Pro	His	Leu	
	135				140					145					150	
cag	gta	gga	atc	cta	ata	cca	acc	tgg	agg	ccc	tgg	aag	aat	tta	aga	592
Gln	Val	Gly	Ile	Leu	Ile	Pro	Thr	Trp	Arg	Pro	Trp	Lys	Asn	Leu	Arg	
			155					160						165		
aat	tgg	tgc	agc	aca	agg	gac	tct	cgg	agg	agg	aca	ttt	tca	tgc	ccc	640
Asn	Trp	Cys	Ser	Thr	Arg	Asp	Ser	Arg	Arg	Arg	Thr	Phe	Ser	Cys	Pro	
			170					175					180			
tgc	aga	cgg	gaa	gct	gcg	ttc	tcg	aac	act	agg	cag	ccc	ccg	ggt	ctg	688
Cys	Arg	Arg	Glu	Ala	Ala	Phe	Ser	Asn	Thr	Arg	Gln	Pro	Pro	Gly	Leu	
	185						190					195				
cac	ctc	cag	agc	cca	ccc	tac	cac	cag	aca	cag	agc	ccg	gac	cac	ctg	736
His	Leu	Gln	Ser	Pro	Pro	Tyr	His	Gln	Thr	Gln	Ser	Pro	Asp	His	Leu	
	200					205					210					
gac	cta	ccc	tcc	agc	cat	gac	cct	tcc	ctg	ctc	cca	ccc	acc	tga		781
Asp	Leu	Pro	Ser	Ser	His	Asp	Pro	Ser	Leu	Leu	Pro	Pro	Thr	*		
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<210> 361  
 <211> 2147  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (58) .. (1683)

<400> 361																
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atg	agg	cag	aag	cgg	aaa	gga	gat	ctc	agc	cct	gct	gag	ctg	atg	atg	105
Met	Arg	Gln	Lys	Arg	Lys	Gly	Asp	Leu	Ser	Pro	Ala	Glu	Leu	Met	Met	
1				5					10					15		
ctg	act	ata	gga	gat	gtt	att	aaa	caa	ctg	att	gaa	gcc	cac	gag	cag	153
Leu	Thr	Ile	Gly	Asp	Val	Ile	Lys	Gln	Leu	Ile	Glu	Ala	His	Glu	Gln	
			20					25					30			
ggg	aaa	gac	atc	gat	cta	aat	aag	gtg	aaa	acc	aag	aca	gct	gcc	aaa	201
Gly	Lys	Asp	Ile	Asp	Leu	Asn	Lys	Val	Lys	Thr	Lys	Thr	Ala	Ala	Lys	
		35					40					45				
tat	ggc	ctt	tct	gcc	cag	ccc	cgc	ctg	gtg	gat	atc	att	gct	gcc	gtc	249
Tyr	Gly	Leu	Ser	Ala	Gln	Pro	Arg	Leu	Val	Asp	Ile	Ile	Ala	Ala	Val	
	50					55					60					
cct	cct	cag	tat	cgc	aag	gtc	ttg	atg	ccc	aag	tta	aag	gcg	aaa	ccc	297
Pro	Pro	Gln	Tyr	Arg	Lys	Val	Leu	Met	Pro	Lys	Leu	Lys	Ala	Lys	Pro	

65	70					75					80					
atc aga act gct agt ggg att gct gtc gtg gct gtg atg tgc aaa ccc																345
Ile Arg Thr Ala Ser Gly Ile Ala Val Val Ala Val Met Cys Lys Pro																
	85					90					95					
cac aga tgt cca cac atc agt ttt aca gga aat ata tgt gta tac tgc																393
His Arg Cys Pro His Ile Ser Phe Thr Gly Asn Ile Cys Val Tyr Cys																
	100					105					110					
cct ggt gga cct gat tct gat ttt gag tat tcc acc cag tct tac act																441
Pro Gly Gly Pro Asp Ser Asp Phe Glu Tyr Ser Thr Gln Ser Tyr Thr																
	115					120					125					
ggc tat gag cca acc tcc atg aga gct atc cgt gcc aga tat gac cct																489
Gly Tyr Glu Pro Thr Ser Met Arg Ala Ile Arg Ala Arg Tyr Asp Pro																
	130					135					140					
ttc cta cag aca aga cac cga ata gaa cag tta aaa caa ctt ggt cat																537
Phe Leu Gln Thr Arg His Arg Ile Glu Gln Leu Lys Gln Leu Gly His																
	145					150					155					160
agt gtg gat aaa gtg gag ttt att gtg atg ggt gga acg ttt atg gcc																585
Ser Val Asp Lys Val Glu Phe Ile Val Met Gly Gly Thr Phe Met Ala																
	165					170					175					
ctt cca gaa gaa tac aga gat tat ttt att cga aat tta cat gat gcc																633
Leu Pro Glu Glu Tyr Arg Asp Tyr Phe Ile Arg Asn Leu His Asp Ala																
	180					185					190					
tta tca gga cat act tcc aac aat att tac gag gca gtc aag tat tct																681
Leu Ser Gly His Thr Ser Asn Asn Ile Tyr Glu Ala Val Lys Tyr Ser																
	195					200					205					
gag aga agc ctc aca aag tgt att gga att act att gaa acc aga cca																729
Glu Arg Ser Leu Thr Lys Cys Ile Gly Ile Thr Ile Glu Thr Arg Pro																
	210					215					220					
gat tac tgc atg aag cga cat tta agt gac atg ttg acc tat ggc tgc																777
Asp Tyr Cys Met Lys Arg His Leu Ser Asp Met Leu Thr Tyr Gly Cys																
	225					230					235					240
aca agg ctg gag att ggg gtg cag agt gtt tat gaa gat gtg gct aga																825
Thr Arg Leu Glu Ile Gly Val Gln Ser Val Tyr Glu Asp Val Ala Arg																
	245					250					255					
gac acc aac agg ggc cac act gtg aag gca gtg tgt gag tca ttt cac																873
Asp Thr Asn Arg Gly His Thr Val Lys Ala Val Cys Glu Ser Phe His																
	260					265					270					
ctg gcc aaa gat tcc ggt ttt aaa gtg gtg gcc cat atg atg cct gac																921
Leu Ala Lys Asp Ser Gly Phe Lys Val Val Ala His Met Met Pro Asp																
	275					280					285					
ctg cca aac gtg gga cta gaa aga gac att gaa cag ttc aca gag ttt																969
Leu Pro Asn Val Gly Leu Glu Arg Asp Ile Glu Gln Phe Thr Glu Phe																
	290					295					300					
ttt gag aac cct gct ttt cgt ccc gat ggg ctg aaa ctc tat cct acc																1017
Phe Glu Asn Pro Ala Phe Arg Pro Asp Gly Leu Lys Leu Tyr Pro Thr																
	305					310					315					320
ctg gtg att cgt ggg acc ggg ctt tat gag ctt tgg aaa tca gga aga																1065
Leu Val Ile Arg Gly Thr Gly Leu Tyr Glu Leu Trp Lys Ser Gly Arg																

325	330	335	
gat aag agt tac tct cct agt gac ctg gtt gaa ttg gtg gct cgg atc Asp Lys Ser Tyr Ser Pro Ser Asp Leu Val Glu Leu Val Ala Arg Ile 340 345 350			1113
cta gcc ctg gtg cct cca tgg act cga gtg tac cga gta cag agg gat Leu Ala Leu Val Pro Pro Trp Thr Arg Val Tyr Arg Val Gln Arg Asp 355 360 365			1161
att cca atg cct tta gtt agc tca gga gta gag cat ggt aac ctg aga Ile Pro Met Pro Leu Val Ser Ser Gly Val Glu His Gly Asn Leu Arg 370 375 380			1209
gag ctg gca ctt gca aga atg aaa gac ctg gga ata cag tgt cga gat Glu Leu Ala Leu Ala Arg Met Lys Asp Leu Gly Ile Gln Cys Arg Asp 385 390 395 400			1257
gtg aga acc aga gaa gtt gga atc caa gaa att cat cac aaa gta cgg Val Arg Thr Arg Glu Val Gly Ile Gln Glu Ile His His Lys Val Arg 405 410 415			1305
cca tac cag gtt gaa ttg gta agg aga gat tat gtt gca aat ggt ggc Pro Tyr Gln Val Glu Leu Val Arg Arg Asp Tyr Val Ala Asn Gly Gly 420 425 430			1353
tgg gaa aca ttc ttg tca tac gaa gac cca gat caa gac att ttg att Trp Glu Thr Phe Leu Ser Tyr Glu Asp Pro Asp Gln Asp Ile Leu Ile 435 440 445			1401
ggc ctg cta cga tta cgc aag tgt tca gaa gaa act ttc cgt ttc gaa Gly Leu Leu Arg Leu Arg Lys Cys Ser Glu Glu Thr Phe Arg Phe Glu 450 455 460			1449
ttg ggt gga ggt gtc tcc ata gta cga gag ctg cat gtg tat ggg agt Leu Gly Gly Gly Val Ser Ile Val Arg Glu Leu His Val Tyr Gly Ser 465 470 475 480			1497
gtg gtc cct gtg agc agc cgg gat cct act aaa ttt cag cat cag gga Val Val Pro Val Ser Ser Arg Asp Pro Thr Lys Phe Gln His Gln Gly 485 490 495			1545
ttt ggc atg ctg ctg atg gag gaa gca gaa aga ata gct aga gaa gaa Phe Gly Met Leu Leu Met Glu Glu Ala Glu Arg Ile Ala Arg Glu Glu 500 505 510			1593
cat ggg tct ggg aaa atc gct gtg ata tca gga gtg gat gtc ctg ggg His Gly Ser Gly Lys Ile Ala Val Ile Ser Gly Val Asp Val Leu Gly 515 520 525			1641
cag agg cag agg gga ggc cac cac aga agc tgt tca ctg tag gcacttt Gln Arg Gln Arg Gly Gly His His Arg Ser Cys Ser Leu * 530 535 540			1690
gcaaggggtc ggcaccagga attattatag aaagatcggc tacagattac aaggcccgtg			1750
catggtgaag atgctgaaat aatggccaca ccagtccact cttctgcagt atcctccctg			1810
gcagaacacg gagaatcagg atttcttaaa tactcaacag agaggctgag cagagcaa			1870
ggggggcttc accctcatcc cgcagctgca gagactggaa actgccttca aggccacggc			1930
tggtcatctg ctgaccacac cccagatccg ccctctcctg cgtgcacccc aaaaaatcac			1990

ttgcgttttt gaggtttaa tcactatcc agtttctaca ttttgcata ggcctgcagg 2050  
 tggcctatatt tgactcagac ggtgaaaaaa gcaaattaac tcatttggac accataactc 2110  
 atgcaataaaa actgattgtc attcgaaaaa aaaaaaa 2147

<210> 362  
 <211> 2076  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (58)..(1701)

<400> 362  
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 Met Arg Gln Lys Arg Lys Gly Asp Leu Ser Pro Ala Glu Leu Met Met  
 1 5 10 15  
 ctg act ata gga gat gtt att aaa caa ctg att gaa gcc cac gag cag 153  
 Leu Thr Ile Gly Asp Val Ile Lys Gln Leu Ile Glu Ala His Glu Gln  
 20 25 30  
 ggg aaa gac atc gat cta aat aag gtg aaa acc aag aca gct gcc aaa 201  
 Gly Lys Asp Ile Asp Leu Asn Lys Val Lys Thr Lys Thr Ala Ala Lys  
 35 40 45  
 tat ggc ctt tct gcc cag ccc cgc ctg gtg gat atc att gct gcc gtc 249  
 Tyr Gly Leu Ser Ala Gln Pro Arg Leu Val Asp Ile Ile Ala Ala Val  
 50 55 60  
 cct cct cag tat cgc aag gtc ttg atg ccc aag tta aag gcg aaa ccc 297  
 Pro Pro Gln Tyr Arg Lys Val Leu Met Pro Lys Leu Lys Ala Lys Pro  
 65 70 75 80  
 atc aga act gct agt ggg att gct gtc gtg gct gtg atg tgc aaa ccc 345  
 Ile Arg Thr Ala Ser Gly Ile Ala Val Val Ala Val Met Cys Lys Pro  
 85 90 95  
 cac aga tgt cca cac atc agt ttt aca gga aat ata tgt gta tac tgc 393  
 His Arg Cys Pro His Ile Ser Phe Thr Gly Asn Ile Cys Val Tyr Cys  
 100 105 110  
 cct ggt gga cct gat tct gat ttt gag tat tcc acc cag tct tac act 441  
 Pro Gly Gly Pro Asp Ser Asp Phe Glu Tyr Ser Thr Gln Ser Tyr Thr  
 115 120 125  
 ggc tat gag cca acc tcc atg aga gct atc cgt gcc aga tat gac cct 489  
 Gly Tyr Glu Pro Thr Ser Met Arg Ala Ile Arg Ala Arg Tyr Asp Pro  
 130 135 140  
 ttc cta cag aca aga cac cga ata gaa cag tta aaa caa ctt ggt cat 537  
 Phe Leu Gln Thr Arg His Arg Ile Glu Gln Leu Lys Gln Leu Gly His  
 145 150 155 160  
 agt gtg gat aaa gtg gag ttt att gtg atg ggt gga acg ttt atg gcc 585  
 Ser Val Asp Lys Val Glu Phe Ile Val Met Gly Gly Thr Phe Met Ala  
 165 170 175

ctt cca gaa gaa tac aga gat tat ttt att cga aat tta cat gat gcc	633
Leu Pro Glu Glu Tyr Arg Asp Tyr Phe Ile Arg Asn Leu His Asp Ala	
180 185 190	
tta tca gga cat act tcc aac aat att tac gag gca gtc aag tat tct	681
Leu Ser Gly His Thr Ser Asn Asn Ile Tyr Glu Ala Val Lys Tyr Ser	
195 200 205	
gag aga agc ctc aca aag tgt att gga att act att gaa acc aga cca	729
Glu Arg Ser Leu Thr Lys Cys Ile Gly Ile Thr Ile Glu Thr Arg Pro	
210 215 220	
gat tac tgc atg aag cga cat tta agt gac atg ttg acc tat ggc tgc	777
Asp Tyr Cys Met Lys Arg His Leu Ser Asp Met Leu Thr Tyr Gly Cys	
225 230 235 240	
aca agg ctg gag att ggg gtg cag agt gtt tat gaa gat gtg gct aga	825
Thr Arg Leu Glu Ile Gly Val Gln Ser Val Tyr Glu Asp Val Ala Arg	
245 250 255	
gac acc aac agg ggc cac act gtg aag gca gtg tgt gag tca ttt cac	873
Asp Thr Asn Arg Gly His Thr Val Lys Ala Val Cys Glu Ser Phe His	
260 265 270	
ctg gcc aaa gat tcc ggt ttt aaa gtg gtg gcc cat atg atg cct gac	921
Leu Ala Lys Asp Ser Gly Phe Lys Val Val Ala His Met Met Pro Asp	
275 280 285	
ctg cca aac gtg gga cta gaa aga gac att gaa cag ttc aca gag ttt	969
Leu Pro Asn Val Gly Leu Glu Arg Asp Ile Glu Gln Phe Thr Glu Phe	
290 295 300	
ttt gag aac cct gct ttt cgt ccc gat ggg ctg aaa ctc tat cct acc	1017
Phe Glu Asn Pro Ala Phe Arg Pro Asp Gly Leu Lys Leu Tyr Pro Thr	
305 310 315 320	
ctg gtg att cgt ggg acc ggg ctt tat gag ctt tgg aaa tca gga aga	1065
Leu Val Ile Arg Gly Thr Gly Leu Tyr Glu Leu Trp Lys Ser Gly Arg	
325 330 335	
gat aag agt tac tct cct agt gac ctg gtt gaa ttg gtg gct cgg atc	1113
Asp Lys Ser Tyr Ser Pro Ser Asp Leu Val Glu Leu Val Ala Arg Ile	
340 345 350	
cta gcc ctc gtg cct cca tgg act cga gtg tac cga gta cag agg gat	1161
Leu Ala Leu Val Pro Pro Trp Thr Arg Val Tyr Arg Val Gln Arg Asp	
355 360 365	
att cca atg cct tta gtt agc tca gga gta gag cat ggt aac ctg aga	1209
Ile Pro Met Pro Leu Val Ser Ser Gly Val Glu His Gly Asn Leu Arg	
370 375 380	
gag ctg gca ctt gca aga atg aaa gac ctc gga ata cag tgt cga gat	1257
Glu Leu Ala Leu Ala Arg Met Lys Asp Leu Gly Ile Gln Cys Arg Asp	
385 390 395 400	
gtg aga acc aga gaa gtt gga atc caa gaa att cat cac aaa gta cgg	1305
Val Arg Thr Arg Glu Val Gly Ile Gln Glu Ile His His Lys Val Arg	
405 410 415	
cca tac cag gtt gaa ttg gta agg aga gat tat gtt gca aat ggt ggc	1353
Pro Tyr Gln Val Glu Leu Val Arg Arg Asp Tyr Val Ala Asn Gly Gly	
420 425 430	

tgg gaa aca ttc ttg tca tac gaa gac cca gat caa gac att ttg att 1401  
 Trp Glu Thr Phe Leu Ser Tyr Glu Asp Pro Asp Gln Asp Ile Leu Ile  
 435 440 445  
 ggc ctc cta cga tta cgc aag tgt tca gaa gaa act ttc cgt ttc gaa 1449  
 Gly Leu Leu Arg Leu Arg Lys Cys Ser Glu Glu Thr Phe Arg Phe Glu  
 450 455 460  
 ttg ggt gga ggt gtc tcc ata gta cga gag ctg cat gtg tat ggg agt 1497  
 Leu Gly Gly Gly Val Ser Ile Val Arg Glu Leu His Val Tyr Gly Ser  
 465 470 475 480  
 gtg gtc cct gtg agc agc cgg gat cct act aaa ttt cag cat cag gga 1545  
 Val Val Pro Val Ser Ser Arg Asp Pro Thr Lys Phe Gln His Gln Gly  
 485 490 495  
 ttt ggc atg ctg ctg atg gag gaa gca gaa aga ata gct aga gaa gaa 1593  
 Phe Gly Met Leu Leu Met Glu Glu Ala Glu Arg Ile Ala Arg Glu Glu  
 500 505 510  
 cat ggg tct ggg aaa atc gct gtg ata tca ggg gtc ggc acc agg aat 1641  
 His Gly Ser Gly Lys Ile Ala Val Ile Ser Gly Val Gly Thr Arg Asn  
 515 520 525  
 tat tat aga aag atc ggc tac aga tta caa ggc ccg tac atg gtg aag 1689  
 Tyr Tyr Arg Lys Ile Gly Tyr Arg Leu Gln Gly Pro Tyr Met Val Lys  
 530 535 540  
 atg ctg aaa taa tgg ccacaccagt ccactcttct gcagtatcct ccctggcaga 1744  
 Met Leu Lys \*  
 545  
 acacggagaa tcaggatttc ttaaatactc aacagagagg ctgagcagag caaatggggg 1804  
 gcttcaccct catcccgag ctgcagagac tggaaactgc cttcaaggcc acggctggtc 1864  
 atctgctgac cacaccccag atccgccctc tccctgcgtgc accccaaaaa atcacttgcg 1924  
 tttttgaggc ttaaatactc tatccagttt ctacattttg catgaggcct gcaggtggcc 1984  
 tattttgact cagacggtga aaaaagcaaa ttaactcatt tggacaccat aactcatgca 2044  
 ataaaactga ttgtcattcg aaaaaaaaaa aa 2076

<210> 363  
 <211> 2123  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (71) .. (487)

<400> 363  
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 cggggtcgcc atg gct gag ctg cag cag ctc cgg gtg cag gag gcg gtg 109  
 Met Ala Glu Leu Gln Gln Leu Arg Val Gln Glu Ala Val  
 1 5 10  
 gag tcc atg gtg aag agt ctg gaa aga gag aac atc cgg aag atg cag 157



Glu	Ser	Met	Val	Lys	Ser	Leu	Glu	Arg	Glu	Asn	Ile	Arg	Lys	Met	Gln	
15						20					25					
ggt	ctc	atg	ttc	cgg	tgc	agc	gcc	agc	tgt	tgt	gag	gac	agc	cag	gcc	205
Gly	Leu	Met	Phe	Arg	Cys	Ser	Ala	Ser	Cys	Cys	Glu	Asp	Ser	Gln	Ala	
30					35				40					45		
tcc	atg	aag	cag	gtg	cac	cag	tgc	atc	gag	cgc	tgc	cat	gtg	cct	ctg	253
Ser	Met	Lys	Gln	Val	His	Gln	Cys	Ile	Glu	Arg	Cys	His	Val	Pro	Leu	
				50				55					60			
gct	caa	gcc	cag	gct	ttg	gtc	acc	agt	gag	ctg	gag	aag	ttc	cag	gac	301
Ala	Gln	Ala	Gln	Ala	Leu	Val	Thr	Ser	Glu	Leu	Glu	Lys	Phe	Gln	Asp	
			65				70						75			
cgc	ctg	gcc	cgg	tgc	acc	atg	cat	tgc	aac	gac	aaa	gcc	aaa	gat	tca	349
Arg	Leu	Ala	Arg	Cys	Thr	Met	His	Cys	Asn	Asp	Lys	Ala	Lys	Asp	Ser	
		80					85					90				
ata	gat	gct	ggg	agt	aag	gag	ctt	cag	gtg	aag	cag	cag	ctg	gac	agt	397
Ile	Asp	Ala	Gly	Ser	Lys	Glu	Leu	Gln	Val	Lys	Gln	Gln	Leu	Asp	Ser	
	95					100					105					
tgt	gtg	acc	aag	tgt	gtg	gat	gac	cac	atg	cac	ctc	atc	cca	act	atg	445
Cys	Val	Thr	Lys	Cys	Val	Asp	Asp	His	Met	His	Leu	Ile	Pro	Thr	Met	
110					115				120					125		
acc	aag	aag	atg	aag	gag	gct	ctc	tta	tca	att	gga	aaa	taa	aagtatt		494
Thr	Lys	Lys	Met	Lys	Glu	Ala	Leu	Leu	Ser	Ile	Gly	Lys	*			
			130					135								
tgccagtggc	catcagggct	gagggcaaga	atatatTTTT	tataaggaat	tggaatttt											554
agtcTTTTaa	gcaaagttta	cgaatgaaga	aatgaaggat	ggccacaagc	gtaaggcata											614
tgtcacttgc	ctctggacac	tggttatttt	atgtttcagt	ccctaaaaaa	tgaaatggaa											674
aaaagtgggtg	ctaaatcgag	tcagagatat	tacaggagag	ttttagagct	tattatttcc											734
tgtggccagt	gcttgtcctg	gcagtaaggc	tttccctgt	aacaagccag	agccctccaa											794
ggtaccagac	tcttcttact	acacaggtac	taacaggctg	gcaggttaga	gttggtggag											854
tctgaggaga	gatattttct	ctttgttgcc	aacatcctgt	ttaccaaaag	tgtcacccca											914
ccatcttcca	taagctgtga	aacaaaatca	atgaggtcac	taacttagaa	gggaaagaaa											974
gttttctggg	tctttgtttt	cttgatttgg	ggtaatttat	acaagggcat	acaagttgat											1034
tttaagatgt	ggaactggga	ggtagactag	tttgataag	aactttgaaa	tgttccttgt											1094
ggatcccat	ttctggtcac	caagatgtgg	atgtacattt	cttaaaatta	ttacatgctg											1154
catctttcag	cctggagact	gtgcagaaac	atgagagggtg	atgacacact	aattatggga											1214
agcagaatta	ctggctgatg	gcccctgagg	ctgtgtgtaa	caaatgaca	ggacaatctt											1274
gcagtaacac	tttcccttg	aagagaaggg	ggttttgatt	gtgatata	ctagtatcta											1334
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Met Asn Arg Glu Asp Arg Asn Val Leu Arg Met Lys Glu Arg Glu Arg
1 5 10 15

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Arg Asn Gln Glu Ile Gln Gln Gly Glu Asp Ala Phe Pro Pro Ser Ser
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cct ctc ttt gca gag cca tac aaa gtt act agc aaa gaa gat aag tta 203
Pro Leu Phe Ala Glu Pro Tyr Lys Val Thr Ser Lys Glu Asp Lys Leu
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Ser Ser Arg Ile Gln Ser Met Leu Gly Asn Tyr Asp Glu Met Lys Asp
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ttc ata gga gac aga tct ata cca aag ctt gtt gca att ccc aag cct 299
Phe Ile Gly Asp Arg Ser Ile Pro Lys Leu Val Ala Ile Pro Lys Pro
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Thr Val Pro Pro Ser Ala Asp Glu Lys Ser Asn Pro Asn Phe Phe Glu
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Gln Arg His Gly Gly Ser His Gln Ser Ser Lys Trp Thr Pro Val Gly
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 Glu Ile Gln Gln Lys Cys Gly Phe Ser Glu Leu Tyr Ser Trp Gln Arg  
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 gaa aga aaa gta aag aca gaa ttt tgc ctt cat gat gga cct cct tat 325  
 Glu Arg Lys Val Lys Thr Glu Phe Cys Leu His Asp Gly Pro Pro Tyr  
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 gca aac ggt gac cct cat gtt gga cat gct tta aat aag att ttg aaa 373  
 Ala Asn Gly Asp Pro His Val Gly His Ala Leu Asn Lys Ile Leu Lys  
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 Asp Ile Ala Asn Arg Phe His Met Met Asn Gly Ser Lys Ile His Phe  
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Glu Gly Thr Asp Val Val Ile Lys Met Leu Gln Thr Ala Lys Asn Leu			
	370	375	380
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Leu Lys Glu Glu Lys Leu Val His Ser Tyr Pro Tyr Asp Trp Arg Thr			
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Lys Lys Pro Val Val Ile Arg Ala Ser Lys Gln Trp Phe Ile Asn Ile			
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Pro Tyr Trp Cys Ile Ser Arg Gln Arg Val Trp Gly Val Pro Ile Pro			
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gtg ttt cat cat aag acc aag gat gaa tac ttg atc aac agc caa acc			1621
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Thr Glu His Ile Val Lys Leu Val Glu Gln His Gly Ser Asp Ile Trp			
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Trp Thr Leu Pro Pro Glu Gln Leu Leu Pro Lys Glu Val Leu Ser Glu			
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Val Gly Gly Pro Asp Ala Leu Glu Tyr Val Pro Gly Gln Asp Ile Leu			
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Gly Trp Phe Gln Ser Ser Leu Leu Thr Ser Val Ala Ala Arg Lys Arg			
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Ala Pro Tyr Lys Thr Val Ile Val His Gly Phe Thr Leu Gly Glu Lys			
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Asp Val Leu Arg Trp Trp Val Ala Asp Ser Asn Val Phe Thr Glu Val				
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Tyr Lys Gln Tyr Asp Phe Gly Lys Val Val Arg Leu Leu Arg Thr Phe				
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tat acc aga gag ctc tct aac ttt tat ttc agt ata atc aaa gat agg				2389
Tyr Thr Arg Glu Leu Ser Asn Phe Tyr Phe Ser Ile Ile Lys Asp Arg				
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ctc tat tgt gaa aag gaa aat gac ccc aaa cga cgc tct tgt cag act				2437
Leu Tyr Cys Glu Lys Glu Asn Asp Pro Lys Arg Arg Ser Cys Gln Thr				
	735	740	745	
gca tta gtt gaa att ttg gat gta ata gtt cgt tct ttt gct ccc att				2485
Ala Leu Val Glu Ile Leu Asp Val Ile Val Arg Ser Phe Ala Pro Ile				
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Arg Leu Ser Leu *				
	830			
gtctgaagag acttccagca cctctcagtt gaatgaatta atgatggctt ctgagtcaac				2792

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tttactggct caggaaccac gagagatgac tgcagatgta atcgagctta aagggaaatt 2852
cctcatcaac ttagaaggtg gtgatattcg tgaagagtct tcctataaag taattgtcat 2912
gccgactacg aaagaaaaat gcccccgttg ttggaagtat acagcggagt cttcagatac 2972
actgtgtcct cgatgtgcag aagttgtcag tggaaaatag tattaacagc tcaactcgagc 3032
aagaaccctc ctgacagtac tggctggaag tttggatgga ttatttacia tatagggaag 3092
aaagccaaga tttaggtaat gagtggatga gtaaattggtg gaggatggga gcaaaataga 3152
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<210> 366
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<212> DNA
<213> Homo sapiens

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<220>
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<222> (66)..(1835)

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gcaca      atg agg ccc agg aga ccc ttg gtc ttc atg tct ttg gtg tgt 107
            Met Arg Pro Arg Arg Pro Leu Val Phe Met Ser Leu Val Cys
            1                5                10

gca ctc ttg aac aca tgc cag gca cac agg gtg cat gac gac aag cct 155
Ala Leu Leu Asn Thr Cys Gln Ala His Arg Val His Asp Asp Lys Pro
15                20                25                30

aat att gtc cta atc atg gtt gat gac ctg ggt att gga gat ctg ggc 203
Asn Ile Val Leu Ile Met Val Asp Asp Leu Gly Ile Gly Asp Leu Gly
35                40                45

tgc tac ggc aat gac acc atg agg acg cct cac atc gac cgc ctt gcc 251
Cys Tyr Gly Asn Asp Thr Met Arg Thr Pro His Ile Asp Arg Leu Ala
50                55                60

agg gaa ggc gtg cga ctg act cag cac atc tct gcc gcc tcc ctc tgc 299
Arg Glu Gly Val Arg Leu Thr Gln His Ile Ser Ala Ala Ser Leu Cys
65                70                75

agc cca agc cgg tcc gcg ttc ttg acg gga aga tac ccc atc cga tca 347
Ser Pro Ser Arg Ser Ala Phe Leu Thr Gly Arg Tyr Pro Ile Arg Ser
80                85                90

ggg atg gtt tct agt ggt aat aga cgt gtc atc caa aat ctt gca gtc 395
Gly Met Val Ser Ser Gly Asn Arg Arg Val Ile Gln Asn Leu Ala Val
95                100                105                110

ccc gca ggc ctc cct ctt aat gag aca aca ctt gca gcc ttg cta aag 443
Pro Ala Gly Leu Pro Leu Asn Glu Thr Thr Leu Ala Ala Leu Leu Lys
115                120                125

aag caa gga tac agc acg ggg ctt ata ggc aaa tgg cac caa ggc ttg 491
Lys Gln Gly Tyr Ser Thr Gly Leu Ile Gly Lys Trp His Gln Gly Leu
130                135                140

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aac tgc gac tcc cga agt gac cag tgc cac cat cca tat aat tat ggg Asn Cys Asp Ser Arg Ser Asp Gln Cys His His Pro Tyr Asn Tyr Gly 145 150 155	539
ttt gac tac tac tat ggc atg ccg ttc act ctc gtt gac agc tgc tgg Phe Asp Tyr Tyr Tyr Gly Met Pro Phe Thr Leu Val Asp Ser Cys Trp 160 165 170	587
ccg gac ccc tct cgt aac acg gaa tta gcc ttt gag agt cag ctc tgg Pro Asp Pro Ser Arg Asn Thr Glu Leu Ala Phe Glu Ser Gln Leu Trp 175 180 185 190	635
ctc tgt gtg cag cta gtt gcc att gcc atc ctc acc cta acc ttt ggg Leu Cys Val Gln Leu Val Ala Ile Ala Ile Leu Thr Leu Thr Phe Gly 195 200 205	683
aag ctg agc ggc tgg gtc tct gtt ccc tgg ctc ctg atc ttc tcc atg Lys Leu Ser Gly Trp Val Ser Val Pro Trp Leu Leu Ile Phe Ser Met 210 215 220	731
att ctg ttt att ttc ctc ttg ggc tat gct tgg ttc tcc agc cac acg Ile Leu Phe Ile Phe Leu Leu Gly Tyr Ala Trp Phe Ser Ser His Thr 225 230 235	779
tcc cct tta tac tgg gac tgc ctc ctc atg cgg ggg cac gag atc acg Ser Pro Leu Tyr Trp Asp Cys Leu Leu Met Arg Gly His Glu Ile Thr 240 245 250	827
gag cag ccc atg aag gct gaa cga gct gga tcc att atg gtg aag gaa Glu Gln Pro Met Lys Ala Glu Arg Ala Gly Ser Ile Met Val Lys Glu 255 260 265 270	875
gcg att tcc ttt tta gaa agg cac agt aag gaa act ttc ctt ctc ttt Ala Ile Ser Phe Leu Glu Arg His Ser Lys Glu Thr Phe Leu Leu Phe 275 280 285	923
ttc tcc ttt ctt cac gtg cac aca cct ctc ccc acc acg gac gat ttc Phe Ser Phe Leu His Val His Thr Pro Leu Pro Thr Thr Asp Asp Phe 290 295 300	971
act ggc acc agc aag cat ggc ttg tat ggg gat aat gtg gaa gag atg Thr Gly Thr Ser Lys His Gly Leu Tyr Gly Asp Asn Val Glu Glu Met 305 310 315	1019
gac tcc atg gtg ggc aag att ctt gat gct atc gat gat ttt ggc cta Asp Ser Met Val Gly Lys Ile Leu Asp Ala Ile Asp Asp Phe Gly Leu 320 325 330	1067
agg aac aac acc ctt gtc tac ttt aca tca gat cac gga ggg cat ttg Arg Asn Asn Thr Leu Val Tyr Phe Thr Ser Asp His Gly Gly His Leu 335 340 345 350	1115
gaa gct agg cga ggg cat gcc caa ctt ggt gga tgg aat gga ata tac Glu Ala Arg Arg Gly His Ala Gln Leu Gly Gly Trp Asn Gly Ile Tyr 355 360 365	1163
aaa ggt gga aaa ggc atg ggg ggc tgg gaa ggt gga atc cgc gtc cca Lys Gly Gly Lys Gly Met Gly Gly Trp Glu Gly Gly Ile Arg Val Pro 370 375 380	1211
gga att gtc cga tgg cct gga aag gta cca gct gga cgg ttg att aag Gly Ile Val Arg Trp Pro Gly Lys Val Pro Ala Gly Arg Leu Ile Lys 385 390 395	1259

gaa cct aca agt tta atg gat att tta cca act gtc gca tca gtg tca 1307  
 Glu Pro Thr Ser Leu Met Asp Ile Leu Pro Thr Val Ala Ser Val Ser  
 400 405 410

gga gga agt ctc cct cag gac agg gtc att gac ggc cga gac ctc atg 1355  
 Gly Gly Ser Leu Pro Gln Asp Arg Val Ile Asp Gly Arg Asp Leu Met  
 415 420 425 430

ccc ttg ctg cag ggc aac gtc agg cac tcg gag cat gaa ttt ctt ttc 1403  
 Pro Leu Leu Gln Gly Asn Val Arg His Ser Glu His Glu Phe Leu Phe  
 435 440 445

cac tac tgt ggc tcc tac ctg cac gcc gtg cgg tgg atc ccc aag gac 1451  
 His Tyr Cys Gly Ser Tyr Leu His Ala Val Arg Trp Ile Pro Lys Asp  
 450 455 460

gac agt ggg tca gtt tgg aag gct cac tat gtg acc ccg gta ttc cag 1499  
 Asp Ser Gly Ser Val Trp Lys Ala His Tyr Val Thr Pro Val Phe Gln  
 465 470 475

cca cca gct tct ggt ggc tgc tat gtc acc tca tta tgc aga tgt ttc 1547  
 Pro Pro Ala Ser Gly Gly Cys Tyr Val Thr Ser Leu Cys Arg Cys Phe  
 480 485 490

gga gaa cag gtt acc tac cac aac ccc cct ctg ctc ttc gat ctc tcc 1595  
 Gly Glu Gln Val Thr Tyr His Asn Pro Pro Leu Leu Phe Asp Leu Ser  
 495 500 505 510

agg gac ccc tca gag tcc aca ccc ctg aca cct gcc aca gag ccc ctc 1643  
 Arg Asp Pro Ser Glu Ser Thr Pro Leu Thr Pro Ala Thr Glu Pro Leu  
 515 520 525

tat gat ttt gtg att aaa aag gtg gcc aac gcc ctg aag gaa cac cag 1691  
 Tyr Asp Phe Val Ile Lys Lys Val Ala Asn Ala Leu Lys Glu His Gln  
 530 535 540

gaa acc atc gtg cct gtg acc tac caa ctc tca gaa ctg aat cag ggc 1739  
 Glu Thr Ile Val Pro Val Thr Tyr Gln Leu Ser Glu Leu Asn Gln Gly  
 545 550 555

agg acg tgg ctg aag cct tgc tgt ggg gtg ttc cca ttt tgt ctg tgt 1787  
 Arg Thr Trp Leu Lys Pro Cys Cys Gly Val Phe Pro Phe Cys Leu Cys  
 560 565 570

gac aag gaa gag gaa gtc tct cag cct cgg ggt cct aac gag aag aga 1835  
 Asp Lys Glu Glu Glu Val Ser Gln Pro Arg Gly Pro Asn Glu Lys Arg  
 575 580 585 590

taattacaat caggctacca gaggaagcct ttggctcctaa cgagaagaga taattacaat 1895

caggctacca aaggaagcac taactttggt gctttcaagt tggcaaggag tgcatttaat 1955

agtcaataaa ttcattctacc attccagatt attaaaaaaaa aaaaa 2000

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&lt;222&gt; (9) .. (2255)

&lt;400&gt; 367

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1 5 10	
gac gac cag ctg ctg cag aag ctc agg gcc agt cgc cgc cgc ttc cag	98
Asp Asp Gln Leu Leu Gln Lys Leu Arg Ala Ser Arg Arg Arg Phe Gln	
15 20 25 30	
agg cgc atg cag cgg ctg ata gag aag tac aac cag ccc ttc gag gac	146
Arg Arg Met Gln Arg Leu Ile Glu Lys Tyr Asn Gln Pro Phe Glu Asp	
35 40 45	
acc ccg gtg gtg caa atg gcc acg ctg acc tac gag acg cca cag gga	194
Thr Pro Val Val Gln Met Ala Thr Leu Thr Tyr Glu Thr Pro Gln Gly	
50 55 60	
ttg aga att tgg ggt gga aga cta ata aag gaa aga aac gaa gga gag	242
Leu Arg Ile Trp Gly Gly Arg Leu Ile Lys Glu Arg Asn Glu Gly Glu	
65 70 75	
atc cag gac tcc tcc atg aag ccc gcg gac agg aca gat ggc tcc gtg	290
Ile Gln Asp Ser Ser Met Lys Pro Ala Asp Arg Thr Asp Gly Ser Val	
80 85 90	
caa gct gca gcc tgg ggt cct gag ctt ccc tcg cac cgc aca gtc ctg	338
Gln Ala Ala Ala Trp Gly Pro Glu Leu Pro Ser His Arg Thr Val Leu	
95 100 105 110	
gga gcc gat tca aaa agc ggt gag gtc gat gcc acg tca gac cag gaa	386
Gly Ala Asp Ser Lys Ser Gly Glu Val Asp Ala Thr Ser Asp Gln Glu	
115 120 125	
gag tca gtt gct tgg gcc tta gca cct gca gtg cct caa agc cct ttg	434
Glu Ser Val Ala Trp Ala Leu Ala Pro Ala Val Pro Gln Ser Pro Leu	
130 135 140	
aaa aat gaa tta aga agg aaa tac ttg acc caa gtg gat ata ctg cta	482
Lys Asn Glu Leu Arg Arg Lys Tyr Leu Thr Gln Val Asp Ile Leu Leu	
145 150 155	
caa ggt gca gag tat ttt gag tgt gca ggt aac aga gct gga agg gat	530
Gln Gly Ala Glu Tyr Phe Glu Cys Ala Gly Asn Arg Ala Gly Arg Asp	
160 165 170	
gta cgt gtg act ccg ctg cct tca ctg gcc tca cct gcc gtg cct gcc	578
Val Arg Val Thr Pro Leu Pro Ser Leu Ala Ser Pro Ala Val Pro Ala	
175 180 185 190	
ccc gga tac tgc agt cgt atc tcc aga aag agt cct ggt gac cca gcg	626
Pro Gly Tyr Cys Ser Arg Ile Ser Arg Lys Ser Pro Gly Asp Pro Ala	
195 200 205	
aaa cca gct tca tct ccc aga gaa tgg gat cct ttg cat cct tcc tcc	674
Lys Pro Ala Ser Ser Pro Arg Glu Trp Asp Pro Leu His Pro Ser Ser	
210 215 220	
aca gac atg gcc tta gta cct aga aat gac agc ctc tcc cta caa gag	722
Thr Asp Met Ala Leu Val Pro Arg Asn Asp Ser Leu Ser Leu Gln Glu	
225 230 235	

acc agt agc agc agc ttc tta agc agc cag ccc ttt gaa gat gat gac	770
Thr Ser Ser Ser Phe Leu Ser Ser Gln Pro Phe Glu Asp Asp Asp	
240 245 250	
att tgc aat gtg acc atc agt gac ctg tac gca ggg atg ctg cac tcc	818
Ile Cys Asn Val Thr Ile Ser Asp Leu Tyr Ala Gly Met Leu His Ser	
255 260 265 270	
atg agc cgg ctg ttg agc aca aag cca tca agc atc atc tcc acc aaa	866
Met Ser Arg Leu Leu Ser Thr Lys Pro Ser Ser Ile Ile Ser Thr Lys	
275 280 285	
acg ttc atc atg caa aac tgg aac tgc agg agg agg cac aga tat aag	914
Thr Phe Ile Met Gln Asn Trp Asn Cys Arg Arg Arg His Arg Tyr Lys	
290 295 300	
agc agg atg aac aaa aca tat tgc aaa gga gcc aga cgt tct cag agg	962
Ser Arg Met Asn Lys Thr Tyr Cys Lys Gly Ala Arg Arg Ser Gln Arg	
305 310 315	
agc tcc aag gag aac ttc ata ccc tgc tct gag cct gtg aaa ggg aca	1010
Ser Ser Lys Glu Asn Phe Ile Pro Cys Ser Glu Pro Val Lys Gly Thr	
320 325 330	
ggg gca tta aga gat tgc aag aac gta tta gat gtt tct tgc cgt aag	1058
Gly Ala Leu Arg Asp Cys Lys Asn Val Leu Asp Val Ser Cys Arg Lys	
335 340 345 350	
aca ggt tta aaa ttg gaa aaa gct ttt ctt gaa gtc aac aga ccc caa	1106
Thr Gly Leu Lys Leu Glu Lys Ala Phe Leu Glu Val Asn Arg Pro Gln	
355 360 365	
atc cat aag tta gat cca agt tgg aag gag cgc aaa gtg aca ccc tcg	1154
Ile His Lys Leu Asp Pro Ser Trp Lys Glu Arg Lys Val Thr Pro Ser	
370 375 380	
aag tat tct tcc ttg att tac ttc gac tcc agt gca aca tat aat ctt	1202
Lys Tyr Ser Ser Leu Ile Tyr Phe Asp Ser Ser Ala Thr Tyr Asn Leu	
385 390 395	
gat gag gaa aat aga ttt agg aca tta aaa tgg tta att tct cct gta	1250
Asp Glu Glu Asn Arg Phe Arg Thr Leu Lys Trp Leu Ile Ser Pro Val	
400 405 410	
aaa ata gtt tcc aga cca aca ata cga cag ggc cat gga gag aac cgt	1298
Lys Ile Val Ser Arg Pro Thr Ile Arg Gln Gly His Gly Glu Asn Arg	
415 420 425 430	
cag agg gag att gaa atc cga ttt gat cag ctt cat cgg gaa tat tgc	1346
Gln Arg Glu Ile Glu Ile Arg Phe Asp Gln Leu His Arg Glu Tyr Cys	
435 440 445	
ctg agt ccc agg aac cag cct cgc cgg atg tgc ctc ccg gac tcc tgg	1394
Leu Ser Pro Arg Asn Gln Pro Arg Arg Met Cys Leu Pro Asp Ser Trp	
450 455 460	
gcc atg aac atg tac aga ggg ggt cct gcg agt cct ggt ggc ctt cag	1442
Ala Met Asn Met Tyr Arg Gly Gly Pro Ala Ser Pro Gly Gly Leu Gln	
465 470 475	
ggc tta gaa acc cgc agg ctg agt tta cct tcc agc aaa gca aaa gca	1490
Gly Leu Glu Thr Arg Arg Leu Ser Leu Pro Ser Ser Lys Ala Lys Ala	
480 485 490	

aaa agt tta agt gag gct ttt gaa aac cta ggc aaa aga tct ctg gaa	1538
Lys Ser Leu Ser Glu Ala Phe Glu Asn Leu Gly Lys Arg Ser Leu Glu	
495 500 505 510	
gca ggt agg tgc ctg ccc aag agc gat tca tct tca tca ctt cca aag	1586
Ala Gly Arg Cys Leu Pro Lys Ser Asp Ser Ser Ser Ser Leu Pro Lys	
515 520 525	
acc aac ccc aca cac agc gca act cgc ccg cag cag aca tct gac ctt	1634
Thr Asn Pro Thr His Ser Ala Thr Arg Pro Gln Gln Thr Ser Asp Leu	
530 535 540	
cac gtt cag gga aat agt tct gga ata ttt aga aag tca gtg tca ccc	1682
His Val Gln Gly Asn Ser Ser Gly Ile Phe Arg Lys Ser Val Ser Pro	
545 550 555	
agc aaa act ctt tca gtc cca gat aaa gaa gtg cca ggc cac gga agg	1730
Ser Lys Thr Leu Ser Val Pro Asp Lys Glu Val Pro Gly His Gly Arg	
560 565 570	
aat cgt tac gat gaa att aaa gaa gaa ttt gac aag ctt cat caa aag	1778
Asn Arg Tyr Asp Glu Ile Lys Glu Glu Phe Asp Lys Leu His Gln Lys	
575 580 585 590	
tat tgc ctc aaa tct cct ggg cag atg aca gtg cct tta tgt att gga	1826
Tyr Cys Leu Lys Ser Pro Gly Gln Met Thr Val Pro Leu Cys Ile Gly	
595 600 605	
gtg tct aca gat aaa gca agt atg gaa gtt cga tat caa aca gaa ggc	1874
Val Ser Thr Asp Lys Ala Ser Met Glu Val Arg Tyr Gln Thr Glu Gly	
610 615 620	
ttc tta gga aaa tta aat cca gac cct cac ttc cag ggt ttc cag aag	1922
Phe Leu Gly Lys Leu Asn Pro Asp Pro His Phe Gln Gly Phe Gln Lys	
625 630 635	
ttg cca tca tca ccc ctg ggg tgc aga aaa agt cta ctg ggc tca act	1970
Leu Pro Ser Ser Pro Leu Gly Cys Arg Lys Ser Leu Leu Gly Ser Thr	
640 645 650	
gca att gag gct cct tca tct aca tgt gtt gct cgt gcc atc acg agg	2018
Ala Ile Glu Ala Pro Ser Ser Thr Cys Val Ala Arg Ala Ile Thr Arg	
655 660 665 670	
gat ggc acg agg gac cat cag ttc cct gca aaa aga ccc agg cta tca	2066
Asp Gly Thr Arg Asp His Gln Phe Pro Ala Lys Arg Pro Arg Leu Ser	
675 680 685	
gaa ccc cag ggc tcc gga cgc cag ggc aat tcc ctg ggt gcc tca gat	2114
Glu Pro Gln Gly Ser Gly Arg Gln Gly Asn Ser Leu Gly Ala Ser Asp	
690 695 700	
ggg gtg gac aac acc gtc aga ccg gga gac cag ggc agc tct tca cag	2162
Gly Val Asp Asn Thr Val Arg Pro Gly Asp Gln Gly Ser Ser Ser Gln	
705 710 715	
ccc aac tca gaa gag aga gga gag aac acg tct tac agg atg gaa gag	2210
Pro Asn Ser Glu Glu Arg Gly Glu Asn Thr Ser Tyr Arg Met Glu Glu	
720 725 730	
aaa agt gat ttc atg cta gaa aaa ttg gaa act aaa agt gtg tag cta	2258
Lys Ser Asp Phe Met Leu Glu Lys Leu Glu Thr Lys Ser Val *	
735 740 745	

ggttatttcg gagtgttatt tatcttccca cttgctctct gtttgtattt ttgttttgtt 2318  
 tttgattctt gagactgtga ggacttggtt gacttctctg cccttaaagt aaatattagt 2378  
 gaaattgggt ccatcagaga taacctcgag ttcttggtgt agaaattatg tgaataaagt 2438  
 tgctcaatta gaattttaaa aaaaaaaaaa a 2469

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 <212> DNA  
 <213> Homo sapiens

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 Met Asp Pro Ala Leu Ala Ala Gln Met Ser Glu Ala Val Ala Glu Lys  
 1 5 10 15  
 atg ctc cag tac cgg cgg gac aca gca ggc tgg aag att tgc cgg gaa 154  
 Met Leu Gln Tyr Arg Arg Asp Thr Ala Gly Trp Lys Ile Cys Arg Glu  
 20 25 30  
 ggc aat gga gtt tca gtt tcc tgg agg cca tct gtg gag ttt cca ggg 202  
 Gly Asn Gly Val Ser Val Ser Trp Arg Pro Ser Val Glu Phe Pro Gly  
 35 40 45  
 aac ctg tac cga gga gaa ggc att gta tat ggg aca cta gag gag gtg 250  
 Asn Leu Tyr Arg Gly Glu Gly Ile Val Tyr Gly Thr Leu Glu Glu Val  
 50 55 60  
 tgg gac tgt gtg aag cca gct gtt gga ggc cta cga gtg aag tgg gat 298  
 Trp Asp Cys Val Lys Pro Ala Val Gly Gly Leu Arg Val Lys Trp Asp  
 65 70 75 80  
 gag aat gtg acc ggt ttt gaa att atc caa agc atc act gac acc ctg 346  
 Glu Asn Val Thr Gly Phe Glu Ile Ile Gln Ser Ile Thr Asp Thr Leu  
 85 90 95  
 tgt gta agc aga acc tcc act ccc tcc gct gcc atg aag ctc att tct 394  
 Cys Val Ser Arg Thr Ser Thr Pro Ser Ala Ala Met Lys Leu Ile Ser  
 100 105 110  
 ccc aga gat ttt gtg gac ttg gtg cta gtc aag aga tat gag gat ggg 442  
 Pro Arg Asp Phe Val Asp Leu Val Leu Val Lys Arg Tyr Glu Asp Gly  
 115 120 125  
 acc atc agt tcc aac gcc acc cat gtg gag cat ccg tta tgt ccc ccg 490  
 Thr Ile Ser Ser Asn Ala Thr His Val Glu His Pro Leu Cys Pro Pro  
 130 135 140  
 aag cca ggt ttt gtg aga gga ttt aac cat cct tgt ggt tgc ttc tgt 538  
 Lys Pro Gly Phe Val Arg Gly Phe Asn His Pro Cys Gly Cys Phe Cys  
 145 150 155 160  
 gaa cct ctt cca ggg gaa ccc acc aag acc aac ctg gtc aca ttc ttc 586  
 Glu Pro Leu Pro Gly Glu Pro Thr Lys Thr Asn Leu Val Thr Phe Phe

	165	170	175	
cat acc gac ctc agc ggt tac ctc cca cag aac gtg gtg gac tcc ttc				634
His Thr Asp Leu Ser Gly Tyr Leu Pro Gln Asn Val Val Asp Ser Phe				
	180	185	190	
ttc ccc cgc agc atg acc cgg ttt tat gcc aac ctt cag aaa gca gtg				682
Phe Pro Arg Ser Met Thr Arg Phe Tyr Ala Asn Leu Gln Lys Ala Val				
	195	200	205	
aag caa ttc cat gag taa tgctat cggtacttct tggcaaagaa ctcccgtgac				736
Lys Gln Phe His Glu *				
	210			
tcatacgagga gctccagctg ttgggacacc aaggagcctg ggagcacgca gaggcctgtg				796
ttcactcttt ggaacaagct gatggactgc gcactctctga gaatgccaac cagaggcggc				856
agcccaccct tcctgcctcc tgcccactc agggttggcg tgtgatgagc cattcatgtg				916
ttccaaactc catctgcctg ttacccaaac acgcctctcc tggcagggta gaccaggcc				976
tctaaccatc tgacagagac tcggcctgga caccatgcga tgcactctgg caccaaggct				1036
ttatgtgccc atcactctca gagaccacgt ttccctgact gtcatagaga atcatcatcg				1096
ccactgaaaa ccaggccctg ttgcctttta agcatgtacc gctccctcag tcctgtgctg				1156
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<210> 369  
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 <212> DNA  
 <213> Homo sapiens

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 <222> (256)..(1329)

<220>  
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 <222> (1)...(1501)  
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ccgaacatcg tgaagttgca caagtactgg ctggatacct ctgaggcctg cgcgagggtc	180
atcttcatca cagagtacgt gtcatacaggc agcctcaagc aattcctcaa aaagaccaag	240
aagaaccaca aggcc atg aac gcc cgg gcc tgg aag cgc tgg tgc acg cag	291
Met Asn Ala Arg Ala Trp Lys Arg Trp Cys Thr Gln	
1 5 10	
atc ctg tct gcg ctc agc ttc ctg cac gcc tgc acc ccc cca atc atc	339
Ile Leu Ser Ala Leu Ser Phe Leu His Ala Cys Thr Pro Pro Ile Ile	
15 20 25	

cac ggg aac ctg acc agc gac acc atc ttc att cag cac aac ggc ctc	387
His Gly Asn Leu Thr Ser Asp Thr Ile Phe Ile Gln His Asn Gly Leu	
30 35 40	
atc aag atc ggc tcc gtg tgg cac cga atc ttc tcc aat gca ctt cca	435
Ile Lys Ile Gly Ser Val Trp His Arg Ile Phe Ser Asn Ala Leu Pro	
45 50 55 60	
gat gat ctc cga agc ccc atc cgc gct gag cga gag gaa ctt cgg aac	483
Asp Asp Leu Arg Ser Pro Ile Arg Ala Glu Arg Glu Glu Leu Arg Asn	
65 70 75	
ctg cac ttc ttc ccc cca gag tat gga gag gtg gcc gat ggg acc gct	531
Leu His Phe Phe Pro Pro Glu Tyr Gly Glu Val Ala Asp Gly Thr Ala	
80 85 90	
gtg gac atc ttc tcc ttt ggg atg tgt gcg ctg gag atg gct gta ctg	579
Val Asp Ile Phe Ser Phe Gly Met Cys Ala Leu Glu Met Ala Val Leu	
95 100 105	
gaa atc cag acc aat ggg gac acc cgg gtc aca gag gag gcc att gct	627
Glu Ile Gln Thr Asn Gly Asp Thr Arg Val Thr Glu Glu Ala Ile Ala	
110 115 120	
cgc gcc agg cac tcg ctg agt gac ccc aac atg cgg gag ttc atc ctt	675
Arg Ala Arg His Ser Leu Ser Asp Pro Asn Met Arg Glu Phe Ile Leu	
125 130 135 140	
tgc tgc ctg gcc cgg gac cct gcc cgc cgg ccc tct gcc cac agc ctc	723
Cys Cys Leu Ala Arg Asp Pro Ala Arg Arg Pro Ser Ala His Ser Leu	
145 150 155	
ctc ttc cac cgc gtg ctc ttc gag gtg cac tcg ctg aag ctc ctg gca	771
Leu Phe His Arg Val Leu Phe Glu Val His Ser Leu Lys Leu Leu Ala	
160 165 170	
gcc cac tgc ttc atc cag cac cag tac ctc atg cct gag aat gtg gtg	819
Ala His Cys Phe Ile Gln His Gln Tyr Leu Met Pro Glu Asn Val Val	
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gag gag aag acc aag gcc atg gac ctg cac gcg gtc ttg gcg gag ctt	867
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Pro Arg Pro Arg Arg Pro Pro Leu Gln Trp Arg Tyr Ser Glu Val Ser	
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Phe Met Glu Leu Asp Lys Phe Leu Glu Asp Val Arg Asn Gly Ile Tyr	
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Leu Ala Pro Pro Pro Glu Glu Val Gln Lys Ala Lys Thr Pro Thr Pro	
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Glu Pro Phe Asp Ser Glu Thr Arg Lys Val Ile Gln Met Gln Cys Asn	
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 Leu Glu Arg Ser Glu Asp Lys Ala Arg Trp His Leu Thr Leu Leu Leu  
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 Val Leu Glu Asp Arg Leu His Arg Gln Leu Thr Tyr Asp Leu Leu Pro  
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160 165 170 175	
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cac ttg agc gaa gga acc aag ggc cgg cag gtg gga agt gga ggt gat His Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly Ser Gly Gly Asp 420 425 430	1654
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 Leu Arg Gly Gly Arg Gly Ile Asp Lys Thr Asn Gly Ala Pro Glu Gln  
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 Ile Gly Leu Asp Glu Ser Gly Gly Gly Gly Gly Ser Asp Pro Gly Glu  
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 Ala Pro Thr Arg Ala Ala Pro Gly Glu Leu Arg Ser Ala Arg Gly Pro  
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 Leu Ser Ser Ala Pro Glu Ile Val His Glu Asp Leu Lys Met Gly Ser  
 65 70 75  
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 Asp Gly Glu Ser Asp Gln Ala Ser Ala Thr Ser Ser Asp Glu Val Gln  
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 Ser Pro Val Arg Val Arg Met Arg Asn His Pro Pro Arg Lys Ile Ser  
 95 100 105 110

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Thr Glu Asp Ile Asn Lys Arg Leu Ser Leu Pro Ala Asp Ile Arg Leu	
115 120 125	
cct gag ggc tac ctg gag aag ctg acc ctc aat agc ccc atc ttt gac	611
Pro Glu Gly Tyr Leu Glu Lys Leu Thr Leu Asn Ser Pro Ile Phe Asp	
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aag ccc ctc agc cgc cgc ctc cgt cgt gtc agc cta tct gag att ggc	659
Lys Pro Leu Ser Arg Arg Leu Arg Arg Val Ser Leu Ser Glu Ile Gly	
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Phe Gly Lys Leu Glu Thr Tyr Ile Lys Leu Asp Lys Leu Gly Glu Gly	
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Thr Tyr Ala Thr Val Tyr Lys Gly Lys Ser Lys Leu Thr Asp Asn Leu	
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Val Ala Leu Lys Glu Ile Arg Leu Glu His Glu Glu Gly Ala Pro Cys	
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Leu Arg Gly Leu Ala Tyr Cys His Arg Gln Lys Val Leu His Arg Asp	
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Leu Lys Pro Gln Asn Leu Leu Ile Asn Glu Arg Gly Glu Leu Lys Leu	
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gaa aat gcc agt gct aat cct cca tct gga att gaa gat gaa act gct      317
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Glu Asn Gly Val Pro Lys Pro Lys Val Thr Glu Thr Glu Asp Asp Ser
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gat agt gac agc gat gat gat gaa gat gat gtt cat gtc act ata gga      413
Asp Ser Asp Ser Asp Asp Asp Glu Asp Asp Val His Val Thr Ile Gly
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gac att aaa acg gga gca cca cag tat ggg agt tat ggt aca gca cct      461
Asp Ile Lys Thr Gly Ala Pro Gln Tyr Gly Ser Tyr Gly Thr Ala Pro
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gta aat ctt aac atc aag aca ggg gga aga gtt tat gga act aca ggg      509
Val Asn Leu Asn Ile Lys Thr Gly Gly Arg Val Tyr Gly Thr Thr Gly
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aca aaa gtc aaa gga gta gac ctt gat gca cct gga agc att aat gga      557
Thr Lys Val Lys Gly Val Asp Leu Asp Ala Pro Gly Ser Ile Asn Gly
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cgt aaa cct ggt gct gat ctt tct gat tat ttt aat tat ggg ttt aat      653
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 Ser Arg Arg Arg His Glu Ser Glu Glu Gly Asp Ser His Arg Arg His  
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 Lys His Lys Lys Ser Lys Arg Ser Lys Glu Gly Lys Glu Ala Gly Ser  
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 Glu Pro Ala Pro Glu Gln Glu Ser Thr Glu Ala Thr Pro Ala Glu \*  
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 Met Glu Gln Thr Asp Cys Lys  
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Thr	Ser	Ser	Ser	Asp	Glu	Ser	Glu	Asp	Gly	Arg	Lys	Pro	Arg	Gln	Ser	
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Tyr	Asn	Ser	Arg	Glu	Thr	Leu	His	Glu	Tyr	Asn	Gln	Glu	Leu	Arg	Met	
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Gln	Glu	Met	Glu	Phe	Cys	Glu	Thr	Ser	His	Thr	Leu	Cys	Ser	Gly	Tyr	
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Gln	Thr	Asp	Met	His	Ser	Val	Ser	Arg	His	Gly	Tyr	Gln	Leu	Glu	Met	
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Cys	Asp	Met	Glu	Ala	Gln	Ala	Gly	Ser	Thr	Gln	Asp	Val	Gln	Ser	Ser	
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Pro	His	Asn	Gln	Phe	Thr	Phe	Arg	Pro	Leu	Pro	Pro	Pro	Pro	Pro	Pro	
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Pro	His	Ala	Cys	Thr	Cys	Ala	Arg	Lys	Pro	Pro	Pro	Ala	Ala	Asp	Ser	
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Leu	Gln	Arg	Arg	Ser	Met	Thr	Thr	Arg	Ser	Gln	Pro	Ser	Pro	Ala	Ala	
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cca	gct	ccc	cca	acc	agc	acg	cag	gat	tca	gtc	cat	ctg	cat	aac	agc	1131
Pro	Ala	Pro	Pro	Thr	Ser	Thr	Gln	Asp	Ser	Val	His	Leu	His	Asn	Ser	
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Trp	Val	Leu	Asn	Ser	Asn	Ile	Pro	Leu	Glu	Thr	Arg	His	Phe	Leu	Phe	
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Lys	His	Gly	Ser	Gly	Ser	Ser	Ala	Ile	Phe	Ser	Ala	Ala	Ser	Gln	Asn	
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Tyr	Pro	Leu	Thr	Ser	Asn	Thr	Val	Tyr	Ser	Pro	Pro	Pro	Arg	Pro	Leu	
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cct	cga	agc	acc	ttt	tcc	cga	cct	gcc	ttt	acc	ttt	aac	aaa	cct	tac	1323
Pro	Arg	Ser	Thr	Phe	Ser	Arg	Pro	Ala	Phe	Thr	Phe	Asn	Lys	Pro	Tyr	
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Arg	Cys	Cys	Asn	Trp	Lys	Cys	Thr	Ala	Leu	Ser	Ala	Thr	Ala	Ile	Thr	
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Val	Thr	Leu	Ala	Leu	Leu	Leu	Ala	Tyr	Val	Ile	Ala	Val	His	Leu	Phe	
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Gln	Lys	Gly	Arg	Ala	Ile	Asp	Thr	Gly	Glu	Val	Asp	Ile	Gly	Ala	Gln	
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Val	Met	Gln	Thr	Ile	Pro	Pro	Gly	Leu	Phe	Trp	Arg	Phe	Gln	Ile	Thr	
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Ile	His	His	Pro	Ile	Tyr	Leu	Lys	Phe	Asn	Ile	Ser	Leu	Ala	Lys	Asp	
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Gln	Phe	Asp	Phe	Val	Lys	Leu	Met	Asp	Gly	Lys	Gln	Leu	Val	Lys	Gln	
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Asp	Ser	Lys	Gly	Ser	Asp	Asp	Thr	Gln	His	Ser	Pro	Arg	Asn	Leu	Ile	
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Pro	Trp	Tyr	Leu	Ala	Phe	Tyr	Asn	Asp	Gly	Lys	Lys	Met	Glu	Gln	Val	
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Phe Val Leu Thr Thr Ala Ile Glu Ile Met Asp Asp Cys Ser Thr Asn 520 525 530 535	
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Cys	Pro	Glu	Arg	Gly	Thr	Ile	Val	Pro	Glu	Leu	Gln	Val	Val	Gln	Glu	
1000					1005				1010					1015		
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Phe Ile Ser Gln Gln Pro Pro Val Ile Ser Thr Ile Met Gly Asn Gly	
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Asn Lys Leu Phe Ala Pro Val Ala Leu Ala Ser Gly Pro Asp Gly Ser	
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Tyr Leu Ala Met Asp Pro Val Ser Glu Ser Leu Tyr Leu Ser Asp Thr	
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Ala Gly Arg Pro Ile His Cys Gln Val Pro Gly Ile Asp His Phe Leu	
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Val Ser Lys Val Ala Ile His Ser Thr Leu Glu Ser Ala Arg Ala Ile	
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Ser Val Ser His Ser Gly Leu Leu Phe Ile Ala Glu Thr Asp Glu Arg	
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Ile Ala Gly Ala Pro Thr Asp Cys Asp Cys Lys Ile Asp Pro Asn Cys	
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Asp Leu Gly Asn Val Arg Ile Arg Thr Ile Ser Arg Asn Gln Ala His	
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Leu Asn Asp Met Asn Ile Tyr Glu Ile Ala Ser Pro Ala Asp Gln Glu	
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Leu Tyr Gln Phe Thr Val Asn Gly Thr His Leu His Thr Leu Asn Leu	
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Ile Thr Arg Asp Tyr Val Tyr Asn Phe Thr Tyr Asn Ser Glu Gly Asp	
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Leu Gly Ala Ile Thr Ser Ser Asn Gly Asn Ser Val His Ile Arg Arg	
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Tyr Trp Leu Thr Ile Ser Ser Asn Gly Val Leu Lys Arg Val Ser Ala	
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Leu Ala Thr Lys Ser Asn Glu Asn Gly Trp Thr Thr Val Tyr Glu Tyr	
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Asp Phe Asp His Ile Thr Arg Thr Gly Lys Ile Tyr Asp Asp His Arg	
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Lys Phe Thr Leu Arg Ile Leu Tyr Asp Gln Thr Gly Arg Pro Ile Leu	
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Trp Ser Pro Val Ser Arg Tyr Asn Glu Val Asn Ile Thr Tyr Ser Pro	
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Leu Ser Val Thr Met Pro Ser Met Val Arg His Ser Leu Gln Thr Met	
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 aacatggctg agtgtctcag tcccaaaca taaagaactt gaagaggttt agccggaaac 1505  
 tttgaagaca gaaaatctgc ccattatgtt ttccagacat ttcgaggggg cgagcggagg 1565  
 tcattggagc ttgaagccca tttggaaggc tggtcctctg gcctgcgttt tctccttggc 1625  
 cctttgaagg gccccccagc tcacagggca cttccatcct agtctgccga tttcgagctg 1685  
 gagaggggct ggggtccac attcgaggtc ccttcccacg taggcatcca ggtgatggct 1745  
 tccgcccaca ccaggaagga gacgagaggc ccgccaggaa gaagacttgg gtccgggatg 1805

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<210> 375
<211> 2041
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (140)..(1645)
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<400> 375
ttgtcgctg tcgattcggc acgaggcgac agcaatcccg ccccggcctg tcgggagcgg      60
tggggcagag gctgcggagc cccaggagga tctgcctccg ctttcacagt cctccagatt      120
tttccaagag cagcagaaa atg  aat  aaa  tcc  ctg  ggg  cca  gtg  tca  ttc  aag      172
                Met Asn Lys  Ser  Leu  Gly  Pro  Val  Ser  Phe  Lys
                  1              5              10

gac  gtg  gct  gtg  gac  ttc  acc  cag  gag  gaa  tgg  cag  cag  ctg  gat  cct      220
Asp Val Ala Val Asp Phe Thr Gln Glu Glu Trp Gln Gln Leu Asp Pro
                15              20              25

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gag cag aag ata act tac agg gat gtg atg ctg gag aac tac agc aat Glu Gln Lys Ile Thr Tyr Arg Asp Val Met Leu Glu Asn Tyr Ser Asn 30 35 40	268
cta gtt tct gtg ggg tat cac att atc aaa ccg gat gtt atc agc aag Leu Val Ser Val Gly Tyr His Ile Ile Lys Pro Asp Val Ile Ser Lys 45 50 55	316
ttg gag caa gga gaa gag cca tgg ata gta gaa gga gaa ttc cta ctt Leu Glu Gln Gly Glu Glu Pro Trp Ile Val Glu Gly Glu Phe Leu Leu 60 65 70 75	364
cag agc tat cca gat gaa gtc tgg caa act gat gac cta ata gag aga Gln Ser Tyr Pro Asp Glu Val Trp Gln Thr Asp Asp Leu Ile Glu Arg 80 85 90	412
atc cag gaa gag gaa aat aaa cct tca agg caa act gtg ttc att gag Ile Gln Glu Glu Glu Asn Lys Pro Ser Arg Gln Thr Val Phe Ile Glu 95 100 105	460
acc ctg att gaa gag aga ggt aat gtt cct ggt aaa act ttt gat gta Thr Leu Ile Glu Glu Arg Gly Asn Val Pro Gly Lys Thr Phe Asp Val 110 115 120	508
gaa acg aac cct gtt cct tca aga aaa ata gcc tat aaa aat agc ctc Glu Thr Asn Pro Val Pro Ser Arg Lys Ile Ala Tyr Lys Asn Ser Leu 125 130 135	556
tgt gac tca tgt gaa aag tgt tta acg tct gtt tca gaa tat att agt Cys Asp Ser Cys Glu Lys Cys Leu Thr Ser Val Ser Glu Tyr Ile Ser 140 145 150 155	604
agt gat gga agc tat gca aga atg aaa gct gat gaa tgt agt gga tgt Ser Asp Gly Ser Tyr Ala Arg Met Lys Ala Asp Glu Cys Ser Gly Cys 160 165 170	652
ggg aaa tca ctc ctc cat att aag ctt gag aaa act cat cca gga gat Gly Lys Ser Leu Leu His Ile Lys Leu Glu Lys Thr His Pro Gly Asp 175 180 185	700
caa gct tat gaa ttt aat caa aat ggg gaa cct tat act cta aat gaa Gln Ala Tyr Glu Phe Asn Gln Asn Gly Glu Pro Tyr Thr Leu Asn Glu 190 195 200	748
gaa agt ctt tat cag aaa att cgt att ttg gag aaa cct ttt gaa tat Glu Ser Leu Tyr Gln Lys Ile Arg Ile Leu Glu Lys Pro Phe Glu Tyr 205 210 215	796
att gaa tgc cag aaa gcc ttc caa aag gac act gtt ttt gtt aat cac Ile Glu Cys Gln Lys Ala Phe Gln Lys Asp Thr Val Phe Val Asn His 220 225 230 235	844
atg gaa gaa aag ccc tat aag tgg aat gga tct gaa ata gcc ttt ctc Met Glu Glu Lys Pro Tyr Lys Trp Asn Gly Ser Glu Ile Ala Phe Leu 240 245 250	892
cag atg tcg gac ctc act gta cat cag aca tct cat atg gaa atg aag Gln Met Ser Asp Leu Thr Val His Gln Thr Ser His Met Glu Met Lys 255 260 265	940
ccc tat gaa tgc agt gaa tgt ggg aaa tcc ttc tgt aaa aag tca aaa Pro Tyr Glu Cys Ser Glu Cys Gly Lys Ser Phe Cys Lys Lys Ser Lys 270 275 280	988



ttt att ata cat cag agg act cac aca gga gag aaa cct tac gaa tgt	1036
Phe Ile Ile His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys	
285 290 295	
aat cag tgt ggg aaa tcc ttc tgc cag aag gga acc ctt act gtg cat	1084
Asn Gln Cys Gly Lys Ser Phe Cys Gln Lys Gly Thr Leu Thr Val His	
300 305 310 315	
cag aga aca cac aca ggg gag aag ccc tat gaa tgt aat gaa tgt ggg	1132
Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys Gly	
320 325 330	
aag aac ttt tac cag aag tta cac ctc att cag cat cag aga act cac	1180
Lys Asn Phe Tyr Gln Lys Leu His Leu Ile Gln His Gln Arg Thr His	
335 340 345	
tca gga gag aag ccc tat gaa tgt agt tat tgt gga aaa tcc ttt tgc	1228
Ser Gly Glu Lys Pro Tyr Glu Cys Ser Tyr Cys Gly Lys Ser Phe Cys	
350 355 360	
cag aag aca cac ctc aca caa cat cag aga aca cat tca gga gag aga	1276
Gln Lys Thr His Leu Thr Gln His Gln Arg Thr His Ser Gly Glu Arg	
365 370 375	
cct tat gtt tgt cat gac tgt ggg aaa acc ttc tcg cag aag tca gca	1324
Pro Tyr Val Cys His Asp Cys Gly Lys Thr Phe Ser Gln Lys Ser Ala	
380 385 390 395	
ctt aat gac cat cag aaa att cac aca ggt gtg aaa ctc tac aag tgt	1372
Leu Asn Asp His Gln Lys Ile His Thr Gly Val Lys Leu Tyr Lys Cys	
400 405 410	
agt gaa tgt ggg aaa tgc ttc tgc cgc aag tct act ctc acg acc cac	1420
Ser Glu Cys Gly Lys Cys Phe Cys Arg Lys Ser Thr Leu Thr Thr His	
415 420 425	
ctg agg acc cac aca gga gag aaa ccg tat gaa tgt aat gag tgt gga	1468
Leu Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys Gly	
430 435 440	
aaa gcc ttc tct cgg atg tca tac ctc act gta cat tat aga act cat	1516
Lys Ala Phe Ser Arg Met Ser Tyr Leu Thr Val His Tyr Arg Thr His	
445 450 455	
tca gga gag aaa ccc tat gag tgt act gaa tgt gga aaa aaa ttc tac	1564
Ser Gly Glu Lys Pro Tyr Glu Cys Thr Glu Cys Gly Lys Lys Phe Tyr	
460 465 470 475	
cac aaa tca gca ttc aac agc cat cag aga att cat agg aga ggc aat	1612
His Lys Ser Ala Phe Asn Ser His Gln Arg Ile His Arg Arg Gly Asn	
480 485 490	
atg aat gta ata gat gtg gga agg ctt ctc tga agtcagac ctcattttat	1663
Met Asn Val Ile Asp Val Gly Arg Leu Leu *	
495 500	
atcagagaac cctttcagta tagtgaatca gaaactcctg cctgaagtca aacaccttgt	1723
acatcagaga gttcacacag gttagtgtgg acatcccctt gtgtgttgga ctcataatct	1783
gaagactcac agaatggaaa ccatgattat aacaagacca catggtataa caatactaga	1843
ctatagacaa gtaaaaattt ataaatatta agaatgtata tacatgtcac catggattgg	1903

aactgttttg catatcaggg aaatcatagc caaggggaaa tctatcagta taaggaatgt 1963  
 ggaagacata atccttttga aactgttaat actaaaagat atgttttctga tacaatagca 2023  
 aacttgaaaa aaaaaaaaaa 2041

<210> 376  
 <211> 1316  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (192)..(1058)

<400> 376  
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 tcctccccca gctccagcct ctctcatctt gggaatctgc gtcagaagtc actcgcagtc 120  
 ccgtcagccc agaagacgta aagcaggcta ccagcaattt tgagaacttg caaaaacagc 180  
 ttgcaaggaa a atg aag ctt cct att ttc ata gca gat gca ttc aca gca 230  
                   Met Lys Leu Pro Ile Phe Ile Ala Asp Ala Phe Thr Ala  
                   1                  5                  10  
 aga gca ttt cgt ggg aat cct gct gct gtt tgc ctc cta gaa aat gaa 278  
 Arg Ala Phe Arg Gly Asn Pro Ala Ala Val Cys Leu Leu Glu Asn Glu  
                   15                  20                  25  
 ttg gat gaa gac atg cat cag aaa att gca agg gag atg aac ctc tct 326  
 Leu Asp Glu Asp Met His Gln Lys Ile Ala Arg Glu Met Asn Leu Ser  
                   30                  35                  40                  45  
 gaa act gct ttt atc cga aaa ctg cac ccg aca gac aac ttt gca caa 374  
 Glu Thr Ala Phe Ile Arg Lys Leu His Pro Thr Asp Asn Phe Ala Gln  
                   50                  55                  60  
 agt tcc tgc ttt gga ctg aga tgg ttt aca cca gcg agt gag gtc cca 422  
 Ser Ser Cys Phe Gly Leu Arg Trp Phe Thr Pro Ala Ser Glu Val Pro  
                   65                  70                  75  
 ctc tgt ggc cat gcc acc ctg gct tct gca gct gtg ctg ttt cac aaa 470  
 Leu Cys Gly His Ala Thr Leu Ala Ser Ala Ala Val Leu Phe His Lys  
                   80                  85                  90  
 ata aaa aac atg aat agc acg ctc acg ttt gtc act ctg agt gga gaa 518  
 Ile Lys Asn Met Asn Ser Thr Leu Thr Phe Val Thr Leu Ser Gly Glu  
                   95                  100                  105  
 cta agg gcc aga cga gca gag gac ggc atc gtc ctg gac ttg cct ctt 566  
 Leu Arg Ala Arg Arg Ala Glu Asp Gly Ile Val Leu Asp Leu Pro Leu  
                   110                  115                  120                  125  
 tat cca gcc cac ccc cag gac ttc cat gaa gta gag gac ttg ata aag 614  
 Tyr Pro Ala His Pro Gln Asp Phe His Glu Val Glu Asp Leu Ile Lys  
                   130                  135                  140  
 act gcc ata ggc aac aca ctg gtc cag gac atc tgt tat tct cca gat 662  
 Thr Ala Ile Gly Asn Thr Leu Val Gln Asp Ile Cys Tyr Ser Pro Asp

	145	150	155	
acc caa aag ctc ctc gtc cgc ctc agt gac gtt tac aac agg tcg ttt				710
Thr Gln Lys Leu Leu Val Arg Leu Ser Asp Val Tyr Asn Arg Ser Phe				
	160	165	170	
ctg gag aac ctg aaa gtg aac acg gag aat ctg ctg caa gtt gaa aac				758
Leu Glu Asn Leu Lys Val Asn Thr Glu Asn Leu Leu Gln Val Glu Asn				
	175	180	185	
aca ggg aag gtg aaa ggg ctt att ctt acc ctt aaa gga gag cct ggt				806
Thr Gly Lys Val Lys Gly Leu Ile Leu Thr Leu Lys Gly Glu Pro Gly				
	190	195	200	205
ggg cag acc caa gca ttt gac ttt tac tca aga tat ttt gca ccg tgg				854
Gly Gln Thr Gln Ala Phe Asp Phe Tyr Ser Arg Tyr Phe Ala Pro Trp				
	210	215	220	
gtt ggt gtg gct gaa gac cca gtg aca ggg tct gca cac gct gtt ctc				902
Val Gly Val Ala Glu Asp Pro Val Thr Gly Ser Ala His Ala Val Leu				
	225	230	235	
agc agc tac tgg tcc cag cat ctg ggg aag aaa gaa atg cat gct ttt				950
Ser Ser Tyr Trp Ser Gln His Leu Gly Lys Lys Glu Met His Ala Phe				
	240	245	250	
cag tgt tcc cac cga gga gga gag ctg gga att tcc ctt cgt cca gac				998
Gln Cys Ser His Arg Gly Gly Glu Leu Gly Ile Ser Leu Arg Pro Asp				
	255	260	265	
gga agg gtt gac att aga gga ggt gca gct gtt gtt tta gag ggc aca				1046
Gly Arg Val Asp Ile Arg Gly Gly Ala Ala Val Val Leu Glu Gly Thr				
	270	275	280	285
ctg aca gcc tag agg tggttatgct gtgacgctgc tgtctctaac caccaagtat				1101
Leu Thr Ala *				
tttctgctta aaaagaaatg taaggggctg ccttttagcaa atgtgcgtag tagtctactt				1161
aatcctcatg ttaaaaatcg aaaaatgggc caggcgcagt ggctcatgcc tgtaatcgta				1221
gcactttgag aggccaaggt ggggtggatca cctgagggtca ggggttcgac accagcctgg				1281
ccaacatggt gaaacctcgt ctctataaaaa aaaaa				1316

<210> 377  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (172) .. (456)

<400> 377	
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ctttggtgat tcagccctga cttctcaaaa agcactgcac agaggaggag gcagcagaac	120
cccatttcag cttcttagga ctctgcactt cccagaagg aagaattaaa a atg aat	177

Met Asn

1

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atg ttc aag gaa gca gtg acc ttc aag gac gtg gct gtg acc ttc acg      225
Met Phe Lys Glu Ala Val Thr Phe Lys Asp Val Ala Val Thr Phe Thr
      5              10              15

gag gag gaa ttg ggg ctg ctg ggc cct gcc cag agg aag ctg tac cga      273
Glu Glu Glu Leu Gly Leu Leu Gly Pro Ala Gln Arg Lys Leu Tyr Arg
      20              25              30

gat gtg atg gtg gag aac ttt agg aac ctg ctg tca gtg ggg cat cca      321
Asp Val Met Val Glu Asn Phe Arg Asn Leu Leu Ser Val Gly His Pro
      35              40              45              50

ccc ttc aaa caa gat gta tca cct ata gaa aga aat gag cag ctt tgg      369
Pro Phe Lys Gln Asp Val Ser Pro Ile Glu Arg Asn Glu Gln Leu Trp
      55              60              65

ata atg acg aca gca acc cga aga cag gga aat tta gat acc tta ctt      417
Ile Met Thr Thr Ala Thr Arg Arg Gln Gly Asn Leu Asp Thr Leu Leu
      70              75              80

gta aaa gct ctt ttg ctc tat gac ctg gct caa act taa acttgattt      466
Val Lys Ala Leu Leu Leu Tyr Asp Leu Ala Gln Thr *
      85              90              95

gaagttagaa gaaatgttgg aagtcattta tatatgaaga aatgttggaa ggactcatat      526

atgcatacat tccttgagtg actatgaatg actgccgggc agtaacttct gggctgtggt      586

tgtaaactgt gagcactaca aaatgttttt ccttattgat accatattat ggtaggaaag      646

acatggaata aaaaatttag atagtaaaaa aaaaaaaaaa                        685

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<210> 378  
 <211> 917  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (160)..(714)

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<400> 378
ccggaattcc cgggtcgacc cagcgtccg cccacgcgtc cggcgagcgg cggtgacttg      60

ccagtaaggg tttggagtca tcagcagggt taatttttga ggaactttac aggtttggct      120

ccagcagctg ctgttgccac caccactagt tcaagcacc   atg cag ttt acc tca      174
                                         Met Gln Phe Thr Ser
                                         1              5

ata tca aat tct ttg acc tcc act gct gct att ggg ctc tca ttt aca      222
Ile Ser Asn Ser Leu Thr Ser Thr Ala Ala Ile Gly Leu Ser Phe Thr
      10              15              20

act tca acg act acc acc gcc act ttc acc acc aac act act acc aca      270
Thr Ser Thr Thr Thr Thr Ala Thr Phe Thr Thr Asn Thr Thr Thr Thr
      25              30              35

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atc acc agt ggc ttt act gtg aac caa aac caa ctg tta tca aga ggg 318  
 Ile Thr Ser Gly Phe Thr Val Asn Gln Asn Gln Leu Leu Ser Arg Gly  
 40 45 50

ttt gaa aac ctt gta cct tat act tca act gtt agt gta gta gca act 366  
 Phe Glu Asn Leu Val Pro Tyr Thr Ser Thr Val Ser Val Val Ala Thr  
 55 60 65

cct gtg atg aca tat ggt cat ctg gag ggt ctt ata aat gag tgg aac 414  
 Pro Val Met Thr Tyr Gly His Leu Glu Gly Leu Ile Asn Glu Trp Asn  
 70 75 80 85

ctt gag ctg gaa gat caa gag aag tac ttt ctt ctc cag gcc act cag 462  
 Leu Glu Leu Glu Asp Gln Glu Lys Tyr Phe Leu Leu Gln Ala Thr Gln  
 90 95 100

gtc aat gct tgg gac cat aca ttg att gag aat ggt gag atg att cgt 510  
 Val Asn Ala Trp Asp His Thr Leu Ile Glu Asn Gly Glu Met Ile Arg  
 105 110 115

att tta cat gga gaa gtg aac aaa gtg aaa ctg gat cag aaa aga ttg 558  
 Ile Leu His Gly Glu Val Asn Lys Val Lys Leu Asp Gln Lys Arg Leu  
 120 125 130

gaa caa gaa ttg gat ttt atc ctg tca cag cag cag gaa cta gaa ttt 606  
 Glu Gln Glu Leu Asp Phe Ile Leu Ser Gln Gln Gln Glu Leu Glu Phe  
 135 140 145

ctg ttg act tat tta gag gag tct acg cgc gac cag agt gga ctt cat 654  
 Leu Leu Thr Tyr Leu Glu Glu Ser Thr Arg Asp Gln Ser Gly Leu His  
 150 155 160 165

tat ctg cag gat gca gat gag gag cat gtg gag atc tcc acc aga tct 702  
 Tyr Leu Gln Asp Ala Asp Glu Glu His Val Glu Ile Ser Thr Arg Ser  
 170 175 180

gca gaa ttc tga atg cccatatgga ctccctgcag tggattgatc ggaattcagg 757  
 Ala Glu Phe \*  
 185

catgctgcga aggaaggtag aagtggtaac acgggttttt cgaggattat cattcacgag 817  
 gggctctttca catcatgttc atcactgttt tttagtgtat tgaccctttt ttcagcttgt 877  
 cgtttctgga ttattatcta ctaattcttt tgtttatttt 917

<210> 379  
 <211> 1631  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (459) .. (1511)

<400> 379  
 gaatttaata cgatcactat aggggaatttg gccctcgagg catagaattc ggcacgaggg 60  
 ctggccaagt aagccactaa cctaggtcat aaagagttag ctttgggacc atttatttcc 120  
 atgatcaaaa taaatacatc tgggtttaac ctgaatcacc atttagtaac atagtcatca 180

951



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atg agt ttt gtc atg gaa tat gtt gga gag gta atc aca agt gaa gaa      1145
Met Ser Phe Val Met Glu Tyr Val Gly Glu Val Ile Thr Ser Glu Glu
      215                      220                      225

gct gaa aga cga gga cag ttc tat gac aac aag gga atc acg tat ctc      1193
Ala Glu Arg Arg Gly Gln Phe Tyr Asp Asn Lys Gly Ile Thr Tyr Leu
230                      235                      240                      245

ttt gat ctg gac tat gag tct gat gaa ttc aca gtg gat gcg gct cga      1241
Phe Asp Leu Asp Tyr Glu Ser Asp Glu Phe Thr Val Asp Ala Ala Arg
                      250                      255                      260

tac ggc aat gtg tct cat ttt gtg aat cac agc tgt gac cca aat ctt      1289
Tyr Gly Asn Val Ser His Phe Val Asn His Ser Cys Asp Pro Asn Leu
                      265                      270                      275

cag gtg ttc aat gtt ttc att gat aac ctc gat act cgt ctt ccc cga      1337
Gln Val Phe Asn Val Phe Ile Asp Asn Leu Asp Thr Arg Leu Pro Arg
                      280                      285                      290

ata gca ttg ttt tcc aca aga acc ata aat gct gga gaa gag ctg act      1385
Ile Ala Leu Phe Ser Thr Arg Thr Ile Asn Ala Gly Glu Glu Leu Thr
                      295                      300                      305

ttt gat tat caa atg aaa ggt tct gga gat ata tct tca gat tct att      1433
Phe Asp Tyr Gln Met Lys Gly Ser Gly Asp Ile Ser Ser Asp Ser Ile
310                      315                      320                      325

gac cac agc cca gcc aaa aag agg gtc aga aca gta tgt aaa tgt gga      1481
Asp His Ser Pro Ala Lys Lys Arg Val Arg Thr Val Cys Lys Cys Gly
                      330                      335                      340

gct gtg act tgc aga ggt tac ctc aac tga a ctttttcagg aaatagagct      1532
Ala Val Thr Cys Arg Gly Tyr Leu Asn *
                      345                      350

gatgattata atattttttt cctaattgtta acattttttaa aaatacatat ttgggactct      1592

tattatcaag gttctaccta tgtaatttta cgattcatg      1631

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<210> 380
<211> 4884
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (116)..(4666)

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<400> 380
aaggatcctt aattaaatta atcccccccc cccagcggg aagagccggc cgaagcgtgg      60

cggccacaga ctgtgggtac cgggtccgag ggactcgcgc ttttctctcc gtgcc atg      118
Met
1

gcg cca gcg aaa gcc acg aac gtg gtg cgg ctg cta cta ggc tcc aca      166
Ala Pro Ala Lys Ala Thr Asn Val Val Arg Leu Leu Leu Gly Ser Thr
5                      10                      15

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gcg ctg tgg ctt tcg cag ctc ggc tcc ggg acg gtc gcc gcg tcc aag	214
Ala Leu Trp Leu Ser Gln Leu Gly Ser Gly Thr Val Ala Ala Ser Lys	
20 25 30	
tcg gtg act gcc cac ttg gcc gcg aag tgg ccc gag acc ccg ctg ctg	262
Ser Val Thr Ala His Leu Ala Ala Lys Trp Pro Glu Thr Pro Leu Leu	
35 40 45	
ctg gag gca agt gaa ttt atg gca gaa gaa agt aat gaa aaa ttt tgg	310
Leu Glu Ala Ser Glu Phe Met Ala Glu Glu Ser Asn Glu Lys Phe Trp	
50 55 60 65	
cag ttt ttg gaa act gtg caa gaa tta gca att tat aag caa aca gaa	358
Gln Phe Leu Glu Thr Val Gln Glu Leu Ala Ile Tyr Lys Gln Thr Glu	
70 75 80	
tca gat tat tct tat tac aac tta atc ctg aag aaa gct gga cag ttt	406
Ser Asp Tyr Ser Tyr Tyr Asn Leu Ile Leu Lys Lys Ala Gly Gln Phe	
85 90 95	
cta gac aat tta cac atc aac ctt tta aag ttt gct ttc tct ata agg	454
Leu Asp Asn Leu His Ile Asn Leu Leu Lys Phe Ala Phe Ser Ile Arg	
100 105 110	
gca tac tcc cca gct att cag atg ttt cag cag att gca gct gat gag	502
Ala Tyr Ser Pro Ala Ile Gln Met Phe Gln Gln Ile Ala Ala Asp Glu	
115 120 125	
cca cca cca gat ggt tgt aat gca ttt gtg gtt att cat aag aag cac	550
Pro Pro Pro Asp Gly Cys Asn Ala Phe Val Val Ile His Lys Lys His	
130 135 140 145	
acc tgt aaa att aat gag att aaa aag ctg ctg aag aaa gct gct tca	598
Thr Cys Lys Ile Asn Glu Ile Lys Lys Leu Leu Lys Lys Ala Ala Ser	
150 155 160	
agg act aga cct tat cta ttt aaa gga gat cac aaa ttt cct aca aac	646
Arg Thr Arg Pro Tyr Leu Phe Lys Gly Asp His Lys Phe Pro Thr Asn	
165 170 175	
aaa gag aac tta cca gtg gtg att ctc tat gcc gaa atg ggt act aga	694
Lys Glu Asn Leu Pro Val Val Ile Leu Tyr Ala Glu Met Gly Thr Arg	
180 185 190	
aca ttt agt gca ttt cac aaa gta ttg tct gaa aaa gct caa aat gag	742
Thr Phe Ser Ala Phe His Lys Val Leu Ser Glu Lys Ala Gln Asn Glu	
195 200 205	
gaa att ctg tat gtt ctt cgc cat tat att cag aaa cca agc tca cgg	790
Glu Ile Leu Tyr Val Leu Arg His Tyr Ile Gln Lys Pro Ser Ser Arg	
210 215 220 225	
aaa atg tac tta tct ggg tat ggt gtg gag cta gca att aag agt aca	838
Lys Met Tyr Leu Ser Gly Tyr Gly Val Glu Leu Ala Ile Lys Ser Thr	
230 235 240	
gaa tac aaa gca ctg gat gat acc caa gtt aaa act gtg act aat act	886
Glu Tyr Lys Ala Leu Asp Asp Thr Gln Val Lys Thr Val Thr Asn Thr	
245 250 255	
act gta gag gat gag act gaa aca aat gaa gtt caa gga ttt ctc ttt	934
Thr Val Glu Asp Glu Thr Glu Thr Asn Glu Val Gln Gly Phe Leu Phe	
260 265 270	

ggg	aaa	cta	aaa	gaa	ata	tat	tca	gat	ctt	aga	gat	aat	ctg	aca	gca	982
Gly	Lys	Leu	Lys	Glu	Ile	Tyr	Ser	Asp	Leu	Arg	Asp	Asn	Leu	Thr	Ala	
275						280					285					
ttc	caa	aaa	tac	ctg	att	gag	agt	aac	aaa	caa	atg	atg	cct	ttg	aaa	1030
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 Pro Glu Gly Leu Gly Arg Lys Gln Ala Cys Leu Ala Met Leu Leu His  
 5 10 15

ttc ttg gac acc tac cag ggg ctg ctt caa gag gaa gag ggg gcc ggc 631  
 Phe Leu Asp Thr Tyr Gln Gly Leu Leu Gln Glu Glu Gly Ala Gly



20	25	30	35	
cac atc atc aag gat cta tac ctg cta att atg aag gac gag tcc ctt				679
His Ile Ile Lys Asp Leu Tyr Leu Leu Ile Met Lys Asp Glu Ser Leu	40	45	50	
tac cag ggc ctc cga gag gac act ctg agg ctg cac cag ctg gtg gag				727
Tyr Gln Gly Leu Arg Glu Asp Thr Leu Arg Leu His Gln Leu Val Glu	55	60	65	
acg gtg gaa cta aag att cca gag gag aac cag cca ccc agc aag cag				775
Thr Val Glu Leu Lys Ile Pro Glu Glu Asn Gln Pro Pro Ser Lys Gln	70	75	80	
gtg aag cca ctc ttc cgc cac ttc cgc cgg ata gac tcc tgt ctg cag				823
Val Lys Pro Leu Phe Arg His Phe Arg Arg Ile Asp Ser Cys Leu Gln	85	90	95	
acc cgg gtg gcc ttc cgg ggc tct gat gag atc ttc tgc cgt gta tac				871
Thr Arg Val Ala Phe Arg Gly Ser Asp Glu Ile Phe Cys Arg Val Tyr	100	105	110	115
atg cct gac cac tct tat gtg acc ata cgc agc cgc ctt tca gca tct				919
Met Pro Asp His Ser Tyr Val Thr Ile Arg Ser Arg Leu Ser Ala Ser	120	125	130	
gtg cag gac att ctg ggc tct gtg acg gag aaa ctt caa tat tca gag				967
Val Gln Asp Ile Leu Gly Ser Val Thr Glu Lys Leu Gln Tyr Ser Glu	135	140	145	
gag ccc gcg ggg cgt gag gat tcc ctc atc ctg gta gct gtg tcc tcc				1015
Glu Pro Ala Gly Arg Glu Asp Ser Leu Ile Leu Val Ala Val Ser Ser	150	155	160	
tct gga gag aag gtc ctt ctc cag ccc act gag gac tgt gtt ttc acc				1063
Ser Gly Glu Lys Val Leu Leu Gln Pro Thr Glu Asp Cys Val Phe Thr	165	170	175	
gca ctg ggc atc aac agc cac ctg ttt gcc tgt act cgg gac agc tat				1111
Ala Leu Gly Ile Asn Ser His Leu Phe Ala Cys Thr Arg Asp Ser Tyr	180	185	190	195
gag gct ctg gtg ccc ctc ccc gag gag atc cag gtc tcc cct gga gac				1159
Glu Ala Leu Val Pro Leu Pro Glu Glu Ile Gln Val Ser Pro Gly Asp	200	205	210	
aca gag atc cac cga gtg gag cct gag gac gtt gcc aac cac cta act				1207
Thr Glu Ile His Arg Val Glu Pro Glu Asp Val Ala Asn His Leu Thr	215	220	225	
gcc ttc cac tgg gag ctg ttc cga tgt gtg cat gag ctg gag ttc gtg				1255
Ala Phe His Trp Glu Leu Phe Arg Cys Val His Glu Leu Glu Phe Val	230	235	240	
gac tac gtg ttc cac ggg gag cgc ggc cgc cgg gag acg gcc aac ttg				1303
Asp Tyr Val Phe His Gly Glu Arg Gly Arg Arg Glu Thr Ala Asn Leu	245	250	255	
gag ctg ctg ctg cag cgc tgc agc gag gtc acg cac tgg gtg gcc acc				1351
Glu Leu Leu Leu Gln Arg Cys Ser Glu Val Thr His Trp Val Ala Thr	260	265	270	275
gaa gtg ctg ctc tgc gag gcc ccg ggc aag cgc gcg cag ctg ctc aag				1399
Glu Val Leu Leu Cys Glu Ala Pro Gly Lys Arg Ala Gln Leu Leu Lys				

	280	285	290	
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Lys Phe Ile Lys Ile Ala Ala Leu Cys Lys Gln Asn Gln Asp Leu Leu				
	295	300	305	
tct ttc tac gcc gtg gtc atg ggg ctg gac aac gcc gct gtc agc cgc				1495
Ser Phe Tyr Ala Val Val Met Gly Leu Asp Asn Ala Ala Val Ser Arg				
	310	315	320	
ctt cga ctc acc tgg gag aag ctg cca ggg aaa ttc aag aac ttg ttt				1543
Leu Arg Leu Thr Trp Glu Lys Leu Pro Gly Lys Phe Lys Asn Leu Phe				
	325	330	335	
cgc aaa ttt gag aac ctg acg gac ccc tgc agg aac cac aaa agc tac				1591
Arg Lys Phe Glu Asn Leu Thr Asp Pro Cys Arg Asn His Lys Ser Tyr				
	340	345	350	355
cga gaa gtg atc tcc aaa atg aag ccc cct gtg att ccc ttc gtg cct				1639
Arg Glu Val Ile Ser Lys Met Lys Pro Pro Val Ile Pro Phe Val Pro				
	360	365	370	
ctg atc ctc aaa gac ctg act ttc ctg cac gaa ggg agt aag acc ctt				1687
Leu Ile Leu Lys Asp Leu Thr Phe Leu His Glu Gly Ser Lys Thr Leu				
	375	380	385	
gta gat ggt ttg gtg aac atc gag aag ctg cat tca gtg gcc gaa aaa				1735
Val Asp Gly Leu Val Asn Ile Glu Lys Leu His Ser Val Ala Glu Lys				
	390	395	400	
gtg agg aca atc cgc aaa tac cgg agc cgg ccc ctt tgc ctg gac atg				1783
Val Arg Thr Ile Arg Lys Tyr Arg Ser Arg Pro Leu Cys Leu Asp Met				
	405	410	415	
gag gca tcc ccc aat cac ctg cag acc aag gcc tat gtg cgc cag ttt				1831
Glu Ala Ser Pro Asn His Leu Gln Thr Lys Ala Tyr Val Arg Gln Phe				
	420	425	430	435
cag gtc atc gac aac cag aac ctc ctc ttc gag ctc tcc tac aag ctg				1879
Gln Val Ile Asp Asn Gln Asn Leu Leu Phe Glu Leu Ser Tyr Lys Leu				
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tcccgagcac agcggcgct atg gac tct cca gga tac aac tgc ttc gtg gac	232
Met Asp Ser Pro Gly Tyr Asn Cys Phe Val Asp	
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aaa gac aag atg gac gct gcc atc cag gac ctg ggg ccc aag gag ctg	280
Lys Asp Lys Met Asp Ala Ala Ile Gln Asp Leu Gly Pro Lys Glu Leu	
15 20 25	
agc tgc act gaa ctg cag gaa ctg aag cag ctg gcg cgc cag ggc tac	328
Ser Cys Thr Glu Leu Gln Glu Leu Lys Gln Leu Ala Arg Gln Gly Tyr	
30 35 40	
tgg gcc caa agc cac gcc ctg cgg gga aag gtg tac cag cgc ctg atc	376
Trp Ala Gln Ser His Ala Leu Arg Gly Lys Val Tyr Gln Arg Leu Ile	
45 50 55	
cgg gac att ccc tgc cgc acg gtc acg cct gac gcc agc gtg tac agc	424
Arg Asp Ile Pro Cys Arg Thr Val Thr Pro Asp Ala Ser Val Tyr Ser	
60 65 70 75	
gac atc gtg ggc aag atc gtg ggc aag cac agc agc agc tgc ctg ccg	472
Asp Ile Val Gly Lys Ile Val Gly Lys His Ser Ser Ser Cys Leu Pro	
80 85 90	
ctg ccc gag ttc gtg gac aac acg cag gtg ccc agc tac tgc ctg aat	520
Leu Pro Glu Phe Val Asp Asn Thr Gln Val Pro Ser Tyr Cys Leu Asn	
95 100 105	
gca cgc ggc gag ggg gcc gtg cgc aag atc ctc ctg tgc ctg gcc aac	568
Ala Arg Gly Glu Gly Ala Val Arg Lys Ile Leu Leu Cys Leu Ala Asn	
110 115 120	
cag ttc ccc gac atc tcc ttc tgc ccc gcc ctg ccg gcc gtg gtg gcc	616
Gln Phe Pro Asp Ile Ser Phe Cys Pro Ala Leu Pro Ala Val Val Ala	
125 130 135	
ctg ctg ctg cac tac agc atc gac gag gcc gag tgc ttc gag aag gcc	664
Leu Leu Leu His Tyr Ser Ile Asp Glu Ala Glu Cys Phe Glu Lys Ala	
140 145 150 155	
tgc cgc atc ctg gcc tgc aat gac ccc ggc agg agg ctg atc gac cag	712
Cys Arg Ile Leu Ala Cys Asn Asp Pro Gly Arg Arg Leu Ile Asp Gln	
160 165 170	
agc ttc ctg gcc ttt gag tcg tcc tgc atg acg ttt ggg gac ctg gtg	760
Ser Phe Leu Ala Phe Glu Ser Ser Cys Met Thr Phe Gly Asp Leu Val	
175 180 185	
aac aag tac tgc cag gcg gcc cac aag ctg atg gtg gcc gtg tcg gag	808
Asn Lys Tyr Cys Gln Ala Ala His Lys Leu Met Val Ala Val Ser Glu	
190 195 200	
gat gtc ctg cag gtc tat gcg gac tgg cag cgc tgg ctg ttt ggg gag	856
Asp Val Leu Gln Val Tyr Ala Asp Trp Gln Arg Trp Leu Phe Gly Glu	
205 210 215	
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Leu Pro Leu Cys Tyr Phe Ala Arg Val Phe Asp Val Phe Leu Val Glu	
220 225 230 235	
ggc tac aag gtg ctg tac cgc gtg gcg ctg gcc atc ctc aag ttc ttc	952
Gly Tyr Lys Val Leu Tyr Arg Val Ala Leu Ala Ile Leu Lys Phe Phe	
240 245 250	
cat aag gtg agg gcc ggg cag ccg ctg gag tcg gac agc gtg aag cag	1000
His Lys Val Arg Ala Gly Gln Pro Leu Glu Ser Asp Ser Val Lys Gln	
255 260 265	
gac atc cgc acg ttc gtc aga gac atc gcg aag acg gtg tcc cct gag	1048
Asp Ile Arg Thr Phe Val Arg Asp Ile Ala Lys Thr Val Ser Pro Glu	
270 275 280	
aag ctg ctg gag aaa gcg ttc gcc atc cgc ctc ttg tcc cgc aag gag	1096
Lys Leu Leu Glu Lys Ala Phe Ala Ile Arg Leu Leu Ser Arg Lys Glu	
285 290 295	
atc cag ctc ctg cag atg gcc aat gag aaa gcc ctg aag cag aag ggc	1144
Ile Gln Leu Leu Gln Met Ala Asn Glu Lys Ala Leu Lys Gln Lys Gly	
300 305 310 315	
atc acc gtg aag cag aag agt gtg tca ctt tct aaa agg cag ttt gta	1192
Ile Thr Val Lys Gln Lys Ser Val Ser Leu Ser Lys Arg Gln Phe Val	
320 325 330	
cac ttg gcc gtc cat gca gag aac ttc cgc tcg gag atc gtc agc gtg	1240
His Leu Ala Val His Ala Glu Asn Phe Arg Ser Glu Ile Val Ser Val	
335 340 345	
agg gag atg aga gac atc tgg tcc tgg gtc ccc gag cgc ttt gcc ctg	1288
Arg Glu Met Arg Asp Ile Trp Ser Trp Val Pro Glu Arg Phe Ala Leu	
350 355 360	
tgc cag ccc ctt ctg ctg ttc tcc tcc ctg cag cac ggg tac agc ctg	1336
Cys Gln Pro Leu Leu Leu Phe Ser Ser Leu Gln His Gly Tyr Ser Leu	
365 370 375	
gcc agg ttc tac ttc cag tgt gaa gga cat gag cct acc ctc ttg ctc	1384
Ala Arg Phe Tyr Phe Gln Cys Glu Gly His Glu Pro Thr Leu Leu Leu	
380 385 390 395	
atc aag acc acg cag aag gag gtg tgt ggt gct tac ctg tcc aca gac	1432
Ile Lys Thr Thr Gln Lys Glu Val Cys Gly Ala Tyr Leu Ser Thr Asp	
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Trp Ser Glu Arg Asn Lys Phe Gly Gly Lys Leu Gly Phe Phe Gly Thr	
415 420 425	
gga gaa tgc ttt gtg ttt agg ctg cag cct gag gtg cag cgc tac gag	1528
Gly Glu Cys Phe Val Phe Arg Leu Gln Pro Glu Val Gln Arg Tyr Glu	
430 435 440	
tgg gtg gtg atc aag cac ccc gag ctg acc aag ccc cca ccc ttg atg	1576
Trp Val Val Ile Lys His Pro Glu Leu Thr Lys Pro Pro Pro Leu Met	
445 450 455	
gct gcc gag ccc acc gcc cca ctc agc cac tcc gcc tcc tca gac ccc	1624
Ala Ala Glu Pro Thr Ala Pro Leu Ser His Ser Ala Ser Ser Asp Pro	
460 465 470 475	
gct gac cgc ctc tcg ccc ttc ctg gcc gct cgc cac ttc aac ctg ccc	1672

Ala Asp Arg Leu Ser Pro Phe Leu Ala Ala Arg His Phe Asn Leu Pro	
480 485 490	
tcc aag acc gag tcc atg ttc atg gcg ggg ggc agc gac tgc ctc atc	1720
Ser Lys Thr Glu Ser Met Phe Met Ala Gly Gly Ser Asp Cys Leu Ile	
495 500 505	
gtc ggg gga gga ggc ggc cag gcg ctc tac atc gat ggg gac ctg aac	1768
Val Gly Gly Gly Gly Gly Gln Ala Leu Tyr Ile Asp Gly Asp Leu Asn	
510 515 520	
cgg ggc cgc aca agc cac tgc gac acc ttc aac aac cag ccc ctc tgc	1816
Arg Gly Arg Thr Ser His Cys Asp Thr Phe Asn Asn Gln Pro Leu Cys	
525 530 535	
tcc gag aac ttc ctc att gct gcc gtg aag gcc tgg ggc ttc cag gac	1864
Ser Glu Asn Phe Leu Ile Ala Ala Val Lys Ala Trp Gly Phe Gln Asp	
540 545 550 555	
cct gac acc cag tga cggcctgtgc cacggtgact gagccgtggt ggggcggtgg	1919
Pro Asp Thr Gln *	
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Met Pro Gly Ser Asp Thr Ala Leu Thr Val	
1 5 10	
gac cgg acc tac tcg gac ccc ggc cgg cac cac cgc tgc aag agc cgg	159
Asp Arg Thr Tyr Ser Asp Pro Gly Arg His His Arg Cys Lys Ser Arg	
15 20 25	
gta gaa cgt cat gac atg aat acc tta agc ctg ccc ctg aac ata cgc	207
Val Glu Arg His Asp Met Asn Thr Leu Ser Leu Pro Leu Asn Ile Arg	
30 35 40	
cga ggg ggg tca gac acc aac ctc aac ttt gat gtc ccg gat ggc atc	255
Arg Gly Gly Ser Asp Thr Asn Leu Asn Phe Asp Val Pro Asp Gly Ile	
45 50 55	
ctg gac ttc cac aag gtc aaa ctc act gca gac agc ctg aag caa aaa	303
Leu Asp Phe His Lys Val Lys Leu Thr Ala Asp Ser Leu Lys Gln Lys	
60 65 70	
att cta aag gta aca gag cag ata aaa att gag caa aca tcg cgc gat	351
Ile Leu Lys Val Thr Glu Gln Ile Lys Ile Glu Gln Thr Ser Arg Asp	

75	80	85	90	
ggg aat gtt gcg gag tat ctg aaa cta gtg aac aac gcg gac aag cag				399
Gly Asn Val Ala Glu Tyr Leu Lys Leu Val Asn Asn Ala Asp Lys Gln				
	95	100	105	
cag gcg gga cgt atc aag caa gtc ttt gag aag aag aat cag aaa tca				447
Gln Ala Gly Arg Ile Lys Gln Val Phe Glu Lys Lys Asn Gln Lys Ser				
	110	115	120	
gct cac tcc atc gcc cag ctg cag aag aag tta gag cag tat cat cga				495
Ala His Ser Ile Ala Gln Leu Gln Lys Lys Leu Glu Gln Tyr His Arg				
	125	130	135	
aag ctc aga gag atc gag cag aat gga gcc tct agg agc tca aag gac				543
Lys Leu Arg Glu Ile Glu Gln Asn Gly Ala Ser Arg Ser Ser Lys Asp				
	140	145	150	
att tcc aaa gac cac ctg aag gat ata cat cgc tct ttg aaa gat gcc				591
Ile Ser Lys Asp His Leu Lys Asp Ile His Arg Ser Leu Lys Asp Ala				
	155	160	165	170
cac gtg aaa tct cga act gcc ccc cat tgc atg gag agc agc aaa tcg				639
His Val Lys Ser Arg Thr Ala Pro His Cys Met Glu Ser Ser Lys Ser				
	175	180	185	
ggc atg cca ggg gtc tca ctt act cca cct gtg ttc gtt ttc aat aag				687
Gly Met Pro Gly Val Ser Leu Thr Pro Pro Val Phe Val Phe Asn Lys				
	190	195	200	
tcc aga gag ttt gcc aac ctg atc cgg aat aag ttt ggc agc gcc gac				735
Ser Arg Glu Phe Ala Asn Leu Ile Arg Asn Lys Phe Gly Ser Ala Asp				
	205	210	215	
aac att gct cac ttg aaa aat tcc tta gag gag ttt agg cca gag gcg				783
Asn Ile Ala His Leu Lys Asn Ser Leu Glu Glu Phe Arg Pro Glu Ala				
	220	225	230	
agt gcc agg gcc tac ggg ggc agc gct acc atc gtg aac aaa ccc aag				831
Ser Ala Arg Ala Tyr Gly Gly Ser Ala Thr Ile Val Asn Lys Pro Lys				
	235	240	245	250
tat ggc agt gat gat gaa tgt tcg agt ggc acg tca ggc tcg gcc gac				879
Tyr Gly Ser Asp Asp Glu Cys Ser Ser Gly Thr Ser Gly Ser Ala Asp				
	255	260	265	
agt aac gga aac cag tcg ttt ggg gct ggt gga gcc agc aca ctg gac				927
Ser Asn Gly Asn Gln Ser Phe Gly Ala Gly Gly Ala Ser Thr Leu Asp				
	270	275	280	
agc cag ggc aag ctc gcc gtg atc ctg gag gaa ctg agg gag atc aag				975
Ser Gln Gly Lys Leu Ala Val Ile Leu Glu Glu Leu Arg Glu Ile Lys				
	285	290	295	
gat acc caa gct cag ctg gct gag gac atc gag gca ctg aag gtg cag				1023
Asp Thr Gln Ala Gln Leu Ala Glu Asp Ile Glu Ala Leu Lys Val Gln				
	300	305	310	
ttt aag aga gaa tat ggt ttt att tct cag acc ctg caa gag gaa aga				1071
Phe Lys Arg Glu Tyr Gly Phe Ile Ser Gln Thr Leu Gln Glu Glu Arg				
	315	320	325	330
tac agg tat gag cga ctg gag gac cag ctg cat gac ctg acg gac ctg				1119
Tyr Arg Tyr Glu Arg Leu Glu Asp Gln Leu His Asp Leu Thr Asp Leu				



	335	340	345	
cat cag cat gag aca gcc aac ctg aag cag gag ctg gcc agc att gag				1167
His Gln His Glu Thr Ala Asn Leu Lys Gln Glu Leu Ala Ser Ile Glu				
	350	355	360	
gag aag gtg gcc tac cag gcc tac gag cgc tcg cgg gac atc cag gaa				1215
Glu Lys Val Ala Tyr Gln Ala Tyr Glu Arg Ser Arg Asp Ile Gln Glu				
	365	370	375	
gcc ttg gaa tcc tgc cag act cgc att tct aag ctg gag ctc cac cag				1263
Ala Leu Glu Ser Cys Gln Thr Arg Ile Ser Lys Leu Glu Leu His Gln				
	380	385	390	
caa gag cag caa gct ctg cag aca gac acc gtg aat gct aaa gtt ctc				1311
Gln Glu Gln Gln Ala Leu Gln Thr Asp Thr Val Asn Ala Lys Val Leu				
	395	400	405	410
ctg ggg agg tgc atc aac gtg atc ctg gcc ttc atg act gtc atc tta				1359
Leu Gly Arg Cys Ile Asn Val Ile Leu Ala Phe Met Thr Val Ile Leu				
	415	420	425	
gtg tgt gtg tcc acc atc gcg aag ttc gtc tca ccc atg atg aag agt				1407
Val Cys Val Ser Thr Ile Ala Lys Phe Val Ser Pro Met Met Lys Ser				
	430	435	440	
cgc tgc cac att ctt ggc acc ttc ttt gcc gtg act ctt ctt gct ata				1455
Arg Cys His Ile Leu Gly Thr Phe Phe Ala Val Thr Leu Leu Ala Ile				
	445	450	455	
ttt tgt aaa aac tgg gac cat atc ctg tgt gcc ata gaa agg atg ata				1503
Phe Cys Lys Asn Trp Asp His Ile Leu Cys Ala Ile Glu Arg Met Ile				
	460	465	470	
ata cca aga tga agc cactggttcc tgccttcaag ttctttcaag tttttatttt				1558
Ile Pro Arg *				
	475			
aaagaaaact ctgtgcatac taccaaattt tacagtgaat gattgtgcgg actcgtgtgt				1618
aagaaaaact aggactgtgt ggtgtaaata actacaattc tcttaactcg gtagcagttg				1678
ccaactcagt ccttgtactt cgttaacacg gatctgtttc agagctctcc taccttgctc				1738
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ctccaggcag cctctggggc ccgcgcccgc gcctgctcag gctcccgtgt tcaggctgcc      240
catccccctcc ccaccggcgt cccggacgtt gggacctgtg accgtggcct cgggctgggc      300
ttccaaagcc ggccgcagcc cggcgacccc cgaggcctct cgccccgggc ccctagacct      360
ctcact    atg acc gcg gcc gcc gcc tcc aac tgg ggg ctg atc acg aac      408
           Met Thr Ala Ala Ala Ala Ser Asn Trp Gly Leu Ile Thr Asn
           1             5             10

atc gtg aac agc atc gta ggg gtc agt gtc ctc acc atg ccc ttc tgc      456
Ile Val Asn Ser Ile Val Gly Val Ser Val Leu Thr Met Pro Phe Cys
15             20             25             30

ttc aaa cag tgc ggc atc gtc ctg ggg gcg ctg ctc ttg gtc ttc tgc      504
Phe Lys Gln Cys Gly Ile Val Leu Gly Ala Leu Leu Leu Val Phe Cys
35             40             45

tca tgg atg acg cac cag tcg tgc atg ttc ttg gtg aag tcg gcc agc      552
Ser Trp Met Thr His Gln Ser Cys Met Phe Leu Val Lys Ser Ala Ser
50             55             60

ctg agc aag cgg agg acc tac gcc ggc ctg gca ttc cac gcc tac ggg      600
Leu Ser Lys Arg Arg Thr Tyr Ala Gly Leu Ala Phe His Ala Tyr Gly
65             70             75

aag gca ggc aag atg ctg gtg gag acc agc atg atc ggg ctg atg ctg      648
Lys Ala Gly Lys Met Leu Val Glu Thr Ser Met Ile Gly Leu Met Leu
80             85             90

ggc acc tgc atc gcc ttc tac gtc gtg atc ggc gac ttg ggg tcc aac      696
Gly Thr Cys Ile Ala Phe Tyr Val Val Ile Gly Asp Leu Gly Ser Asn
95             100            105            110

ttc ttt gcc cgg ctg ttc ggg ttt cag gtg ggc ggc acc ttc cgc atg      744
Phe Phe Ala Arg Leu Phe Gly Phe Gln Val Gly Gly Thr Phe Arg Met
115            120            125

ttc ctg ctg ttc gcc gtg tcg ctg tgc atc gtg ctc ccg ctc agc ctg      792
Phe Leu Leu Phe Ala Val Ser Leu Cys Ile Val Leu Pro Leu Ser Leu
130            135            140

cag cgg aac atg atg gcc tcc atc cag tcc ttc agc gcc atg gcc ctc      840
Gln Arg Asn Met Met Ala Ser Ile Gln Ser Phe Ser Ala Met Ala Leu
145            150            155

ctc ttc tac acc gtg ttt atg ttc gtg atc gtg ctc tcc cct ctc aag      888
Leu Phe Tyr Thr Val Phe Met Phe Val Ile Val Leu Ser Pro Leu Lys
160            165            170

cac ggc ctc ttc agt ggg cag tgg ctg cgg cgg gtc agc tac gtc cgc      936
His Gly Leu Phe Ser Gly Gln Trp Leu Arg Arg Val Ser Tyr Val Arg
175            180            185            190

tgg gag ggc gtc ttc cgc tgc atc ccc atc ttc ggg cat gtc ctt cgc      984
Trp Glu Gly Val Phe Arg Cys Ile Pro Ile Phe Gly His Val Leu Arg
195            200            205

ctg cca gtc cca agt gct gcc cac cta cga cag cct gga tga gccgtca      1033
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210            215            220

gtgat                                             1038

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tctttggact tagaagatga cctggataaa tgataaaaat taagaaagag attttgaagt      180
tttcttattg tcctcttggc atatgcttct ggaataatat tcacc      atg gtt ttg      234
                                   Met Val Leu
                                   1

gat gac ctt cca aac tta gaa gac atc tat act tcc ttg tgt tca tca      282
Asp Asp Leu Pro Asn Leu Glu Asp Ile Tyr Thr Ser Leu Cys Ser Ser
      5                                10                                15

aca atg gaa gac tca gag atg gat ttt gac tct gga cta gaa gat gat      330
Thr Met Glu Asp Ser Glu Met Asp Phe Asp Ser Gly Leu Glu Asp Asp
      20                                25                                30                                35

gac aca aaa agt gat agt att ttg gag gat tcc aca att ttt gtg gcc      378
Asp Thr Lys Ser Asp Ser Ile Leu Glu Asp Ser Thr Ile Phe Val Ala
                                   40                                45                                50

ttc aaa gga aat ata gat gat aaa gac ttc aaa tgg aaa tta gat gca      426
Phe Lys Gly Asn Ile Asp Asp Lys Asp Phe Lys Trp Lys Leu Asp Ala
                                   55                                60                                65

ata ttg aaa aac gtg ccc aat ttg tta cac atg gag tcc agc aag cta      474
Ile Leu Lys Asn Val Pro Asn Leu Leu His Met Glu Ser Ser Lys Leu
                                   70                                75                                80

aaa gta cag aag gtg gag ccc tgg aac agc gtg cgt gtg aca ttc aac      522
Lys Val Gln Lys Val Glu Pro Trp Asn Ser Val Arg Val Thr Phe Asn
                                   85                                90                                95

atc ccc cgg gaa gca gcg gag cgg cta cgg atc ctt gct cag agc aac      570
Ile Pro Arg Glu Ala Ala Glu Arg Leu Arg Ile Leu Ala Gln Ser Asn
      100                                105                                110                                115

aac cag cag ctt cgg gat tta ggg att ctc tcc gtt cag att gaa ggg      618
Asn Gln Gln Leu Arg Asp Leu Gly Ile Leu Ser Val Gln Ile Glu Gly
                                   120                                125                                130

gaa ggt gct att aac ctg gct ttg gct cag aac cga agc caa gat gtg      666
Glu Gly Ala Ile Asn Leu Ala Leu Ala Gln Asn Arg Ser Gln Asp Val
                                   135                                140                                145

aga atg aat gga ccc atg gga gct gga aat tca gtt agg atg gag gcg      714
Arg Met Asn Gly Pro Met Gly Ala Gly Asn Ser Val Arg Met Glu Ala
                                   150                                155                                160

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gga ttt cct atg gca agt ggt cca gga ata ata agg atg aac aac cct Gly Phe Pro Met Ala Ser Gly Pro Gly Ile Ile Arg Met Asn Asn Pro 165 170 175	762
gcc act gtt atg ata ccc ccg ggt gga aat gtg tca tct tcc atg atg Ala Thr Val Met Ile Pro Pro Gly Gly Asn Val Ser Ser Ser Met Met 180 185 190 195	810
gca cca ggc ccc aat cca gag ctg cag ccc agg act cct cgc cct gct Ala Pro Gly Pro Asn Pro Glu Leu Gln Pro Arg Thr Pro Arg Pro Ala 200 205 210	858
tct cag tca gat gca atg gat cca ctc ctc tct ggg ctc cat ata cag Ser Gln Ser Asp Ala Met Asp Pro Leu Leu Ser Gly Leu His Ile Gln 215 220 225	906
cag caa agt cat ccc tca gga tct tta gct ccc cca cat cac cca atg Gln Gln Ser His Pro Ser Gly Ser Leu Ala Pro Pro His His Pro Met 230 235 240	954
cag cct gtc tct gtg aac aga caa atg aac cca gct aat ttt ccc cag Gln Pro Val Ser Val Asn Arg Gln Met Asn Pro Ala Asn Phe Pro Gln 245 250 255	1002
ctg cag cag cag cag caa caa caa caa cag cag cag cag cag cag Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln 260 265 270 275	1050
cag caa caa cag caa cag cag caa caa cag ttg cag gca aga ccc cca Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Gln Ala Arg Pro Pro 280 285 290	1098
cag caa cat cag cag caa cag cca cag gga att cga ccc cag ttt act Gln Gln His Gln Gln Gln Gln Pro Gln Gly Ile Arg Pro Gln Phe Thr 295 300 305	1146
gcc cca act cag gtg cct gtt cct cca ggc tgg aac cag ctg cct tct Ala Pro Thr Gln Val Pro Val Pro Pro Gly Trp Asn Gln Leu Pro Ser 310 315 320	1194
gga gcc ctt caa cct cct cca gcc cag ggt tct ctg ggc aca atg act Gly Ala Leu Gln Pro Pro Pro Ala Gln Gly Ser Leu Gly Thr Met Thr 325 330 335	1242
gca aac caa ggg tgg aag aag gct ccc ttg ccc ggc cca atg caa cag Ala Asn Gln Gly Trp Lys Lys Ala Pro Leu Pro Gly Pro Met Gln Gln 340 345 350 355	1290
caa ctc cag gca aga cca tcc tta gcc acg gta cag acg cct tcc cac Gln Leu Gln Ala Arg Pro Ser Leu Ala Thr Val Gln Thr Pro Ser His 360 365 370	1338
cct ccc cct cca tat ccc ttt ggc agc cag caa gcc tca caa gcc cac Pro Pro Pro Pro Tyr Pro Phe Gly Ser Gln Gln Ala Ser Gln Ala His 375 380 385	1386
aca aac ttt cct cag atg agc aac cca ggc cag ttc aca gct cct cag Thr Asn Phe Pro Gln Met Ser Asn Pro Gly Gln Phe Thr Ala Pro Gln 390 395 400	1434
atg aag agt ttg cag gga ggg ccc tct agg gtc cca act ccc ttg cag Met Lys Ser Leu Gln Gly Gly Pro Ser Arg Val Pro Thr Pro Leu Gln 405 410 415	1482

cag ccc cac ctc acc aac aag tct cct gcc tcc tca ccc tcc tcc ttc	1530
Gln Pro His Leu Thr Asn Lys Ser Pro Ala Ser Ser Pro Ser Ser Phe	
420 425 430 435	
cag cag gga tcc cct gca tcc tcc cca acg gtt aac caa act cag cag	1578
Gln Gln Gly Ser Pro Ala Ser Ser Pro Thr Val Asn Gln Thr Gln Gln	
440 445 450	
cag atg gga cca agg cca cct caa aat aac cca ctt ccc cag gga ttt	1626
Gln Met Gly Pro Arg Pro Pro Gln Asn Asn Pro Leu Pro Gln Gly Phe	
455 460 465	
cag cag cct gtc agc tct ccg ggt cgg aat cct atg gtt caa cag gga	1674
Gln Gln Pro Val Ser Ser Pro Gly Arg Asn Pro Met Val Gln Gln Gly	
470 475 480	
aat gtg cca cct aac ttc atg gtg atg cag cag caa cca cca aac cag	1722
Asn Val Pro Pro Asn Phe Met Val Met Gln Gln Gln Pro Pro Asn Gln	
485 490 495	
ggg cca cag agt tta cat cca ggc cta gga gga atg cct aaa cgc ctc	1770
Gly Pro Gln Ser Leu His Pro Gly Leu Gly Gly Met Pro Lys Arg Leu	
500 505 510 515	
cca cct ggc ttc tca gca gga cag gcc aat ccg aac ttt atg caa ggt	1818
Pro Pro Gly Phe Ser Ala Gly Gln Ala Asn Pro Asn Phe Met Gln Gly	
520 525 530	
cag gtg cct tcg acc aca gca acc acc cct ggg aat tca gga gcc cct	1866
Gln Val Pro Ser Thr Thr Ala Thr Thr Pro Gly Asn Ser Gly Ala Pro	
535 540 545	
cag ctg caa gca aat caa aat gtc cag cat gca ggt ggt caa gga gct	1914
Gln Leu Gln Ala Asn Gln Asn Val Gln His Ala Gly Gly Gln Gly Ala	
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ggt cct cct caa aac cag atg cag gtg tcc cac ggg ccg cca aat atg	1962
Gly Pro Pro Gln Asn Gln Met Gln Val Ser His Gly Pro Pro Asn Met	
565 570 575	
atg cag ccc agc ctc atg gga att cat ggc aac atg aac aat cag cag	2010
Met Gln Pro Ser Leu Met Gly Ile His Gly Asn Met Asn Asn Gln Gln	
580 585 590 595	
gct ggt act tct ggg gtt cct caa gtg aac ctc agc aac atg caa ggc	2058
Ala Gly Thr Ser Gly Val Pro Gln Val Asn Leu Ser Asn Met Gln Gly	
600 605 610	
cag ccc cag cag ggc cca cca tct cag ctg atg ggc atg cac cag caa	2106
Gln Pro Gln Gln Gly Pro Pro Ser Gln Leu Met Gly Met His Gln Gln	
615 620 625	
atc gtg ccc tcc cag ggc cag atg gtc cag caa caa gga acc ttg aac	2154
Ile Val Pro Ser Gln Gly Gln Met Val Gln Gln Gln Gly Thr Leu Asn	
630 635 640	
cct cag aac cct atg atc ctt tca agg gcc cag ctt atg cca cag ggc	2202
Pro Gln Asn Pro Met Ile Leu Ser Arg Ala Gln Leu Met Pro Gln Gly	
645 650 655	
cag atg atg gtg aac ccc ccg agc caa aat ctt ggg ccc tcg ccc caa	2250
Gln Met Met Val Asn Pro Pro Ser Gln Asn Leu Gly Pro Ser Pro Gln	
660 665 670 675	

agg atg acc cca ccc aag cag atg ctt tcc cag cag ggc cca caa atg	2298
Arg Met Thr Pro Pro Lys Gln Met Leu Ser Gln Gln Gly Pro Gln Met	
680 685 690	
atg gcg cca cat aac cag atg atg ggg cct cag ggg cag gtt ttg ctc	2346
Met Ala Pro His Asn Gln Met Met Gly Pro Gln Gly Gln Val Leu Leu	
695 700 705	
caa cag aac cca atg ata gag cag att atg acc aat caa atg cag ggg	2394
Gln Gln Asn Pro Met Ile Glu Gln Ile Met Thr Asn Gln Met Gln Gly	
710 715 720	
aat aag cag cag ttt aac act cag aac cag tcc aat gtc atg ccg gga	2442
Asn Lys Gln Gln Phe Asn Thr Gln Asn Gln Ser Asn Val Met Pro Gly	
725 730 735	
cca gcc cag ata atg agg gga cca act cca aac atg caa gga aat atg	2490
Pro Ala Gln Ile Met Arg Gly Pro Thr Pro Asn Met Gln Gly Asn Met	
740 745 750 755	
gtg cag ttt acg gga cag atg tca gga cag atg ctg ccc cag caa ggg	2538
Val Gln Phe Thr Gly Gln Met Ser Gly Gln Met Leu Pro Gln Gln Gly	
760 765 770	
cct gtg aac aac agt cca tct cag gtt atg ggc att cag gga cag gtc	2586
Pro Val Asn Asn Ser Pro Ser Gln Val Met Gly Ile Gln Gly Gln Val	
775 780 785	
ctg cgg cca cca ggg ccc agc cca cac atg gcc cag cag cat ggt gat	2634
Leu Arg Pro Pro Gly Pro Ser Pro His Met Ala Gln Gln His Gly Asp	
790 795 800	
cct gct act aca gca aat aac gat gtc agt tta tct cag atg atg cct	2682
Pro Ala Thr Thr Ala Asn Asn Asp Val Ser Leu Ser Gln Met Met Pro	
805 810 815	
gat gtt agc att caa caa acc aac atg gtc ccc cct cat gtg cag gcc	2730
Asp Val Ser Ile Gln Gln Thr Asn Met Val Pro Pro His Val Gln Ala	
820 825 830 835	
atg cag gga aac agt gcc tcg gga aac cac ttc tca ggc cat ggg atg	2778
Met Gln Gly Asn Ser Ala Ser Gly Asn His Phe Ser Gly His Gly Met	
840 845 850	
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Ser Phe Asn Ala Pro Phe Ser Gly Ala Pro Asn Gly Asn Gln Met Ser	
855 860 865	
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Cys Gly Gln Asn Pro Gly Phe Pro Val Asn Lys Asp Val Thr Leu Thr	
870 875 880	
agc cca ttg ttg gtc aac tta ttg cag agt gac ata tct gca ggc cat	2922
Ser Pro Leu Leu Val Asn Leu Leu Gln Ser Asp Ile Ser Ala Gly His	
885 890 895	
ttt ggg gta aac aat aag caa aat aat acc aac gca aat aaa ccg aag	2970
Phe Gly Val Asn Asn Lys Gln Asn Asn Thr Asn Ala Asn Lys Pro Lys	
900 905 910 915	
aag aag aaa ccc cct cgg aag aag aaa aat agt cag caa gat cta aac	3018
Lys Lys Lys Pro Pro Arg Lys Lys Lys Asn Ser Gln Gln Asp Leu Asn	
920 925 930	



acc cca gat act cgc cca gct ggt ctg gaa gag gct gat cag cca ccg Thr Pro Asp Thr Arg Pro Ala Gly Leu Glu Glu Ala Asp Gln Pro Pro	3066
935 940 945	
ttg cct gga gaa caa gga att agc ttg gat aac tca ggc cct aaa ctg Leu Pro Gly Glu Gln Gly Ile Ser Leu Asp Asn Ser Gly Pro Lys Leu	3114
950 955 960	
cca gaa ttt tca aac cgg cca cca ggt tat cct tct caa cca gtt gaa Pro Glu Phe Ser Asn Arg Pro Pro Gly Tyr Pro Ser Gln Pro Val Glu	3162
965 970 975	
cag agg cca ctt cag cag atg cct cct caa ctc atg cag cat gtg gca Gln Arg Pro Leu Gln Gln Met Pro Pro Gln Leu Met Gln His Val Ala	3210
980 985 990 995	
ccc cca cca cag cca cca cag cag cag cca cag cca caa ctg cct cag Pro Pro Pro Gln Pro Pro Gln Gln Gln Pro Gln Pro Gln Leu Pro Gln	3258
1000 1005 1010	
cag cag cag cca cca cct ccc agt cag cca cag tct cag cag cag cag Gln Gln Gln Pro Pro Pro Pro Ser Gln Pro Gln Ser Gln Gln Gln Gln	3306
1015 1020 1025	
cag cag cag caa caa atg atg atg atg ctc atg atg cag cag gat ccc Gln Gln Gln Gln Gln Met Met Met Met Leu Met Met Gln Gln Asp Pro	3354
1030 1035 1040	
aaa tca gtt agg ctt cca gtc tct caa aat gtc cat cct cca agg ggc Lys Ser Val Arg Leu Pro Val Ser Gln Asn Val His Pro Pro Arg Gly	3402
1045 1050 1055	
ccc ctg aac ccc gac tcc cag aga atg ccc atg caa cag agt ggc agt Pro Leu Asn Pro Asp Ser Gln Arg Met Pro Met Gln Gln Ser Gly Ser	3450
1060 1065 1070 1075	
gtg cct gtc atg gtc agt ctg caa gga cct gcc tcc gtg cca cca tca Val Pro Val Met Val Ser Leu Gln Gly Pro Ala Ser Val Pro Pro Ser	3498
1080 1085 1090	
cct gat aaa caa aga atg cca atg cct gtg aat act ccc ttg gga agc Pro Asp Lys Gln Arg Met Pro Met Pro Val Asn Thr Pro Leu Gly Ser	3546
1095 1100 1105	
aat tca agg aaa atg gtc tat cag gag agc ccg cag aat cct tcc agc Asn Ser Arg Lys Met Val Tyr Gln Glu Ser Pro Gln Asn Pro Ser Ser	3594
1110 1115 1120	
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1125 1130 1135	
gca cca tct gtc cca gga ggc cca aac aac atg cct tca cat gta gta Ala Pro Ser Val Pro Gly Gly Pro Asn Asn Met Pro Ser His Val Val	3690
1140 1145 1150 1155	
ctt ccc cag aat cag tta atg atg aca ggg cca aaa cct gga cca tcg Leu Pro Gln Asn Gln Leu Met Met Thr Gly Pro Lys Pro Gly Pro Ser	3738
1160 1165 1170	
ccc ctt tca gca act caa ggt gca act ccc cag caa ccc cct gta aat Pro Leu Ser Ala Thr Gln Gly Ala Thr Pro Gln Gln Pro Pro Val Asn	3786
1175 1180 1185	

tcc ctg ccc agc tct cac ggc cac cac ttc cca aat gtg gct gcg cca Ser Leu Pro Ser Ser His Gly His His Phe Pro Asn Val Ala Ala Pro 1190 1195 1200	3834
acc cag aca tct agg ccc aaa aca cca aac aga gcc agc ccc aga ccc Thr Gln Thr Ser Arg Pro Lys Thr Pro Asn Arg Ala Ser Pro Arg Pro 1205 1210 1215	3882
tat tat cct cag aca ccc aac aac cgc cct ccc agc aca gaa cct tca Tyr Tyr Pro Gln Thr Pro Asn Asn Arg Pro Pro Ser Thr Glu Pro Ser 1220 1225 1230 1235	3930
gaa atc agt ctg tca cca gaa aga ctc aat gcc tcc ata gca gga ctc Glu Ile Ser Leu Ser Pro Glu Arg Leu Asn Ala Ser Ile Ala Gly Leu 1240 1245 1250	3978
ttc cct cca cag att aat att cct tta cct cct agg cca aat tta aac Phe Pro Pro Gln Ile Asn Ile Pro Leu Pro Pro Arg Pro Asn Leu Asn 1255 1260 1265	4026
agg ggc ttt gat caa caa ggc cta aat ccg aca att ttg aag gcc atc Arg Gly Phe Asp Gln Gln Gly Leu Asn Pro Thr Ile Leu Lys Ala Ile 1270 1275 1280	4074
ggg caa gca cct tca aat ctt acc atg aat cct tcc aat ttt gct acc Gly Gln Ala Pro Ser Asn Leu Thr Met Asn Pro Ser Asn Phe Ala Thr 1285 1290 1295	4122
cca caa act cac aaa tta gat tct gtg gta gtg aat tct gga aag cag Pro Gln Thr His Lys Leu Asp Ser Val Val Val Asn Ser Gly Lys Gln 1300 1305 1310 1315	4170
tct aat tct gga gca aca aaa cgg gca agt cca agc aac agt cgc agg Ser Asn Ser Gly Ala Thr Lys Arg Ala Ser Pro Ser Asn Ser Arg Arg 1320 1325 1330	4218
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cta ttg cag aat gtg gag ttg ccg aga aat gta ttg gtc agt ccc act Leu Leu Gln Asn Val Glu Leu Pro Arg Asn Val Leu Val Ser Pro Thr 1365 1370 1375	4362
cct ctg gcc aat ccc cct gta cct ggg agc ttt cct aac aac agt ggg Pro Leu Ala Asn Pro Pro Val Pro Gly Ser Phe Pro Asn Asn Ser Gly 1380 1385 1390 1395	4410
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gtt gag gat aac aag gag agc ttg aat gtg cct cag gac agt gat tgc Val Glu Asp Asn Lys Glu Ser Leu Asn Val Pro Gln Asp Ser Asp Cys 1415 1420 1425	4506
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aag gat ggg cag cct tcg gat cct aac aaa ctt ccc agt gtc gaa gag Lys Asp Gly Gln Pro Ser Asp Pro Asn Lys Leu Pro Ser Val Glu Glu 1460 1465 1470 1475	4650
aac aaa aat ttg gtg tct cct gct atg agg gaa gca cca aca tcg tta Asn Lys Asn Leu Val Ser Pro Ala Met Arg Glu Ala Pro Thr Ser Leu 1480 1485 1490	4698
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cct ggg ctt aca gat ctg gaa gta aca cct cca gta gtt tct ggg gag Pro Gly Leu Thr Asp Leu Glu Val Thr Pro Pro Val Val Ser Gly Glu 1510 1515 1520	4794
gac ctg aaa aaa gca tct gtc att ccc aca ctg cag gat ctg tct tct Asp Leu Lys Lys Ala Ser Val Ile Pro Thr Leu Gln Asp Leu Ser Ser 1525 1530 1535	4842
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Leu His Ile Pro Gln Asn Ile Lys Phe Ser Ser Ala Pro Val Pro Pro	
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Leu Val Leu Ser Ser Arg Ala Thr Pro Val Gln Leu Pro Ser Pro Pro	
1735 1740 1745	
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Cys Thr Ser Ser Pro Val Val Pro Ser His Pro Pro Val Gln Gln Val	
1750 1755 1760	
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Lys Glu Leu Asn Pro Asp Glu Ala Ser Pro Gln Val Asn Thr Ser Ala	
1765 1770 1775	
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Asp Gln Asn Thr Leu Pro Ser Ser Gln Ser Thr Thr Met Val Ser Pro	
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Leu Leu Thr Asn Ser Pro Gly Ser Ser Gly Asn Arg Arg Ser Pro Val	
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Ser Ser Ser Lys Gly Lys Gly Lys Val Asp Lys Ile Gly Gln Ile Leu	
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Leu Thr Lys Ala Cys Lys Lys Val Thr Gly Ser Leu Glu Lys Gly Glu	
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Glu Gln Tyr Gly Ala Asp Gly Glu Thr Glu Gly Gln Gly Leu Asp Thr	
1845 1850 1855	
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Thr Ala Pro Gly Leu Met Gly Thr Glu Gln Leu Ser Thr Glu Leu Asp	
1860 1865 1870 1875	
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Ser Lys Thr Pro Thr Pro Pro Ala Pro Thr Leu Leu Lys Met Thr Ser	
1880 1885 1890	
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Ser Pro Val Gly Pro Gly Thr Ala Ser Ala Gly Pro Ser Leu Pro Gly	
1895 1900 1905	
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Gly Ala Leu Pro Thr Ser Val Arg Ser Ile Val Thr Thr Leu Val Pro	
1910 1915 1920	
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Ser Glu Leu Ile Ser Ala Val Pro Thr Thr Lys Ser Asn His Gly Gly	
1925 1930 1935	
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Ile Ala Ser Glu Ser Leu Ala Gly Gly Leu Val Glu Glu Lys Val Gly	
1940 1945 1950 1955	

tcc cat cca gaa ctt cta ccc agc ata gcc ccg tcg cag aat tta gtc 6138  
 Ser His Pro Glu Leu Leu Pro Ser Ile Ala Pro Ser Gln Asn Leu Val  
 1960 1965 1970  
 tca aag gaa act tca acc aca gca ctg cag gcc tct gtt gcc aga cca 6186  
 Ser Lys Glu Thr Ser Thr Thr Ala Leu Gln Ala Ser Val Ala Arg Pro  
 1975 1980 1985  
 gag ctg gag gta aat gct gcc ata gtc tct gga caa agc agt gag ccc 6234  
 Glu Leu Glu Val Asn Ala Ala Ile Val Ser Gly Gln Ser Ser Glu Pro  
 1990 1995 2000  
 aaa gag ata gtt gaa aag tcc aaa atc cca ggc cga aga aac tcc cga 6282  
 Lys Glu Ile Val Glu Lys Ser Lys Ile Pro Gly Arg Arg Asn Ser Arg  
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Ala Gln Lys Ser His Ser Gly Ala Tyr Gln Cys Phe Ala Thr Arg Lys	
70 75 80	
gcc cag acc gcc cag gac ttt gcc atc att gca ctt gag gat ggc acg	883
Ala Gln Thr Ala Gln Asp Phe Ala Ile Ile Ala Leu Glu Asp Gly Thr	
85 90 95	
ccc cgc atc gtc tcg tcc ttc agc gag aag gtg gtc aac ccc ggg gag	931
Pro Arg Ile Val Ser Ser Phe Ser Glu Lys Val Val Asn Pro Gly Glu	
100 105 110	
cag ttc tca ctg atg tgt gcg gcc aag ggc gcc ccg ccc ccc acg gtc	979
Gln Phe Ser Leu Met Cys Ala Ala Lys Gly Ala Pro Pro Pro Thr Val	
115 120 125 130	
acc tgg gcc ctc gac gat gag ccc atc gtg cgg gat ggc agc cac cgc	1027
Thr Trp Ala Leu Asp Asp Glu Pro Ile Val Arg Asp Gly Ser His Arg	
135 140 145	
acc aac cag tac acc atg tcg gac ggc acc acc atc agc cac atg aac	1075
Thr Asn Gln Tyr Thr Met Ser Asp Gly Thr Thr Ile Ser His Met Asn	
150 155 160	
gtc aca ggc ccc cag atc cgc gac ggg ggc gtg tac cgg tgc aca gcg	1123
Val Thr Gly Pro Gln Ile Arg Asp Gly Gly Val Tyr Arg Cys Thr Ala	
165 170 175	
cgg aac ttg gtg ggc agt gct gaa tat cag gcg cga ata aac gta aga	1171



Arg	Asn	Leu	Val	Gly	Ser	Ala	Glu	Tyr	Gln	Ala	Arg	Ile	Asn	Val	Arg		
180						185					190						
ggc	cca	ccc	agc	atc	cgg	gct	atg	cgg	aac	atc	aca	gca	gtc	gcc	ggg	1219	
Gly	Pro	Pro	Ser	Ile	Arg	Ala	Met	Arg	Asn	Ile	Thr	Ala	Val	Ala	Gly		
195					200					205					210		
cgg	gac	acc	ctt	atc	aac	tgc	agg	gtc	atc	ggc	tat	ccc	tac	tac	tcc	1267	
Arg	Asp	Thr	Leu	Ile	Asn	Cys	Arg	Val	Ile	Gly	Tyr	Pro	Tyr	Tyr	Ser		
				215					220					225			
atc	aag	tgg	tac	aag	gat	gcc	ctg	ctg	ctg	cca	gac	aac	cac	cgc	cag	1315	
Ile	Lys	Trp	Tyr	Lys	Asp	Ala	Leu	Leu	Leu	Pro	Asp	Asn	His	Arg	Gln		
			230					235					240				
gtg	gtg	ttt	gag	aat	ggg	acc	ctc	aag	ctg	act	gac	gtg	cag	aag	ggc	1363	
Val	Val	Phe	Glu	Asn	Gly	Thr	Leu	Lys	Leu	Thr	Asp	Val	Gln	Lys	Gly		
		245					250					255					
atg	gat	gag	ggg	gag	tac	ctg	tgc	agt	gtc	ctc	atc	cag	ccc	cag	ctc	1411	
Met	Asp	Glu	Gly	Glu	Tyr	Leu	Cys	Ser	Val	Leu	Ile	Gln	Pro	Gln	Leu		
	260					265					270						
tcc	atc	agc	cag	agc	gtt	cac	gta	gcc	gtc	aaa	gtg	ccc	cct	ctg	atc	1459	
Ser	Ile	Ser	Gln	Ser	Val	His	Val	Ala	Val	Lys	Val	Pro	Pro	Leu	Ile		
275					280					285					290		
cag	ccc	ttc	gaa	ttc	cca	ccc	gcc	tcc	atc	ggc	cag	ctg	ctc	tac	att	1507	
Gln	Pro	Phe	Glu	Phe	Pro	Pro	Ala	Ser	Ile	Gly	Gln	Leu	Leu	Tyr	Ile		
				295					300					305			
ccc	tgt	gtg	gtg	tcc	tcg	ggg	gac	atg	ccc	atc	cgt	atc	acc	tgg	agg	1555	
Pro	Cys	Val	Val	Ser	Ser	Gly	Asp	Met	Pro	Ile	Arg	Ile	Thr	Trp	Arg		
			310					315					320				
aag	gac	gga	cag	gtg	atc	atc	tca	ggc	tcg	ggc	gtg	acc	atc	gag	agc	1603	
Lys	Asp	Gly	Gln	Val	Ile	Ile	Ser	Gly	Ser	Gly	Val	Thr	Ile	Glu	Ser		
		325					330					335					
aag	gaa	ttc	atg	agc	tcc	ctg	cag	atc	tct	agc	gtc	tcc	ctc	aag	cac	1651	
Lys	Glu	Phe	Met	Ser	Ser	Leu	Gln	Ile	Ser	Ser	Val	Ser	Leu	Lys	His		
	340					345					350						
aac	ggc	aac	tat	aca	tgc	atc	gcc	agc	aac	gca	gcc	gcc	acc	gtg	agc	1699	
Asn	Gly	Asn	Tyr	Thr	Cys	Ile	Ala	Ser	Asn	Ala	Ala	Ala	Thr	Val	Ser		
355					360					365					370		
cgg	gag	cgc	cag	ctc	atc	gtg	cgt	gtg	ccc	cct	cga	ttt	gtg	gtg	caa	1747	
Arg	Glu	Arg	Gln	Leu	Ile	Val	Arg	Val	Pro	Pro	Arg	Phe	Val	Val	Gln		
				375					380					385			
ccc	aac	aac	cag	gat	ggc	atc	tac	ggc	aaa	gct	ggt	gtg	ctc	aac	tgc	1795	
Pro	Asn	Asn	Gln	Asp	Gly	Ile	Tyr	Gly	Lys	Ala	Gly	Val	Leu	Asn	Cys		
			390					395					400				
tcg	gtg	gac	ggc	tac	ccc	cca	ccc	aag	gtc	atg	tgg	aag	cat	gcc	aag	1843	
Ser	Val	Asp	Gly	Tyr	Pro	Pro	Pro	Lys	Val	Met	Trp	Lys	His	Ala	Lys		
		405					410					415					
ggg	agc	ggg	aac	ccc	cag	cag	tac	cac	cct	gtg	ccc	ctc	act	ggc	cgc	1891	
Gly	Ser	Gly	Asn	Pro	Gln	Gln	Tyr	His	Pro	Val	Pro	Leu	Thr	Gly	Arg		
	420					425					430						
atc	cag	atc	ctg	ccc	aac	agc	tcg	ctg	ctg	atc	cgc	cac	gtc	cta	gaa	1939	

Ile	Gln	Ile	Leu	Pro	Asn	Ser	Ser	Leu	Leu	Ile	Arg	His	Val	Leu	Glu	
435					440					445					450	
gag	gac	atc	ggc	tac	tac	ctc	tgc	cag	gcc	agc	aac	ggc	gta	ggc	acc	1987
Glu	Asp	Ile	Gly	Tyr	Tyr	Leu	Cys	Gln	Ala	Ser	Asn	Gly	Val	Gly	Thr	
				455					460					465		
gac	atc	agc	aag	tcc	atg	ttc	ctc	aca	gtc	aag	atc	ccg	gcc	atg	atc	2035
Asp	Ile	Ser	Lys	Ser	Met	Phe	Leu	Thr	Val	Lys	Ile	Pro	Ala	Met	Ile	
			470					475					480			
act	tcc	cac	ccc	aac	acc	acc	atc	gcc	atc	aag	ggc	cat	gcg	aag	gag	2083
Thr	Ser	His	Pro	Asn	Thr	Thr	Ile	Ala	Ile	Lys	Gly	His	Ala	Lys	Glu	
		485					490					495				
cta	aac	tgc	acg	gca	cgg	ggc	gag	cgg	ccc	atc	atc	atc	cgc	tgg	gag	2131
Leu	Asn	Cys	Thr	Ala	Arg	Gly	Glu	Arg	Pro	Ile	Ile	Ile	Arg	Trp	Glu	
	500					505						510				
aag	ggg	gac	aca	gtc	atc	gac	cct	gac	cgc	gtc	atg	cgg	tat	gcc	atc	2179
Lys	Gly	Asp	Thr	Val	Ile	Asp	Pro	Asp	Arg	Val	Met	Arg	Tyr	Ala	Ile	
515					520					525					530	
gcc	acc	aag	gac	aac	ggc	gac	gag	gtc	gtc	tcc	aca	ctg	aag	ctc	aag	2227
Ala	Thr	Lys	Asp	Asn	Gly	Asp	Glu	Val	Val	Ser	Thr	Leu	Lys	Leu	Lys	
				535					540					545		
ccc	gct	gac	cgt	ggg	gac	tct	gtg	ttc	ttc	agc	tgc	cat	gcc	atc	aac	2275
Pro	Ala	Asp	Arg	Gly	Asp	Ser	Val	Phe	Phe	Ser	Cys	His	Ala	Ile	Asn	
			550					555					560			
tcg	tat	ggg	gag	gac	cgg	ggc	ttg	atc	caa	ctc	act	gtg	caa	gag	ccc	2323
Ser	Tyr	Gly	Glu	Asp	Arg	Gly	Leu	Ile	Gln	Leu	Thr	Val	Gln	Glu	Pro	
		565					570					575				
ccc	gac	ccc	cca	gag	ctg	gag	atc	cgg	gag	gtg	aag	gcc	cgg	agc	atg	2371
Pro	Asp	Pro	Pro	Glu	Leu	Glu	Ile	Arg	Glu	Val	Lys	Ala	Arg	Ser	Met	
		580				585					590					
aac	ctg	cgc	tgg	acc	cag	cga	ttc	gac	ggg	aac	agc	atc	atc	acg	ggc	2419
Asn	Leu	Arg	Trp	Thr	Gln	Arg	Phe	Asp	Gly	Asn	Ser	Ile	Ile	Thr	Gly	
595					600					605					610	
ttc	gac	att	gaa	tac	aag	aac	aaa	tca	gat	tcc	tgg	gac	ttc	aag	cag	2467
Phe	Asp	Ile	Glu	Tyr	Lys	Asn	Lys	Ser	Asp	Ser	Trp	Asp	Phe	Lys	Gln	
				615					620					625		
tcc	aca	cgc	aac	atc	tcc	ccc	acc	atc	aac	cag	gcc	aac	att	gtg	gac	2515
Ser	Thr	Arg	Asn	Ile	Ser	Pro	Thr	Ile	Asn	Gln	Ala	Asn	Ile	Val	Asp	
			630					635					640			
ttg	cac	ccg	gca	tct	gtg	tac	agc	atc	cgc	atg	tac	tct	ttc	aac	aag	2563
Leu	His	Pro	Ala	Ser	Val	Tyr	Ser	Ile	Arg	Met	Tyr	Ser	Phe	Asn	Lys	
		645					650					655				
att	ggc	cgc	agt	gaa	cca	agc	aag	gag	ctc	acc	atc	agc	act	gag	gag	2611
Ile	Gly	Arg	Ser	Glu	Pro	Ser	Lys	Glu	Leu	Thr	Ile	Ser	Thr	Glu	Glu	
	660					665					670					
gcc	gct	ccc	gat	ggg	ccc	ccc	atg	gat	gtt	acc	ttg	cag	cca	gtg	acc	2659
Ala	Ala	Pro	Asp	Gly	Pro	Pro	Met	Asp	Val	Thr	Leu	Gln	Pro	Val	Thr	
675					680				685						690	
tca	cag	agc	atc	cag	gtg	acc	tgg	aag	gca	ccc	aag	aag	gag	ctg	cag	2707

Ser	Gln	Ser	Ile	Gln	Val	Thr	Trp	Lys	Ala	Pro	Lys	Lys	Glu	Leu	Gln	
				695					700						705	
aac	ggt	gtc	atc	cgg	ggc	tac	cag	att	ggc	tac	aga	gag	aac	agc	ccc	2755
Asn	Gly	Val	Ile	Arg	Gly	Tyr	Gln	Ile	Gly	Tyr	Arg	Glu	Asn	Ser	Pro	
			710					715					720			
ggc	agc	aac	ggg	cag	tac	agc	atc	gtg	gag	atg	aag	gcc	acg	ggg	gac	2803
Gly	Ser	Asn	Gly	Gln	Tyr	Ser	Ile	Val	Glu	Met	Lys	Ala	Thr	Gly	Asp	
		725					730					735				
agc	gag	gtc	tac	acc	ctg	gac	aac	ctc	aag	aag	ttc	gcc	cag	tat	ggg	2851
Ser	Glu	Val	Tyr	Thr	Leu	Asp	Asn	Leu	Lys	Lys	Phe	Ala	Gln	Tyr	Gly	
	740					745					750					
gtg	gtg	gtc	caa	gcc	ttc	aat	cgg	gct	ggc	acg	ggg	ccc	tct	tcc	agc	2899
Val	Val	Val	Gln	Ala	Phe	Asn	Arg	Ala	Gly	Thr	Gly	Pro	Ser	Ser	Ser	
755					760				765						770	
gag	atc	aat	gcc	acc	act	ctg	gag	gat	gtg	ccc	agc	cag	ccc	cct	gag	2947
Glu	Ile	Asn	Ala	Thr	Thr	Leu	Glu	Asp	Val	Pro	Ser	Gln	Pro	Pro	Glu	
				775					780					785		
aac	gtc	cgg	gcc	ctg	tcc	atc	act	tct	gac	gtg	gcc	gtc	atc	tcc	tgg	2995
Asn	Val	Arg	Ala	Leu	Ser	Ile	Thr	Ser	Asp	Val	Ala	Val	Ile	Ser	Trp	
			790					795					800			
tca	gag	ccc	ccg	cgc	agc	acc	ctc	aat	ggc	gtc	ctc	aaa	ggc	tat	cgg	3043
Ser	Glu	Pro	Pro	Arg	Ser	Thr	Leu	Asn	Gly	Val	Leu	Lys	Gly	Tyr	Arg	
		805					810					815				
gtc	atc	ttc	tgg	tcc	ctc	tat	gtt	gat	ggg	gag	tgg	ggc	gag	atg	cag	3091
Val	Ile	Phe	Trp	Ser	Leu	Tyr	Val	Asp	Gly	Glu	Trp	Gly	Glu	Met	Gln	
	820					825					830					
aac	atc	acc	acc	acg	cgg	gag	cgg	gtg	gag	ctg	cgg	ggc	atg	gag	aag	3139
Asn	Ile	Thr	Thr	Thr	Arg	Glu	Arg	Val	Glu	Leu	Arg	Gly	Met	Glu	Lys	
835					840				845					850		
ttc	acc	aac	tac	agc	gtc	cag	gtg	ctg	gcc	tac	acc	cag	gct	ggg	gac	3187
Phe	Thr	Asn	Tyr	Ser	Val	Gln	Val	Leu	Ala	Tyr	Thr	Gln	Ala	Gly	Asp	
				855					860					865		
ggc	gta	cgc	agc	agt	gtg	ctc	tac	atc	cag	acc	aag	gag	gac	gtt	cca	3235
Gly	Val	Arg	Ser	Ser	Val	Leu	Tyr	Ile	Gln	Thr	Lys	Glu	Asp	Val	Pro	
			870					875					880			
ggt	ccc	cct	gct	ggc	atc	aaa	gct	gtc	cct	tca	tca	gct	agc	agt	gtg	3283
Gly	Pro	Pro	Ala	Gly	Ile	Lys	Ala	Val	Pro	Ser	Ser	Ala	Ser	Ser	Val	
		885					890					895				
gtt	gtg	tct	tgg	ctc	ccc	cct	acc	aag	ccc	aac	ggg	gtg	atc	cgc	aag	3331
Val	Val	Ser	Trp	Leu	Pro	Pro	Thr	Lys	Pro	Asn	Gly	Val	Ile	Arg	Lys	
	900					905					910					
tac	acc	atc	ttc	tgt	tcc	agc	ccc	ggg	tct	ggc	cag	ccg	gct	ccc	agc	3379
Tyr	Thr	Ile	Phe	Cys	Ser	Ser	Pro	Gly	Ser	Gly	Gln	Pro	Ala	Pro	Ser	
915					920					925					930	
gag	tac	gag	acg	agt	cca	gag	cag	ctc	ttc	tac	cgg	atc	gcc	cac	cta	3427
Glu	Tyr	Glu	Thr	Ser	Pro	Glu	Gln	Leu	Phe	Tyr	Arg	Ile	Ala	His	Leu	
				935				940						945		
aac	cgc	ggt	cag	cag	tat	ctg	ctg	tgg	gtg	gcc	gcc	gtc	acc	tct	gcc	3475

Asn Arg Gly Gln Gln Tyr Leu Leu Trp Val Ala Ala Val Thr Ser Ala	
950 955 960	
ggc cgg ggc aac agc agc gag aag gtg acc atc gag cct gct ggc aag	3523
Gly Arg Gly Asn Ser Ser Glu Lys Val Thr Ile Glu Pro Ala Gly Lys	
965 970 975	
gcc cca gca aag atc atc tcc ttt ggg ggc acc gtg aca aca cct tgg	3571
Ala Pro Ala Lys Ile Ile Ser Phe Gly Gly Thr Val Thr Thr Pro Trp	
980 985 990	
atg aaa gat gtt cgg ctg cct tgc aat tca gtg gga gat cca gcc cct	3619
Met Lys Asp Val Arg Leu Pro Cys Asn Ser Val Gly Asp Pro Ala Pro	
995 1000 1005 1010	
gct gtg aag tgg acc aag gac agt gaa gac tcg gcc att cca gtg tcc	3667
Ala Val Lys Trp Thr Lys Asp Ser Glu Asp Ser Ala Ile Pro Val Ser	
1015 1020 1025	
atg gat ggg cac cgg ctc atc cac acc aat ggc aca ctg ctg ctg cgt	3715
Met Asp Gly His Arg Leu Ile His Thr Asn Gly Thr Leu Leu Leu Arg	
1030 1035 1040	
gca gtg aag gct gag gac tct ggc tac tac acg tgc acg gcc acc aac	3763
Ala Val Lys Ala Glu Asp Ser Gly Tyr Tyr Thr Cys Thr Ala Thr Asn	
1045 1050 1055	
act ggt ggc ttt gac acc atc atc gtc aac ctt ctg gtg caa gtt ccc	3811
Thr Gly Gly Phe Asp Thr Ile Ile Val Asn Leu Leu Val Gln Val Pro	
1060 1065 1070	
ccg gac cag ccc cgc ctc act gtc tcc aaa acc tca gct tcg tcc atc	3859
Pro Asp Gln Pro Arg Leu Thr Val Ser Lys Thr Ser Ala Ser Ser Ile	
1075 1080 1085 1090	
acc ctg acc tgg att cca ggt gac aat ggg ggc agc tcc atc cga ggc	3907
Thr Leu Thr Trp Ile Pro Gly Asp Asn Gly Gly Ser Ser Ile Arg Gly	
1095 1100 1105	
ttc gtg cta cag tac tcg gtg gac aac agc gag gag tgg aag gat gtg	3955
Phe Val Leu Gln Tyr Ser Val Asp Asn Ser Glu Glu Trp Lys Asp Val	
1110 1115 1120	
ttc atc agc tcc agc gag cgc tcc ttc aag ctg gac agc ctc aag tgt	4003
Phe Ile Ser Ser Ser Glu Arg Ser Phe Lys Leu Asp Ser Leu Lys Cys	
1125 1130 1135	
ggc acg tgg tac aag gtg aag ctg gca gcc aag aac agc gtg ggc tct	4051
Gly Thr Trp Tyr Lys Val Lys Leu Ala Ala Lys Asn Ser Val Gly Ser	
1140 1145 1150	
ggg cgc atc agc gag atc atc gag gcc aag acc cac ggg cgg gag ccc	4099
Gly Arg Ile Ser Glu Ile Ile Glu Ala Lys Thr His Gly Arg Glu Pro	
1155 1160 1165 1170	
tcc ttc agc aaa gac caa cac ctc ttc acc cac atc aac tcc acg cat	4147
Ser Phe Ser Lys Asp Gln His Leu Phe Thr His Ile Asn Ser Thr His	
1175 1180 1185	
gct cgg ctt aac ctg cag ggc tgg aac aat ggg ggc tgc cct atc aca	4195
Ala Arg Leu Asn Leu Gln Gly Trp Asn Asn Gly Gly Cys Pro Ile Thr	
1190 1195 1200	
gcc atc gtt ctg gag tac cgg ccc aag ggg acc tgg gcc tgg cag ggc	4243

Ala Ile Val Leu Glu Tyr Arg Pro Lys Gly Thr Trp Ala Trp Gln Gly	
1205 1210 1215	
ctc cgg gcc aac agc tcc ggg gag gtg ttt ctg acg gaa ctg cga gag	4291
Leu Arg Ala Asn Ser Ser Gly Glu Val Phe Leu Thr Glu Leu Arg Glu	
1220 1225 1230	
gcc acg tgg tac gag ctg cgc atg agg gct tgc aac agt gcg ggc tgc	4339
Ala Thr Trp Tyr Glu Leu Arg Met Arg Ala Cys Asn Ser Ala Gly Cys	
1235 1240 1245 1250	
ggc aat gaa aca gcc cag ttc gcc acc ctg gac tac gat ggc agc acc	4387
Gly Asn Glu Thr Ala Gln Phe Ala Thr Leu Asp Tyr Asp Gly Ser Thr	
1255 1260 1265	
att cca ccc atc aag tct gct caa ggt gaa ggg gat gat gtg aag aag	4435
Ile Pro Pro Ile Lys Ser Ala Gln Gly Glu Gly Asp Asp Val Lys Lys	
1270 1275 1280	
ctg ttc acc atc ggc tgc cct gtc atc ctg gcc aca ctg ggg gtg gca	4483
Leu Phe Thr Ile Gly Cys Pro Val Ile Leu Ala Thr Leu Gly Val Ala	
1285 1290 1295	
ctg ctc ttc atc gta cgc aag aag agg aag gag aaa cgg ctg aag cga	4531
Leu Leu Phe Ile Val Arg Lys Lys Arg Lys Glu Lys Arg Leu Lys Arg	
1300 1305 1310	
ctc cga gat gca aag agt ttg gca gaa atg ttg ata agc aag aac aat	4579
Leu Arg Asp Ala Lys Ser Leu Ala Glu Met Leu Ile Ser Lys Asn Asn	
1315 1320 1325 1330	
aga agc ttt gac acc cct gtg aaa ggg cca ccc cag ggc cca cgg cta	4627
Arg Ser Phe Asp Thr Pro Val Lys Gly Pro Pro Gln Gly Pro Arg Leu	
1335 1340 1345	
cac att gac atc ccc agg gtc cag ctg ctc atc gag gac aaa gaa ggc	4675
His Ile Asp Ile Pro Arg Val Gln Leu Leu Ile Glu Asp Lys Glu Gly	
1350 1355 1360	
atc aag caa ctg gga gat gac aag gcc acc atc cct gtg aca gat gct	4723
Ile Lys Gln Leu Gly Asp Asp Lys Ala Thr Ile Pro Val Thr Asp Ala	
1365 1370 1375	
gag ttc agc caa gct gtc aac cca cag agc ttc tgt act ggc gtc tcc	4771
Glu Phe Ser Gln Ala Val Asn Pro Gln Ser Phe Cys Thr Gly Val Ser	
1380 1385 1390	
ttg cac cac cca acc ctc atc cag agc aca gga ccc ctc atc gac atg	4819
Leu His His Pro Thr Leu Ile Gln Ser Thr Gly Pro Leu Ile Asp Met	
1395 1400 1405 1410	
tct gac atc cgg cca gga acc aat cca gtg tcc agg aag aat gtg aag	4867
Ser Asp Ile Arg Pro Gly Thr Asn Pro Val Ser Arg Lys Asn Val Lys	
1415 1420 1425	
tca gcc cac agc acc cgg aac cgg tac tca agc cag tgg acc ctg acc	4915
Ser Ala His Ser Thr Arg Asn Arg Tyr Ser Ser Gln Trp Thr Leu Thr	
1430 1435 1440	
aag tgc cag gcc tcc aca cct gcc cgc acc ctc acc tcc gac tgg cgc	4963
Lys Cys Gln Ala Ser Thr Pro Ala Arg Thr Leu Thr Ser Asp Trp Arg	
1445 1450 1455	
acc gtg ggc tcc cag cat ggt gtc acg gtc act gag agt gac agc tac	5011

Thr Val Gly Ser Gln His Gly Val Thr Val Thr Glu Ser Asp Ser Tyr	
1460 1465 1470	
agt gcc agc ctg tcc cag gac aca gac aaa gga agg aac agc atg gtg	5059
Ser Ala Ser Leu Ser Gln Asp Thr Asp Lys Gly Arg Asn Ser Met Val	
1475 1480 1485 1490	
tcc act gag agt gcc tct tcc acc tac gag gag ctg gcc cgg gcc tat	5107
Ser Thr Glu Ser Ala Ser Ser Thr Tyr Glu Glu Leu Ala Arg Ala Tyr	
1495 1500 1505	
gag cat gcc aag ctg gag gag cag ctg cag cac gcc aag ttt gag atc	5155
Glu His Ala Lys Leu Glu Glu Gln Leu Gln His Ala Lys Phe Glu Ile	
1510 1515 1520	
acc gag tgc ttc atc tct gac agt tcc tct gac cag atg acc aca ggc	5203
Thr Glu Cys Phe Ile Ser Asp Ser Ser Ser Asp Gln Met Thr Thr Gly	
1525 1530 1535	
acc aac gag aac gcc gac agc atg aca tcc atg agc aca ccc tca gag	5251
Thr Asn Glu Asn Ala Asp Ser Met Thr Ser Met Ser Thr Pro Ser Glu	
1540 1545 1550	
cct ggc atc tgc cgc ttt acc gcc tca cca ccc aag ccc cag gat gcg	5299
Pro Gly Ile Cys Arg Phe Thr Ala Ser Pro Pro Lys Pro Gln Asp Ala	
1555 1560 1565 1570	
gac cgg ggc aaa aac gtg gct gtg ccc atc cct cac cgg gcc aac aag	5347
Asp Arg Gly Lys Asn Val Ala Val Pro Ile Pro His Arg Ala Asn Lys	
1575 1580 1585	
agt gac tac tgc aac ctg ccc ctg tat gcc aag tca gag gcc ttc ttt	5395
Ser Asp Tyr Cys Asn Leu Pro Leu Tyr Ala Lys Ser Glu Ala Phe Phe	
1590 1595 1600	
cga aag gca gat gga cgt gag ccc tgc ccc gtg gtc cca ccc cgt gag	5443
Arg Lys Ala Asp Gly Arg Glu Pro Cys Pro Val Val Pro Pro Arg Glu	
1605 1610 1615	
gcc tcc atc cgg aac ctg gct cga acc tac cac acc cag gct cgc cac	5491
Ala Ser Ile Arg Asn Leu Ala Arg Thr Tyr His Thr Gln Ala Arg His	
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Met Ala Gly Ile Leu Arg Leu
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Val Val Gln Trp Pro Pro Gly Arg Leu Gln Thr Val Thr Lys Gly Val	
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Glu Ser Leu Ile Cys Thr Asp Trp Ile Arg His Lys Phe Thr Arg Ser	
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aga att cca gaa aaa gtg ttt cag gcc tca cct gaa gat cat gaa aaa	315
Arg Ile Pro Glu Lys Val Phe Gln Ala Ser Pro Glu Asp His Glu Lys	
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tac ggt ggg gat cca cag aac cct cat aaa ctg cat att gtt acc aga	363
Tyr Gly Gly Asp Pro Gln Asn Pro His Lys Leu His Ile Val Thr Arg	
60 65 70	
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Ile Lys Ser Thr Arg Arg Arg Pro Tyr Trp Glu Lys Asp Ile Ile Lys	
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Met Leu Gly Leu Glu Lys Ala His Thr Pro Gln Val His Lys Asn Ile	
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Pro Ser Val Asn Ala Lys Leu Lys Val Val Lys His Leu Ile Arg Ile	
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Leu Ser Asn Gly Ile Lys Lys His Arg Thr Ser Leu Pro Ser Pro Met  
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Gly Met Glu Leu Ser Lys Ile Thr Met Pro Val Ile Phe Asn Glu Pro  
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Gly Lys Pro Phe Asn Pro Leu Leu Gly Glu Thr Tyr Glu Leu Val Arg  
110 115 120  
gat gac ctt gga ttt aga ctc atc tcc gaa cag gtc agc cat cac cca 493  
Asp Asp Leu Gly Phe Arg Leu Ile Ser Glu Gln Val Ser His His Pro  
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Pro Ile Ser Ala Phe His Ala Glu Gly Leu Asn Asn Asp Phe Ile Phe  
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Ala Glu Pro Lys Gly Thr Ile Thr Leu Glu Leu Leu Glu His Asn Glu  
175 180 185  
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Lys Thr Gly Asp Lys Cys Val Leu Asn Phe Lys Pro Cys Gly Leu Phe  
225 230 235  
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Gly Lys Glu Leu His Lys Val Glu Gly Tyr Ile Gln Asp Lys Ser Lys	
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Lys Lys Leu Cys Ala Leu Tyr Gly Lys Trp Thr Glu Cys Leu Tyr Ser	
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Val Asp Pro Ala Thr Phe Asp Ala Tyr Lys Lys Asn Asp Lys Lys Asn	
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285 290 295 300	
gat gaa atg cca gtg ccg gat tct gaa agt gta ttc att atc cct gga	1021
Asp Glu Met Pro Val Pro Asp Ser Glu Ser Val Phe Ile Ile Pro Gly	
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Ser Val Leu Leu Trp Arg Ile Ala Pro Arg Pro Pro Asn Ser Ala Gln	
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Met Tyr Asn Phe Thr Ser Phe Ala Met Val Leu Asn Glu Val Asp Lys	
335 340 345	
gac atg gag agt gtg att ccc aag aca gac tgc agg tta cgg cct gac	1165
Asp Met Glu Ser Val Ile Pro Lys Thr Asp Cys Arg Leu Arg Pro Asp	
350 355 360	
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Lys Arg Leu Glu Glu Lys Gln Arg Ala Ala Arg Lys Asn Arg Ser Lys	
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Ser Glu Glu Asp Trp Lys Thr Arg Trp Phe His Gln Gly Pro Asn Pro	
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 <222> (1) .. (4692)

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Ser Leu Ser Arg Ile Lys Ser Asn Val Asp Gly Arg Tyr Leu Val Asp	
20 25 30	
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Gly Val Pro Phe Ser Cys Cys Asn Pro Ser Ser Pro Arg Pro Cys Ile	
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cag tat cag atc acc aac aac tca gca cac tac agt tac gac cac cag	192
Gln Tyr Gln Ile Thr Asn Asn Ser Ala His Tyr Ser Tyr Asp His Gln	
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85 90 95	
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Ile Trp Leu Phe Glu Val Thr Ile Thr Ile Gly Leu Arg Tyr Leu Gln	
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Thr Ser Leu Asp Gly Val Ser Asn Pro Glu Glu Ser Glu Ser Glu Ser	
115 120 125	
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Glu Gly Trp Leu Leu Glu Lys Ser Val Pro Glu Thr Trp Lys Ala Phe	
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Leu Asn Lys Tyr Arg Cys Leu Leu Leu Glu Asp Ala Met Arg Ile Asn	
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Pro Ser Ala Glu Met Val Met Ile Asp Arg Met Phe Asn Gln Glu Glu	



210	215	220	
aga gct tcc ctg tcc cga gac aag cgt ttg gca ctt gta gac cct gag			720
Arg Ala Ser Leu Ser Arg Asp Lys Arg Leu Ala Leu Val Asp Pro Glu			
225	230	235	240
ggt ttt cag gct gat ttc tgt tgt tcc ttc aaa ctt gat aaa gct gct			768
Gly Phe Gln Ala Asp Phe Cys Cys Ser Phe Lys Leu Asp Lys Ala Ala			
	245	250	255
cat gag aca cag ttt ggc cgg agt gac cag cat ggc agt aaa gca agc			816
His Glu Thr Gln Phe Gly Arg Ser Asp Gln His Gly Ser Lys Ala Ser			
	260	265	270
agc tct ctg caa ccg cca gcc aag gcc caa ggc aga gac cga gcc aaa			864
Ser Ser Leu Gln Pro Pro Ala Lys Ala Gln Gly Arg Asp Arg Ala Lys			
	275	280	285
acc ggt gtg acg gaa ccc atg aat cat gac cag ttt cat cta gtg cct			912
Thr Gly Val Thr Glu Pro Met Asn His Asp Gln Phe His Leu Val Pro			
	290	295	300
aat cac atc gtg gtc tct gca gaa gga aac att tct aaa aaa aca gaa			960
Asn His Ile Val Val Ser Ala Glu Gly Asn Ile Ser Lys Lys Thr Glu			
305	310	315	320
tgc ctt ggc aga gca ctg aaa ttt gac aaa gtg ggc tta gtg cag tac			1008
Cys Leu Gly Arg Ala Leu Lys Phe Asp Lys Val Gly Leu Val Gln Tyr			
	325	330	335
cag agc acg tct gaa gag aag gcc agc cgg aga gag cct ctg aag gcc			1056
Gln Ser Thr Ser Glu Glu Lys Ala Ser Arg Arg Glu Pro Leu Lys Ala			
	340	345	350
agt cag tgc tct ccc ggc cct gag ggg cac cgg aaa acc tca tcc aga			1104
Ser Gln Cys Ser Pro Gly Pro Glu Gly His Arg Lys Thr Ser Ser Arg			
	355	360	365
tcg gat cat ggt act gag agc aaa ctg tca agc atc cta gca gat tcg			1152
Ser Asp His Gly Thr Glu Ser Lys Leu Ser Ser Ile Leu Ala Asp Ser			
	370	375	380
cac ttg gag atg acg tgt aac aat tcc ttc cag gac aaa agt ctg agg			1200
His Leu Glu Met Thr Cys Asn Asn Ser Phe Gln Asp Lys Ser Leu Arg			
385	390	395	400
aat tct cca aag aat gaa gtt tta cac aca gac atc atg aaa ggg tca			1248
Asn Ser Pro Lys Asn Glu Val Leu His Thr Asp Ile Met Lys Gly Ser			
	405	410	415
ggc gaa ccc cag cca gat ctc cag ctg aca aag agc ttg gaa acc aca			1296
Gly Glu Pro Gln Pro Asp Leu Gln Leu Thr Lys Ser Leu Glu Thr Thr			
	420	425	430
ttt aag aac atc ttg gaa ctc aaa aag gcg gga cgg cag ccc cag agt			1344
Phe Lys Asn Ile Leu Glu Leu Lys Lys Ala Gly Arg Gln Pro Gln Ser			
	435	440	445
gac ccc acg gtt agc ggc tct gtt gag tta gat ttc ccc aac ttt tct			1392
Asp Pro Thr Val Ser Gly Ser Val Glu Leu Asp Phe Pro Asn Phe Ser			
	450	455	460
cct atg gct tca cag gaa aac tgc ctg gaa aag ttc atc ccg gac cac			1440
Pro Met Ala Ser Gln Glu Asn Cys Leu Glu Lys Phe Ile Pro Asp His			

465	470	475	480	
agt gac gtt gtc atg gat gat gat gat gac tcg tgt ctc ctt gat ctt				1488
Ser Asp Val Val Met Asp Asp Asp Asp Asp Ser Cys Leu Leu Asp Leu				
485		490	495	
att gga gac cca caa gca ttg aac tat ttt cta cat gga cct agt aat				1536
Ile Gly Asp Pro Gln Ala Leu Asn Tyr Phe Leu His Gly Pro Ser Asn				
500		505	510	
aaa tct agc aat gat gac ttg act aat gca gga tat tct gca gcc aat				1584
Lys Ser Ser Asn Asp Asp Leu Thr Asn Ala Gly Tyr Ser Ala Ala Asn				
515		520	525	
tca aat tca att ttc gcc aac tct agt aat gct gat cct aag tca tcc				1632
Ser Asn Ser Ile Phe Ala Asn Ser Ser Asn Ala Asp Pro Lys Ser Ser				
530		535	540	
ctc aaa ggt gta agc aac cag ctt gga gaa ggg ccc agt gat gga ctg				1680
Leu Lys Gly Val Ser Asn Gln Leu Gly Glu Gly Pro Ser Asp Gly Leu				
545		550	555	560
cca ctt tca agt agc ctc cag ttt ctt gaa gat gaa ctc gag tct tct				1728
Pro Leu Ser Ser Ser Leu Gln Phe Leu Glu Asp Glu Leu Glu Ser Ser				
565		570	575	
cct ctt cct gat ctc act gag gac caa cct ttc gac att ctt cag aaa				1776
Pro Leu Pro Asp Leu Thr Glu Asp Gln Pro Phe Asp Ile Leu Gln Lys				
580		585	590	
tcc ttg caa gag gcc aat atc act gaa cag aca ttg gca gaa gag gca				1824
Ser Leu Gln Glu Ala Asn Ile Thr Glu Gln Thr Leu Ala Glu Glu Ala				
595		600	605	
tat ttg gat gcc agt ata ggt tca agc caa cag ttt gca caa gct cag				1872
Tyr Leu Asp Ala Ser Ile Gly Ser Ser Gln Gln Phe Ala Gln Ala Gln				
610		615	620	
ctt cat cct tct tca tca gca tcc ttt act cag gct tct aat gtt tct				1920
Leu His Pro Ser Ser Ser Ala Ser Phe Thr Gln Ala Ser Asn Val Ser				
625		630	635	640
aat tac tca ggt cag acg ctg cag cct ata ggg gtg acg cat gtg cct				1968
Asn Tyr Ser Gly Gln Thr Leu Gln Pro Ile Gly Val Thr His Val Pro				
645		650	655	
gtt gga gca tcg ttt gca agc aat aca gtg ggt gta caa cat ggc ttt				2016
Val Gly Ala Ser Phe Ala Ser Asn Thr Val Gly Val Gln His Gly Phe				
660		665	670	
atg caa cat gtg ggg atc agt gtt ccc agc cag cat ttg tct aat agc				2064
Met Gln His Val Gly Ile Ser Val Pro Ser Gln His Leu Ser Asn Ser				
675		680	685	
agt cag att agt ggt tct ggt caa ata cag tta att ggg tca ttt ggt				2112
Ser Gln Ile Ser Gly Ser Gly Gln Ile Gln Leu Ile Gly Ser Phe Gly				
690		695	700	
aat cat cct tcc atg atg act att aat aac cta gat gga tct caa atc				2160
Asn His Pro Ser Met Met Thr Ile Asn Asn Leu Asp Gly Ser Gln Ile				
705		710	715	720
ata tta aag ggc agc ggg cag caa gcc cca tca aat gtg agt gga ggg				2208
Ile Leu Lys Gly Ser Gly Gln Gln Ala Pro Ser Asn Val Ser Gly Gly				

725								730				735				
ctc	ctg	gtt	cat	aga	cag	act	cct	aat	ggc	aac	tcc	ttg	ttt	ggg	aac	2256
Leu	Leu	Val	His	Arg	Gln	Thr	Pro	Asn	Gly	Asn	Ser	Leu	Phe	Gly	Asn	
740				745				750								
tct	agt	tcc	agt	cca	gta	gca	cag	cct	gtt	acc	gtt	cca	ttt	aac	agc	2304
Ser	Ser	Ser	Ser	Pro	Val	Ala	Gln	Pro	Val	Thr	Val	Pro	Phe	Asn	Ser	
755				760				765								
aca	aat	ttt	caa	aca	tct	tta	cct	gtg	cat	aac	atc	atc	ata	caa	agg	2352
Thr	Asn	Phe	Gln	Thr	Ser	Leu	Pro	Val	His	Asn	Ile	Ile	Ile	Gln	Arg	
770				775				780								
ggc	ctt	gca	cca	aat	tca	aat	aaa	gtc	cca	att	aat	ata	cag	cca	aag	2400
Gly	Leu	Ala	Pro	Asn	Ser	Asn	Lys	Val	Pro	Ile	Asn	Ile	Gln	Pro	Lys	
785				790				795				800				
cct	atc	cag	atg	ggc	cag	caa	aat	aca	tac	aat	gtg	aac	aat	ttg	gga	2448
Pro	Ile	Gln	Met	Gly	Gln	Gln	Asn	Thr	Tyr	Asn	Val	Asn	Asn	Leu	Gly	
805				810				815								
att	cag	cag	cac	cac	gta	caa	caa	ggc	atc	tct	ttt	gct	tct	gca	agc	2496
Ile	Gln	Gln	His	His	Val	Gln	Gln	Gly	Ile	Ser	Phe	Ala	Ser	Ala	Ser	
820				825				830								
tca	ccc	cag	ggc	tca	gta	gtt	ggc	cca	cac	atg	tct	gtg	aac	att	gta	2544
Ser	Pro	Gln	Gly	Ser	Val	Val	Gly	Pro	His	Met	Ser	Val	Asn	Ile	Val	
835				840				845								
aac	caa	cag	aac	aca	aga	aag	cca	gtc	acc	tca	cag	gca	gtg	agc	agc	2592
Asn	Gln	Gln	Asn	Thr	Arg	Lys	Pro	Val	Thr	Ser	Gln	Ala	Val	Ser	Ser	
850				855				860								
act	ggg	ggc	agt	att	gtt	att	cat	tcc	ccc	atg	ggc	caa	cct	cac	gca	2640
Thr	Gly	Gly	Ser	Ile	Val	Ile	His	Ser	Pro	Met	Gly	Gln	Pro	His	Ala	
865				870				875				880				
ccc	caa	agt	cag	ttc	ctt	ata	cct	aca	agc	ctt	tct	gtc	agt	tcc	aac	2688
Pro	Gln	Ser	Gln	Phe	Leu	Ile	Pro	Thr	Ser	Leu	Ser	Val	Ser	Ser	Asn	
885				890				895								
tcg	gta	cac	cac	gtc	cag	act	ata	aat	ggg	caa	ctt	ctt	caa	act	caa	2736
Ser	Val	His	His	Val	Gln	Thr	Ile	Asn	Gly	Gln	Leu	Leu	Gln	Thr	Gln	
900				905				910								
ccc	tct	cag	ctc	att	tct	ggc	caa	gtg	gcc	tca	gag	cat	gtc	atg	ttg	2784
Pro	Ser	Gln	Leu	Ile	Ser	Gly	Gln	Val	Ala	Ser	Glu	His	Val	Met	Leu	
915				920				925								
aac	aga	aac	tct	tcc	aac	atg	ctc	agg	acc	aac	caa	cca	tat	act	gga	2832
Asn	Arg	Asn	Ser	Ser	Asn	Met	Leu	Arg	Thr	Asn	Gln	Pro	Tyr	Thr	Gly	
930				935				940								
ccg	atg	ctt	aac	aac	cag	aat	act	gct	gtc	cac	tta	gtg	tct	ggg	cag	2880
Pro	Met	Leu	Asn	Asn	Gln	Asn	Thr	Ala	Val	His	Leu	Val	Ser	Gly	Gln	
945				950				955				960				
aca	ttt	gct	gcc	tct	gga	agt	cca	gtg	ata	gcc	aat	cat	gcc	tct	cct	2928
Thr	Phe	Ala	Ala	Ser	Gly	Ser	Pro	Val	Ile	Ala	Asn	His	Ala	Ser	Pro	
965				970				975								
cag	ctt	gtg	ggc	gga	cag	atg	ccc	ttg	cag	cag	gca	tcc	cca	act	gta	2976
Gln	Leu	Val	Gly	Gly	Gln	Met	Pro	Leu	Gln	Gln	Ala	Ser	Pro	Thr	Val	

	980	985	990	
tta cac ctg tca cct ggg cag agc agc gtt tcc caa gga aga cct ggc				3024
Leu His Leu Ser Pro Gly Gln Ser Ser Val Ser Gln Gly Arg Pro Gly				
995	1000	1005		
ttc gcc acc atg cca tcg gtg aca agc atg tca gga cct agt cgg ttc				3072
Phe Ala Thr Met Pro Ser Val Thr Ser Met Ser Gly Pro Ser Arg Phe				
1010	1015	1020		
cct gct gtc agc tca gcc agc act gcc cat cct agt ctt ggg tct gca				3120
Pro Ala Val Ser Ser Ala Ser Thr Ala His Pro Ser Leu Gly Ser Ala				
1025	1030	1035	1040	
gtt cag tct ggt tca tca gga tca aac ttt aca gga gat cag ctg acc				3168
Val Gln Ser Gly Ser Ser Gly Ser Asn Phe Thr Gly Asp Gln Leu Thr				
1045	1050	1055		
cag cca aac agg act cca gta cca gtc agt gtg tct cat cgt ctt cca				3216
Gln Pro Asn Arg Thr Pro Val Pro Val Ser Val Ser His Arg Leu Pro				
1060	1065	1070		
gtt tct tct tcc aag tct acc agc acc ttc agt aac aca cct gga aca				3264
Val Ser Ser Ser Lys Ser Thr Ser Thr Phe Ser Asn Thr Pro Gly Thr				
1075	1080	1085		
gga acc cag caa caa ttc ttc tgc cag gct cag aaa aaa tgt ctg aat				3312
Gly Thr Gln Gln Gln Phe Phe Cys Gln Ala Gln Lys Lys Cys Leu Asn				
1090	1095	1100		
cag act tcc ccc att tct gct ccc aag acc aca gac ggc ctg agg caa				3360
Gln Thr Ser Pro Ile Ser Ala Pro Lys Thr Thr Asp Gly Leu Arg Gln				
1105	1110	1115	1120	
gca cag atc cct ggg ctc ttg agc acc aca ctg cca ggg cag gat tct				3408
Ala Gln Ile Pro Gly Leu Leu Ser Thr Thr Leu Pro Gly Gln Asp Ser				
1125	1130	1135		
gga agc aaa gtt ata tcc gca tcc tta gga acc gca caa cca cag cag				3456
Gly Ser Lys Val Ile Ser Ala Ser Leu Gly Thr Ala Gln Pro Gln Gln				
1140	1145	1150		
gaa aaa gta gtt gga tca tct cct ggc cat cca gct gtg cag gtg gag				3504
Glu Lys Val Val Gly Ser Ser Pro Gly His Pro Ala Val Gln Val Glu				
1155	1160	1165		
agt cat tcg gga gga caa aaa agg cct gct gcg aaa cag cta acg aaa				3552
Ser His Ser Gly Gly Gln Lys Arg Pro Ala Ala Lys Gln Leu Thr Lys				
1170	1175	1180		
gga gct ttc att ctc cag cag ttg cag agg gac caa gcc cac act gtg				3600
Gly Ala Phe Ile Leu Gln Gln Leu Gln Arg Asp Gln Ala His Thr Val				
1185	1190	1195	1200	
aca cca gac aaa agt cac ttc cga tca cta agt gat gcg gta cag aga				3648
Thr Pro Asp Lys Ser His Phe Arg Ser Leu Ser Asp Ala Val Gln Arg				
1205	1210	1215		
ctg ctc tcc tac cac gtg tgc cag ggc tcc atg ccc act gaa gaa gac				3696
Leu Leu Ser Tyr His Val Cys Gln Gly Ser Met Pro Thr Glu Glu Asp				
1220	1225	1230		
ttg aga aaa gtg gac aat gaa ttt gag aca gtt gcc act cag ctc cta				3744
Leu Arg Lys Val Asp Asn Glu Phe Glu Thr Val Ala Thr Gln Leu Leu				

1235	1240	1245	
aaa agg acc caa gct atg ctt aac aaa tac aga tgc ctg ctc cta gaa Lys Arg Thr Gln Ala Met Leu Asn Lys Tyr Arg Cys Leu Leu Leu Glu 1250	1255	1260	3792
gat gcc atg cga atc aat ccc tct gct gag atg gtg atg atc gat agg Asp Ala Met Arg Ile Asn Pro Ser Ala Glu Met Val Met Ile Asp Arg 1265	1270	1275	3840
atg ttc aac cag gag gaa aga gct tcc ctg tcc cga gac aag cgt ttg Met Phe Asn Gln Glu Glu Arg Ala Ser Leu Ser Arg Asp Lys Arg Leu 1285	1290	1295	3888
gca ctt gta gac cct gag ggt ttt cag gct gat ttc tgt tgt tcc ttc Ala Leu Val Asp Pro Glu Gly Phe Gln Ala Asp Phe Cys Cys Ser Phe 1300	1305	1310	3936
aaa ctt gat aaa gct gct cat gag aca cag ttt ggc cgg agt gac cag Lys Leu Asp Lys Ala Ala His Glu Thr Gln Phe Gly Arg Ser Asp Gln 1315	1320	1325	3984
cat ggc agt aaa gca agc agc tct ctg caa ccg cca gcc aag gcc caa His Gly Ser Lys Ala Ser Ser Ser Leu Gln Pro Pro Ala Lys Ala Gln 1330	1335	1340	4032
ggc aga gac cga gcc aaa acc ggt gtg acg gaa ccc atg aat cat gac Gly Arg Asp Arg Ala Lys Thr Gly Val Thr Glu Pro Met Asn His Asp 1345	1350	1355	4080
cag ttt cat cta gtg cct aat cac atc gtg gtc tct gca gaa gga aac Gln Phe His Leu Val Pro Asn His Ile Val Val Ser Ala Glu Gly Asn 1365	1370	1375	4128
att tct aaa aaa aca gaa tgc ctt ggc aga gca ctg aaa ttt gac aaa Ile Ser Lys Lys Thr Glu Cys Leu Gly Arg Ala Leu Lys Phe Asp Lys 1380	1385	1390	4176
gtg ggc tta gtg cag tac cag agc acg tct gaa gag aag gcc agc cgg Val Gly Leu Val Gln Tyr Gln Ser Thr Ser Glu Glu Lys Ala Ser Arg 1395	1400	1405	4224
aga gag cct ctg aag gcc agt cag tgc tct ccc ggc cct gag ggg cac Arg Glu Pro Leu Lys Ala Ser Gln Cys Ser Pro Gly Pro Glu Gly His 1410	1415	1420	4272
cgg aaa acc tca tcc aga tgc gat cat ggt act gag agc aaa ctg tca Arg Lys Thr Ser Ser Arg Ser Asp His Gly Thr Glu Ser Lys Leu Ser 1425	1430	1435	4320
agc atc cta gca gat tgc cac ttg gag atg acg tgt aac aat tcc ttc Ser Ile Leu Ala Asp Ser His Leu Glu Met Thr Cys Asn Asn Ser Phe 1445	1450	1455	4368
cag gac aaa agt ctg agg aat tct cca aag aat gaa gtt tta cac aca Gln Asp Lys Ser Leu Arg Asn Ser Pro Lys Asn Glu Val Leu His Thr 1460	1465	1470	4416
gac atc atg aaa ggg tca ggc gaa ccc cag cca gat ctc cag ctg aca Asp Ile Met Lys Gly Ser Gly Glu Pro Gln Pro Asp Leu Gln Leu Thr 1475	1480	1485	4464
aag agc ttg gaa acc aca ttt aag aac atc ttg gaa ctc aaa aag gcg Lys Ser Leu Glu Thr Thr Phe Lys Asn Ile Leu Glu Leu Lys Lys Ala			4512

1490	1495	1500	
gga cgg cag ccc cag agt gac ccc acg gtt agc ggc tct gtt gag tta			4560
Gly Arg Gln Pro Gln Ser Asp Pro Thr Val Ser Gly Ser Val Glu Leu			
1505	1510	1515	1520
gat ttc ccc aac ttt tct cct atg gct tca cag gaa aac tgc ctg gaa			4608
Asp Phe Pro Asn Phe Ser Pro Met Ala Ser Gln Glu Asn Cys Leu Glu			
	1525	1530	1535
aag ttc atc ccg gac cac agt gaa ggt gtt gta gaa act gac tcc att			4656
Lys Phe Ile Pro Asp His Ser Glu Gly Val Val Glu Thr Asp Ser Ile			
	1540	1545	1550
tta gaa gca gct gta aat agt atc cta gag tgt taa tagc agcagtcctc			4706
Leu Glu Ala Ala Val Asn Ser Ile Leu Glu Cys *			
	1555	1560	
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&lt;210&gt; 398

&lt;211&gt; 2530

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (218) .. (775)

&lt;400&gt; 398

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gcacctcctt tctgtccccc ggcagagggc agtagag atg gcc ggc cca agg cct      235
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cgg tgg cgc gac cag ctg ctg ttc atg agc atc ata gtc ctc gtg att      283
Arg Trp Arg Asp Gln Leu Leu Phe Met Ser Ile Ile Val Leu Val Ile
                               10                               15                               20

gtg gtc atc tgc ctg atg tta tac gct ctt ctc tgg gag gct ggc aac      331
Val Val Ile Cys Leu Met Leu Tyr Ala Leu Leu Trp Glu Ala Gly Asn
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ctc act gac ctg ccc aac ctg aga atc ggc ttc tat aac ttc tgc ctg      379
Leu Thr Asp Leu Pro Asn Leu Arg Ile Gly Phe Tyr Asn Phe Cys Leu
                               40                               45                               50

tgg aat gag gac acc agc acc cta cag tgt cac cag ttc cct gag ctg      427
Trp Asn Glu Asp Thr Ser Thr Leu Gln Cys His Gln Phe Pro Glu Leu
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gaa gcc ctg ggg gtg cct cgg gtt ggc ctg ggc ctg gcc agg ctt ggc      475
Glu Ala Leu Gly Val Pro Arg Val Gly Leu Gly Leu Ala Arg Leu Gly
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gtg tac ggg tcc ctg gtc ctc acc ctc ttt gcc ccc cag cct ctc ctc      523
Val Tyr Gly Ser Leu Val Leu Thr Leu Phe Ala Pro Gln Pro Leu Leu
                               90                               95                               100

cta gcc cag tgc aac agt gat gag aga gcg tgg cgg ctg gca gtg ggc      571
Leu Ala Gln Cys Asn Ser Asp Glu Arg Ala Trp Arg Leu Ala Val Gly
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ttc ctg gct gtg tcc tct gtg ctg ctg gcc ggc ggc ctg ggc ctc ttc      619
Phe Leu Ala Val Ser Ser Val Leu Leu Ala Gly Gly Leu Gly Leu Phe
                               120                               125                               130

ctc tcc tat gtg tgg aag tgg gtc agg ctc tcc ctc ccg ggg cct ggg      667
Leu Ser Tyr Val Trp Lys Trp Val Arg Leu Ser Leu Pro Gly Pro Gly
                               135                               140                               145                               150

ttt cta gct ctg ggc agc gcc cag gcc tta ctc atc ctc ttg ctt ata      715
Phe Leu Ala Leu Gly Ser Ala Gln Ala Leu Leu Ile Leu Leu Leu Ile
                               155                               160                               165

gcc atg gct gtg ttc cct ctg agg gct gag agg gct gag agc aag ctt      763
Ala Met Ala Val Phe Pro Leu Arg Ala Glu Arg Ala Glu Ser Lys Leu
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gag agc tgc taa agg cttacgtgat tgcaagggtt cagttccaac catggtcaga      818
Glu Ser Cys *
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&lt;210&gt; 399

&lt;211&gt; 2595

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 Arg Gly Ala Arg Asn Ala Arg Val Leu Arg Gly Ile Leu Ala Gly Ala  
 15 20 25

aca gct aac aag gct tct cat aac agg acc cgg gcc ctg caa agc cac 146  
 Thr Ala Asn Lys Ala Ser His Asn Arg Thr Arg Ala Leu Gln Ser His  
 30 35 40

agc tcc cca gag ggc aag gag gaa cct gaa ccc cta tcc ccg gag ctg 194  
 Ser Ser Pro Glu Gly Lys Glu Glu Pro Glu Pro Leu Ser Pro Glu Leu  
 45 50 55 60

gaa tac att ccc aga aag agg ggc aag aac ccc atg aaa gct gtg gga 242  
 Glu Tyr Ile Pro Arg Lys Arg Gly Lys Asn Pro Met Lys Ala Val Gly  
 65 70 75

ctg gcc tgg tac agc ctg tac acc cgc acc tgg ctc ggg tac ctc ttc 290  
 Leu Ala Trp Tyr Ser Leu Tyr Thr Arg Thr Trp Leu Gly Tyr Leu Phe  
 80 85 90

tac cga cag cag ctg cgc agg gct cgg aat cgc tac cct aaa ggc cac 338  
 Tyr Arg Gln Gln Leu Arg Arg Ala Arg Asn Arg Tyr Pro Lys Gly His  
 95 100 105

tcg aaa acc cag ccc cgc ctc ttc aat gga gtg aag gtg ctt ccc atc 386  
 Ser Lys Thr Gln Pro Arg Leu Phe Asn Gly Val Lys Val Leu Pro Ile  
 110 115 120

cct gtc ctc tcg gac aac tac agc tac ctc atc atc gac acc cag gcc 434  
 Pro Val Leu Ser Asp Asn Tyr Ser Tyr Leu Ile Ile Asp Thr Gln Ala  
 125 130 135 140

cag ctg gct gtg gct gtg gac cct tca gac cct cgg gct gtg cag gct 482  
 Gln Leu Ala Val Ala Val Asp Pro Ser Asp Pro Arg Ala Val Gln Ala  
 145 150 155

tcc att gaa aag gaa ggg gtc acc ttg gtc gcc att ctg tgt act cac 530  
 Ser Ile Glu Lys Glu Gly Val Thr Leu Val Ala Ile Leu Cys Thr His  
 160 165 170

aag cac tgg gac cac agt gga ggg aac cgt gac ctc agc cgg cgg cac 578  
 Lys His Trp Asp His Ser Gly Gly Asn Arg Asp Leu Ser Arg Arg His  
 175 180 185

cgg gac tgt cgg gtg tac ggg agc cct cag gac ggc atc ccc tac ctc 626  
 Arg Asp Cys Arg Val Tyr Gly Ser Pro Gln Asp Gly Ile Pro Tyr Leu  
 190 195 200

acc cat ccc ctg tgt cat caa gat gtg gtc agc gtg gga cgg ctt cag 674  
 Thr His Pro Leu Cys His Gln Asp Val Val Ser Val Gly Arg Leu Gln  
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atc cgg gcc ctg gct aca cct ggc cac aca caa ggc cat ctg gtc tac Ile Arg Ala Leu Ala Thr Pro Gly His Thr Gln Gly His Leu Val Tyr 225 230 235	722
cta ctg gat ggg gag ccc tac aag ggt ccc tcc tgc ctc ttc tca ggg Leu Leu Asp Gly Glu Pro Tyr Lys Gly Pro Ser Cys Leu Phe Ser Gly 240 245 250	770
gac ctg ctc ttc ctc tct ggc tgt ggg cgg acc ttt gag ggc aat gca Asp Leu Leu Phe Leu Ser Gly Cys Gly Arg Thr Phe Glu Gly Asn Ala 255 260 265	818
gag acc atg ctg agc tca ctg gac act gtg ctg ggg cta ggg gat gac Glu Thr Met Leu Ser Ser Leu Asp Thr Val Leu Gly Leu Gly Asp Asp 270 275 280	866
acc ctt ctg tgg cct ggt cat gag tat gca gag gag aac ctg ggc ttt Thr Leu Leu Trp Pro Gly His Glu Tyr Ala Glu Glu Asn Leu Gly Phe 285 290 295 300	914
gca ggt gtg gtg gag ccc gag aac ctg gcc cgg gag agg aag atg cag Ala Gly Val Val Glu Pro Glu Asn Leu Ala Arg Glu Arg Lys Met Gln 305 310 315	962
tgg gtg cag cgg cag cgg ctg gag cgc aag ggc acg tgc cca tct acc Trp Val Gln Arg Gln Arg Leu Glu Arg Lys Gly Thr Cys Pro Ser Thr 320 325 330	1010
ctg gga gag gag cgc tcc tac aac ccg ttc ctg aga acc cac tgc ctg Leu Gly Glu Glu Arg Ser Tyr Asn Pro Phe Leu Arg Thr His Cys Leu 335 340 345	1058
gcg cta cag gag gct ctg ggg ccg ggg ccg ggc ccc act ggg gat gat Ala Leu Gln Glu Ala Leu Gly Pro Gly Pro Gly Pro Thr Gly Asp Asp 350 355 360	1106
gac tac tcc cgg gcc cag ctc ctg gaa gag ctc cgc cgg ctg aag gat Asp Tyr Ser Arg Ala Gln Leu Leu Glu Glu Leu Arg Arg Leu Lys Asp 365 370 375 380	1154
atg cac aag agc aag tga tgcccc cagcgcccc agcccagccc actccccgca Met His Lys Ser Lys * 385	1208
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attcctaaga aactgaagg gctggaatgc tggctggcca ctctctgcct cagtggcctc	1808





tct tgt gaa acc aca aga aat act aca ggc att gaa gaa tca act gat Ser Cys Glu Thr Thr Arg Asn Thr Thr Gly Ile Glu Glu Ser Thr Asp 75 80 85 90	411
ggg atg att tta gga cca gaa gat ctg agt tac caa ata tat gat gtt Gly Met Ile Leu Gly Pro Glu Asp Leu Ser Tyr Gln Ile Tyr Asp Val 95 100 105	459
tcc gga gaa agc aat tca gca gtt tct aca gaa gac cta aaa gaa tgt Ser Gly Glu Ser Asn Ser Ala Val Ser Thr Glu Asp Leu Lys Glu Cys 110 115 120	507
ctg aag aaa caa tta gaa ttc tgt ttt tca cga gaa aat ttt tca aag Leu Lys Lys Gln Leu Glu Phe Cys Phe Ser Arg Glu Asn Phe Ser Lys 125 130 135	555
gat ctt tac ttg ata tct caa atg gat agt gat cag ttc atc cca att Asp Leu Tyr Leu Ile Ser Gln Met Asp Ser Asp Gln Phe Ile Pro Ile 140 145 150	603
tgg aca gtt gcc aac atg gaa gaa ata aaa aag ttg act aca gac cct Trp Thr Val Ala Asn Met Glu Glu Ile Lys Lys Leu Thr Thr Asp Pro 155 160 165 170	651
gat cta att ctt gaa gtg tta aga tct tct ccc atg gta caa gtt gat Asp Leu Ile Leu Glu Val Leu Arg Ser Ser Pro Met Val Gln Val Asp 175 180 185	699
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ctt aga gag att cct gaa aca aca cca ata gag gaa gtg aaa ggt ttg Leu Arg Glu Ile Pro Glu Thr Thr Pro Ile Glu Glu Val Lys Gly Leu 205 210 215	795
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gct ttt aaa tac tta aga gaa gaa gtt aaa aca ttt cag ggc aag cca Ala Phe Lys Tyr Leu Arg Glu Glu Val Lys Thr Phe Gln Gly Lys Pro 255 260 265	939
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tat cga tta atg gat tct agt atc tat agt cac ccc att caa act caa Tyr Arg Leu Met Asp Ser Ser Ile Tyr Ser His Pro Ile Gln Thr Gln 285 290 295	1035
gca cag tat gcc tcc cca gtc ttt atg cag cct gta tat aat cct cac Ala Gln Tyr Ala Ser Pro Val Phe Met Gln Pro Val Tyr Asn Pro His 300 305 310	1083
caa cag tac tcg gtc tat agt att gtg cct cag tct tgg tct cca aat Gln Gln Tyr Ser Val Tyr Ser Ile Val Pro Gln Ser Trp Ser Pro Asn 315 320 325 330	1131

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cct aca cct tac ttt gaa aca cca ctg gct ccc ttt ccc aat ggt agt      1179
Pro Thr Pro Tyr Phe Glu Thr Pro Leu Ala Pro Phe Pro Asn Gly Ser
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ttt gtg aat ggc ttt aat tcg cca gga tct tat aaa aca aat gct gct      1227
Phe Val Asn Gly Phe Asn Ser Pro Gly Ser Tyr Lys Thr Asn Ala Ala
                      350                      355                      360

gct atg aat atg ggt cga cca ttc caa aaa aat cgt gtg aag cct cag      1275
Ala Met Asn Met Gly Arg Pro Phe Gln Lys Asn Arg Val Lys Pro Gln
                      365                      370                      375

ttt agg tca tct ggt ggt tca gaa cac tca aca gag ggc tct gta tcc      1323
Phe Arg Ser Ser Gly Gly Ser Glu His Ser Thr Glu Gly Ser Val Ser
                      380                      385                      390

ttg ggg gat gga cag ttg aac aga tat agt tca aga aac ttt cca gct      1371
Leu Gly Asp Gly Gln Leu Asn Arg Tyr Ser Ser Arg Asn Phe Pro Ala
395                      400                      405                      410

gaa cgg cat aac ccc aca gta act ggg cat cag gag caa act tac ctt      1419
Glu Arg His Asn Pro Thr Val Thr Gly His Gln Glu Gln Thr Tyr Leu
                      415                      420                      425

cag aag gag act tcc act ttg cag gtg gaa cag aat ggg gac tat ggt      1467
Gln Lys Glu Thr Ser Thr Leu Gln Val Glu Gln Asn Gly Asp Tyr Gly
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agg ggc agg taa gaa aataaagtac ctgaaaacct ttgataataa tgtgatcatc      1522
Arg Gly Arg *
                      445

ctgaataatt gaagaacgtg atcttcataa taattaaatg agcatttaat tattggtata      1582

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ctgaccgcaa cccctacccc cgcccaccag c      atg gcc cgg cac gtg ttc cta      172
                                   Met Ala Arg His Val Phe Leu
                                   1                      5

acg ggg ccc cca gga gtt gga aaa aca aca ttg atc cat aaa gcc agt      220
Thr Gly Pro Pro Gly Val Gly Lys Thr Thr Leu Ile His Lys Ala Ser
                      10                      15                      20

gag gtt tta aaa tcc tct ggt gtg cct gtt gat gga ttt tat acc gaa      268
Glu Val Leu Lys Ser Ser Gly Val Pro Val Asp Gly Phe Tyr Thr Glu

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40	45	50	55
tcc ggc acc cgg ggg cct tta tcg aga gtt ggg tta gag cct cca cct			364
Ser Gly Thr Arg Gly Pro Leu Ser Arg Val Gly Leu Glu Pro Pro Pro			
	60	65	70
gga aaa cgt gaa tgc cga gtt ggg cag tat gtg gtc gac ctg act tct			412
Gly Lys Arg Glu Cys Arg Val Gly Gln Tyr Val Val Asp Leu Thr Ser			
	75	80	85
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Phe Glu Gln Leu Ala Leu Pro Val Leu Arg Asn Ala Asp Cys Ser Ser			
	90	95	100
ggc cca ggg caa aga gtg tgc gtc atc gat gag att ggg aag atg gag			508
Gly Pro Gly Gln Arg Val Cys Val Ile Asp Glu Ile Gly Lys Met Glu			
	105	110	115
ctc ttc agt cag ctt ttc att caa gct gtt cgt cag acg ctg tct acc			556
Leu Phe Ser Gln Leu Phe Ile Gln Ala Val Arg Gln Thr Leu Ser Thr			
	120	125	130
cca ggg act ata atc ctt ggc aca atc cca gtt cct aaa gga aag cca			604
Pro Gly Thr Ile Ile Leu Gly Thr Ile Pro Val Pro Lys Gly Lys Pro			
	140	145	150
ctg gct ctt gta gaa gaa atc aga aac aga aag gat gtg aag gtg ttt			652
Leu Ala Leu Val Glu Glu Ile Arg Asn Arg Lys Asp Val Lys Val Phe			
	155	160	165
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Asn Val Thr Lys Glu Asn Arg Asn His Leu Leu Pro Asp Ile Val Thr			
	170	175	180
tgc gtg cag agc agc agg aag tga agacacgtgc attcctgcct tccgtgaagg			754
Cys Val Gln Ser Ser Arg Lys *			
	185	190	
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Glu Pro Val Gly Cys Cys Gly Glu Cys Arg Gly Ser Ser Val Asp Pro	
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cgg agc acc ttc gtg ttg agt aac ctg gcg gag gtg gtg gag cgt gtg	154
Arg Ser Thr Phe Val Leu Ser Asn Leu Ala Glu Val Val Glu Arg Val	
20 25 30	
ctc acc ttc ctg ccc gcc aag gcg ttg ctg cgg gtg gcc tgc gtg tgc	202
Leu Thr Phe Leu Pro Ala Lys Ala Leu Leu Arg Val Ala Cys Val Cys	
35 40 45	
cgc tta tgg agg gag tgt gtg cgc aga gta ttg cgg acc cat cgg agc	250
Arg Leu Trp Arg Glu Cys Val Arg Arg Val Leu Arg Thr His Arg Ser	
50 55 60 65	
gta acc tgg atc tcc gca ggc ctg gcg gag gcc ggc cac ctg gag ggg	298
Val Thr Trp Ile Ser Ala Gly Leu Ala Glu Ala Gly His Leu Glu Gly	
70 75 80	
cat tgc ttg gtt cgc gtg gta gca gag gag ctt gag aat gtt cgc atc	346
His Cys Leu Val Arg Val Val Ala Glu Glu Leu Glu Asn Val Arg Ile	
85 90 95	
tta cca cat aca gtt ctt tac atg gct gat tca gaa act ttc att agt	394
Leu Pro His Thr Val Leu Tyr Met Ala Asp Ser Glu Thr Phe Ile Ser	
100 105 110	
ctg gaa gag tgt cgt ggc cat aag aga gca agg aaa aga act agt atg	442
Leu Glu Glu Cys Arg Gly His Lys Arg Ala Arg Lys Arg Thr Ser Met	
115 120 125	
gaa aca gca ctt gcc ctt gag aag cta ttc ccc aaa caa tgc caa gtc	490
Glu Thr Ala Leu Ala Leu Glu Lys Leu Phe Pro Lys Gln Cys Gln Val	
130 135 140 145	
ctt ggg att gtg acc cca gga att gta gtg act cca atg gga tca ggt	538
Leu Gly Ile Val Thr Pro Gly Ile Val Val Thr Pro Met Gly Ser Gly	
150 155 160	
agc aat cga cct cag gaa ata gaa att gga gaa tct ggt ttt gct tta	586
Ser Asn Arg Pro Gln Glu Ile Glu Ile Gly Glu Ser Gly Phe Ala Leu	
165 170 175	
tta ttc cct caa att gaa gga ata aaa ata caa ccc ttt cat ttt att	634
Leu Phe Pro Gln Ile Glu Gly Ile Lys Ile Gln Pro Phe His Phe Ile	
180 185 190	
aag gat cca aag aat tta aca tta gaa aga cat caa ctc act gaa gta	682
Lys Asp Pro Lys Asn Leu Thr Leu Glu Arg His Gln Leu Thr Glu Val	
195 200 205	
ggt ctt tta gat aac cct gaa ctt cgt gtg gtc ctt gtc ttt ggt tat	730
Gly Leu Leu Asp Asn Pro Glu Leu Arg Val Val Leu Val Phe Gly Tyr	
210 215 220 225	
aat tgc tgt aag gtg gga gcc agt aat tat ctg cag caa gta gtc agc	778
Asn Cys Cys Lys Val Gly Ala Ser Asn Tyr Leu Gln Gln Val Val Ser	
230 235 240	
act ttc agt gat atg aat atc atc ttg gct gga ggc cag gtg gac aac	826
Thr Phe Ser Asp Met Asn Ile Ile Leu Ala Gly Gly Gln Val Asp Asn	
245 250 255	

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Leu Ser Ser Leu Thr Ser Glu Lys Asn Pro Leu Asp Ile Asp Ala Ser	
260 265 270	
ggt gtg gtt gga ctg tca ttt agt gga cac cga atc cag agt gcc act	922
Gly Val Val Gly Leu Ser Phe Ser Gly His Arg Ile Gln Ser Ala Thr	
275 280 285	
gtg ctc ctc aac gag gac gtc agt gat gag aag act gct gag gct gcg	970
Val Leu Leu Asn Glu Asp Val Ser Asp Glu Lys Thr Ala Glu Ala Ala	
290 295 300 305	
atg cag cgc ctc aaa gcg gcc aac att cca gag cat aac acc att ggc	1018
Met Gln Arg Leu Lys Ala Ala Asn Ile Pro Glu His Asn Thr Ile Gly	
310 315 320	
ttc atg ttt gca tgc gtt ggc agg ggc ttt cag tat tac aga gcc aag	1066
Phe Met Phe Ala Cys Val Gly Arg Gly Phe Gln Tyr Tyr Arg Ala Lys	
325 330 335	
ggg aat gtt gag gct gat gca ttt aga aag ttt ttt cct agt gtt ccc	1114
Gly Asn Val Glu Ala Asp Ala Phe Arg Lys Phe Phe Pro Ser Val Pro	
340 345 350	
tta ttc ggc ttc ttt gga aat gga gaa att gga tgt gat cgg ata gtc	1162
Leu Phe Gly Phe Phe Gly Asn Gly Glu Ile Gly Cys Asp Arg Ile Val	
355 360 365	
act ggg aac ttt ata ttg agg aaa tgt aat gag gta aaa gat gat gat	1210
Thr Gly Asn Phe Ile Leu Arg Lys Cys Asn Glu Val Lys Asp Asp Asp	
370 375 380 385	
ctg ttt cat agc tat aca aca ata atg gca ctc ata cat ctg ggg tca	1258
Leu Phe His Ser Tyr Thr Thr Ile Met Ala Leu Ile His Leu Gly Ser	
390 395 400	
tct aaa taa taattaaagt ggctttcata ataaaaaaaa aaaa	1301
Ser Lys *	

<210> 403  
 <211> 932  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (48) .. (728)

<400> 403	
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Met Trp Pro	
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gga ata ttg gca ggg ggg gcc cgg gag gcg tca tgc agg tac ccc gcg	104
Gly Ile Leu Ala Gly Gly Ala Arg Glu Ala Ser Cys Arg Tyr Pro Ala	
5 10 15	
ctg ggg cct cgc ctc gcc gct cac ttt cca gcg cag cgg ccg ccg cag	152

Leu	Gly	Pro	Arg	Leu	Ala	Ala	His	Phe	Pro	Ala	Gln	Arg	Pro	Pro	Gln		
20					25					30					35		
cgg	aca	ctc	cag	aac	ggc	ctg	gcc	ctg	cag	cgg	tgc	ctg	cac	gcg	acg		200
Arg	Thr	Leu	Gln	Asn	Gly	Leu	Ala	Leu	Gln	Arg	Cys	Leu	His	Ala	Thr		
				40					45					50			
gcg	acc	cgg	gct	ctc	ccg	ctc	att	ccc	atc	gtg	gtg	gag	cag	acg	ggt		248
Ala	Thr	Arg	Ala	Leu	Pro	Leu	Ile	Pro	Ile	Val	Val	Glu	Gln	Thr	Gly		
			55					60					65				
cgc	ggc	gag	cgc	gcc	tat	gac	atc	tac	tcg	cgg	ctg	ctg	cgg	gag	cgc		296
Arg	Gly	Glu	Arg	Ala	Tyr	Asp	Ile	Tyr	Ser	Arg	Leu	Leu	Arg	Glu	Arg		
		70					75					80					
atc	gtg	tgc	gtc	atg	ggc	ccg	atc	gat	gac	agc	gtt	gcc	agc	ctt	gtt		344
Ile	Val	Cys	Val	Met	Gly	Pro	Ile	Asp	Asp	Ser	Val	Ala	Ser	Leu	Val		
	85					90					95						
atc	gca	cag	ctc	ctc	ttc	ctg	ctt	ctc	gcc	gcc	ggc	acc	cca	ggc	atg		392
Ile	Ala	Gln	Leu	Leu	Phe	Leu	Leu	Leu	Ala	Ala	Gly	Thr	Pro	Gly	Met		
100					105				110						115		
cgc	cac	tcg	ctc	ccc	aac	tcc	cgt	atc	atg	atc	cac	cag	ccc	tca	gga		440
Arg	His	Ser	Leu	Pro	Asn	Ser	Arg	Ile	Met	Ile	His	Gln	Pro	Ser	Gly		
				120					125					130			
ggc	gcc	cgg	ggc	caa	gcc	aca	gac	att	gcc	atc	cag	gca	gag	gag	atc		488
Gly	Ala	Arg	Gly	Gln	Ala	Thr	Asp	Ile	Ala	Ile	Gln	Ala	Glu	Glu	Ile		
			135					140					145				
atg	aag	ctc	aag	aag	cag	ctc	tat	aac	atc	tac	gcc	aag	cac	acc	aaa		536
Met	Lys	Leu	Lys	Lys	Gln	Leu	Tyr	Asn	Ile	Tyr	Ala	Lys	His	Thr	Lys		
		150					155					160					
cag	agc	ctg	cag	gtg	atc	gag	tcc	gcc	atg	gag	agg	gac	cgc	tac	atg		584
Gln	Ser	Leu	Gln	Val	Ile	Glu	Ser	Ala	Met	Glu	Arg	Asp	Arg	Tyr	Met		
		165				170					175						
agc	ccc	atg	gag	gcc	cag	gag	ttt	ggc	atc	tta	gac	aag	gtt	ctg	gtc		632
Ser	Pro	Met	Glu	Ala	Gln	Glu	Phe	Gly	Ile	Leu	Asp	Lys	Val	Leu	Val		
180					185				190					195			
cac	cct	ccc	cag	gac	ggt	gag	gat	gag	ccc	acg	ctg	gtg	cag	aag	gag		680
His	Pro	Pro	Gln	Asp	Gly	Glu	Asp	Glu	Pro	Thr	Leu	Val	Gln	Lys	Glu		
			200					205						210			
cct	gta	gaa	gca	gcg	ccg	gca	gca	gaa	cct	gtc	cca	gct	agc	acc	tga		728
Pro	Val	Glu	Ala	Ala	Pro	Ala	Ala	Glu	Pro	Val	Pro	Ala	Ser	Thr	*		
			215					220					225				
gagctggggcc	tcctctccag	aatcatgtgg	agggggccaga	ggcctgccag	acccccagct												788
gggccctgct	cacccttgt	tgctgggctt	ggaggggcct	cttgaggaac	ttttaatttg												848
caggggtgcc	cgctatggac	ggggcattcc	agctgagaca	ctgtgatattt	aaattaaatc												908
tttgtggtct	ttaaaaaaaa	aaaa															932

&lt;210&gt; 404

&lt;211&gt; 670



<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (88) .. (312)

<400> 404  
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catcatccgg gaaagacatt agtggtg atg ctg aca tcc ctg tca agg cca 111  
Met Leu Thr Ser Leu Ser Arg Pro  
1 5  
ata act acc atg gct ctc agt gcc ttg gtg tac cct ggg atg tgt ggc 159  
Ile Thr Thr Met Ala Leu Ser Ala Leu Val Tyr Pro Gly Met Cys Gly  
10 15 20  
ctt ctg gcc aag cat ctg tca ttt cat att gtt gga gca ttc ctt ata 207  
Leu Leu Ala Lys His Leu Ser Phe His Ile Val Gly Ala Phe Leu Ile  
25 30 35 40  
acc ctg ggg ttg cag ctc tct gta agt ttg ctg tgg cct gac caa gaa 255  
Thr Leu Gly Leu Gln Leu Ser Val Ser Leu Leu Trp Pro Asp Gln Glu  
45 50 55  
aga agg cat atg cag att tct aca gaa att ata att gaa tta aag aat 303  
Arg Arg His Met Gln Ile Ser Thr Glu Ile Ile Ile Glu Leu Lys Asn  
60 65 70  
ttg agg tga ggaaggc taatatctct cagagtacaa agtgattttg gaacataaag 359  
Leu Arg \*  
75  
tatttctttg ggttgaatta cataaaagtt tgtcactgta cctgtgttcc tgaactatct 419  
gtgaaacatg aatatgtggg ctaagaaatt gtttatctta ataaataatt aacaaaccct 479  
ttaaacgggt aaaaaaaaaa agtcatgggc agtctttttt catatgtata gaccctaac 539  
tactaccgtt aagcaaattc cagacttcat aatttggggg aagtaactat cagatttcat 599  
ctgtactaga atcgtggcaa agtaccattc cacctgctct cgtgccgaat tcttggcctc 659  
gagggcctaa t 670

<210> 405  
<211> 401  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (58) .. (390)

<400> 405  
cccacgcgtc cgggctcctg tggaggcctg ctgggaacgg gacttctaaa aggaact 57  
atg tct gga agg ctg tgg tcc aag gcc att ttt gct ggc tat aag cgg 105  
Met Ser Gly Arg Leu Trp Ser Lys Ala Ile Phe Ala Gly Tyr Lys Arg  
1 5 10 15

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ggt ctc cgg aac caa agg gag cac aca gct ctt ctt aaa att gaa ggt      153
Gly Leu Arg Asn Gln Arg Glu His Thr Ala Leu Leu Lys Ile Glu Gly
                20                      25                      30

ggt tac gcc cga gat gaa aca gaa ttc tat ttg ggc aag aga tgc gct      201
Val Tyr Ala Arg Asp Glu Thr Glu Phe Tyr Leu Gly Lys Arg Cys Ala
                35                      40                      45

tat gta tat aaa gca aag aac aac aca gtc act cct ggc ggc aaa cca      249
Tyr Val Tyr Lys Ala Lys Asn Asn Thr Val Thr Pro Gly Gly Lys Pro
                50                      55                      60

aac aaa acc aga gtc atc tgg gga aaa gta act cgg gcc cat gga aac      297
Asn Lys Thr Arg Val Ile Trp Gly Lys Val Thr Arg Ala His Gly Asn
                65                      70                      75                      80

agt ggc atg gtt cgt gcc aaa ttc cga agc aat ctt cct gct aag gcc      345
Ser Gly Met Val Arg Ala Lys Phe Arg Ser Asn Leu Pro Ala Lys Ala
                85                      90                      95

att gga cac aga atc cga gtg atg ctg tac ccc tca agg att taa act      393
Ile Gly His Arg Ile Arg Val Met Leu Tyr Pro Ser Arg Ile *
                100                      105                      110

aacgaagt                                                                401

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<210> 406
<211> 5759
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (168) .. (2885)

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<400> 406
tttcgtcagg aatttcctt caaggtagca ggagatgaac gcgtgctgct ccaggatttt      60

acagaactga ttctgcagca aagacaaatg ttgcctgtat ttgccagata gtataaacag      120

gagcaaaaagt tgcacagcta aaccaggggc tcattcccag gacagac  atg cag tta      176
                                   Met Gln Leu
                                   1

tgg att ccg aaa gac aag tca agg aca ctg atg aca ttg aaa gtc cta      224
Trp Ile Pro Lys Asp Lys Ser Arg Thr Leu Met Thr Leu Lys Val Leu
                5                      10                      15

aac gca gta tcc gag aca gtg gct aca tcg act gct ggg att ccg agc      272
Asn Ala Val Ser Glu Thr Val Ala Thr Ser Thr Ala Gly Ile Pro Ser
                20                      25                      30                      35

gca gcg act ccc tct ctc ctc ctc gcc acg gca gag atg att cct tcg      320
Ala Ala Thr Pro Ser Leu Leu Leu Ala Thr Ala Glu Met Ile Pro Ser
                40                      45                      50

aca gcc tgg att cct ttg gct ctc gct cgt cgg cag acg cct tca cca      368
Thr Ala Trp Ile Pro Leu Ala Leu Ala Arg Arg Gln Thr Pro Ser Pro
                55                      60                      65

gat gta gtc ctc agg gga agc agc gat ggg aga gga agc gac tct gaa      416

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Asp	Val	Val	Leu	Arg	Gly	Ser	Ser	Asp	Gly	Arg	Gly	Ser	Asp	Ser	Glu	
		70					75					80				
tcc	gac	ttg	cct	cat	cgg	aag	ctg	cca	gat	gtg	aag	aag	gat	gac	atg	464
Ser	Asp	Leu	Pro	His	Arg	Lys	Leu	Pro	Asp	Val	Lys	Lys	Asp	Asp	Met	
	85					90					95					
tct	gca	cgg	cgg	act	tcc	cat	ggt	gag	ccg	aaa	tca	gca	gtg	cct	ttt	512
Ser	Ala	Arg	Arg	Thr	Ser	His	Gly	Glu	Pro	Lys	Ser	Ala	Val	Pro	Phe	
100					105					110					115	
aac	cag	tac	ctc	ccg	aac	aaa	agc	aat	cag	acg	gcc	tac	gtc	ccc	gcg	560
Asn	Gln	Tyr	Leu	Pro	Asn	Lys	Ser	Asn	Gln	Thr	Ala	Tyr	Val	Pro	Ala	
			120						125					130		
cct	ctg	aga	aag	aag	aaa	gca	gag	aga	gag	gaa	tac	cgc	aag	agc	tgg	608
Pro	Leu	Arg	Lys	Lys	Lys	Ala	Glu	Arg	Glu	Glu	Tyr	Arg	Lys	Ser	Trp	
			135					140					145			
agt	acc	gcc	acc	tcc	ccg	ctg	ggt	ggg	gag	agg	ccc	ttc	aga	tac	ggt	656
Ser	Thr	Ala	Thr	Ser	Pro	Leu	Gly	Gly	Glu	Arg	Pro	Phe	Arg	Tyr	Gly	
		150					155					160				
ccg	aga	act	cct	gtg	tct	gat	gac	gca	gag	agc	acc	agc	atg	ttt	gac	704
Pro	Arg	Thr	Pro	Val	Ser	Asp	Asp	Ala	Glu	Ser	Thr	Ser	Met	Phe	Asp	
	165					170					175					
atg	cgg	tgt	gag	gag	gag	gcc	gcg	gtg	cag	ccg	cac	agc	agg	gcc	cgc	752
Met	Arg	Cys	Glu	Glu	Glu	Ala	Ala	Val	Gln	Pro	His	Ser	Arg	Ala	Arg	
180					185					190					195	
cag	gag	cag	ctg	cag	ctg	ata	aat	aac	cag	ctg	agg	gaa	gag	gac	gac	800
Gln	Glu	Gln	Leu	Gln	Leu	Ile	Asn	Asn	Gln	Leu	Arg	Glu	Glu	Asp	Asp	
				200					205					210		
aaa	tgg	caa	gat	gac	ctg	gct	cgt	tgg	aag	agt	cgt	aga	aga	agt	gtt	848
Lys	Trp	Gln	Asp	Asp	Leu	Ala	Arg	Trp	Lys	Ser	Arg	Arg	Arg	Ser	Val	
			215					220					225			
tct	cag	gac	tta	atc	aag	aaa	gag	gaa	gaa	agg	aaa	aaa	atg	gag	aag	896
Ser	Gln	Asp	Leu	Ile	Lys	Lys	Glu	Glu	Glu	Arg	Lys	Lys	Met	Glu	Lys	
		230					235					240				
tta	ctg	gct	gga	gaa	gat	ggg	aca	agt	gaa	cga	agg	aaa	agc	atc	aaa	944
Leu	Leu	Ala	Gly	Glu	Asp	Gly	Thr	Ser	Glu	Arg	Arg	Lys	Ser	Ile	Lys	
	245					250					255					
acc	tac	aga	gaa	att	gtt	caa	gaa	aaa	gag	cgg	aga	gag	aga	gag	ctg	992
Thr	Tyr	Arg	Glu	Ile	Val	Gln	Glu	Lys	Glu	Arg	Arg	Glu	Arg	Glu	Leu	
260					265					270					275	
cat	gaa	gca	tat	aag	aac	gct	cgg	tcc	cag	gag	gag	gca	gag	ggg	atc	1040
His	Glu	Ala	Tyr	Lys	Asn	Ala	Arg	Ser	Gln	Glu	Glu	Ala	Glu	Gly	Ile	
				280					285					290		
ctt	caa	cag	tac	att	gag	agg	ttc	acc	atc	agt	gag	gct	gtt	ctc	gaa	1088
Leu	Gln	Gln	Tyr	Ile	Glu	Arg	Phe	Thr	Ile	Ser	Glu	Ala	Val	Leu	Glu	
			295					300					305			
cgc	ttg	gag	atg	cca	aaa	att	ctg	gaa	aga	agc	cat	tca	aca	gag	cca	1136
Arg	Leu	Glu	Met	Pro	Lys	Ile	Leu	Glu	Arg	Ser	His	Ser	Thr	Glu	Pro	
	310						315					320				
aat	tta	tcc	tcc	ttc	ctg	aat	gac	ccc	aat	ccc	atg	aaa	tac	ctg	cgg	1184

Asn	Leu	Ser	Ser	Phe	Leu	Asn	Asp	Pro	Asn	Pro	Met	Lys	Tyr	Leu	Arg	
325						330					335					
caa	cag	tca	ctg	cct	cca	ccc	aaa	ttc	act	gcc	act	gtt	gaa	acc	acc	1232
Gln	Gln	Ser	Leu	Pro	Pro	Pro	Lys	Phe	Thr	Ala	Thr	Val	Glu	Thr	Thr	
340					345					350					355	
att	gct	cgt	gcc	agt	gtt	ctg	gat	acc	agc	atg	tca	gca	ggc	agt	ggg	1280
Ile	Ala	Arg	Ala	Ser	Val	Leu	Asp	Thr	Ser	Met	Ser	Ala	Gly	Ser	Gly	
				360					365					370		
tct	cca	agc	aaa	act	gtc	act	ccc	aaa	gca	gtg	cct	atg	ctg	aca	ccc	1328
Ser	Pro	Ser	Lys	Thr	Val	Thr	Pro	Lys	Ala	Val	Pro	Met	Leu	Thr	Pro	
			375					380					385			
aag	cct	tac	tcc	cag	ccc	aaa	aat	tct	caa	gat	gtt	ctg	aag	acc	ttt	1376
Lys	Pro	Tyr	Ser	Gln	Pro	Lys	Asn	Ser	Gln	Asp	Val	Leu	Lys	Thr	Phe	
		390					395					400				
aag	gta	gac	ggg	aaa	gtc	agt	gtg	aat	gga	gag	acg	gtt	cat	aga	gag	1424
Lys	Val	Asp	Gly	Lys	Val	Ser	Val	Asn	Gly	Glu	Thr	Val	His	Arg	Glu	
	405					410					415					
gag	gag	aag	gaa	aga	gag	tgt	ccc	acg	gtg	gca	cct	gcc	cac	tcc	tta	1472
Glu	Glu	Lys	Glu	Arg	Glu	Cys	Pro	Thr	Val	Ala	Pro	Ala	His	Ser	Leu	
420					425					430					435	
acc	aaa	tcc	cag	atg	ttt	gaa	ggt	gtg	gcc	aga	gtg	cac	ggg	tct	cca	1520
Thr	Lys	Ser	Gln	Met	Phe	Glu	Gly	Val	Ala	Arg	Val	His	Gly	Ser	Pro	
				440					445					450		
ctg	gag	ctg	aaa	caa	gac	aac	ggt	agc	atc	gag	atc	aac	ata	aag	aag	1568
Leu	Glu	Leu	Lys	Gln	Asp	Asn	Gly	Ser	Ile	Glu	Ile	Asn	Ile	Lys	Lys	
			455				460						465			
cca	aac	tct	gtt	ccc	caa	gag	ctc	gca	gca	acc	act	gag	aaa	acg	gaa	1616
Pro	Asn	Ser	Val	Pro	Gln	Glu	Leu	Ala	Ala	Thr	Thr	Glu	Lys	Thr	Glu	
		470				475						480				
ccg	aat	agt	caa	gag	gac	aag	aat	gat	ggt	gga	aaa	tca	aga	aaa	ggg	1664
Pro	Asn	Ser	Gln	Glu	Asp	Lys	Asn	Asp	Gly	Gly	Lys	Ser	Arg	Lys	Gly	
	485					490					495					
aat	ata	gaa	ctt	gcc	tca	tca	gaa	cca	cag	cat	ttt	aca	aca	act	gtg	1712
Asn	Ile	Glu	Leu	Ala	Ser	Ser	Glu	Pro	Gln	His	Phe	Thr	Thr	Thr	Val	
500				505					510						515	
act	cga	tgc	agc	ccg	acc	gtg	gcc	ttt	gtg	gaa	ttt	ccc	tcc	agc	ccc	1760
Thr	Arg	Cys	Ser	Pro	Thr	Val	Ala	Phe	Val	Glu	Phe	Pro	Ser	Ser	Pro	
				520					525					530		
cag	ctg	aag	aat	gat	gtg	tcg	gaa	gaa	aaa	gac	cag	aag	aaa	cca	gaa	1808
Gln	Leu	Lys	Asn	Asp	Val	Ser	Glu	Glu	Lys	Asp	Gln	Lys	Lys	Pro	Glu	
			535				540						545			
aat	gaa	atg	agt	gga	aag	gtg	gag	ttg	gtg	ctg	tca	caa	aag	gtg	gta	1856
Asn	Glu	Met	Ser	Gly	Lys	Val	Glu	Leu	Val	Leu	Ser	Gln	Lys	Val	Val	
		550				555						560				
aag	cca	aaa	tct	cca	gaa	ccc	gaa	gca	acg	ctg	aca	ttt	cca	ttt	ctg	1904
Lys	Pro	Lys	Ser	Pro	Glu	Pro	Glu	Ala	Thr	Leu	Thr	Phe	Pro	Phe	Leu	
	565					570					575					
gac	aaa	atg	cct	gaa	gcc	aac	caa	cta	cat	ttg	cca	aat	ctc	aat	tct	1952

Asp	Lys	Met	Pro	Glu	Ala	Asn	Gln	Leu	His	Leu	Pro	Asn	Leu	Asn	Ser	
580					585					590					595	
caa	gtg	gat	tct	cca	agc	agt	gag	aag	tca	cct	gtt	acg	aca	cct	ttt	2000
Gln	Val	Asp	Ser	Pro	Ser	Ser	Glu	Lys	Ser	Pro	Val	Thr	Thr	Pro	Phe	
				600					605					610		
aag	ttc	tgg	gca	tgg	gac	cca	gaa	gag	gag	cgc	agg	cga	cag	gaa	aaa	2048
Lys	Phe	Trp	Ala	Trp	Asp	Pro	Glu	Glu	Glu	Arg	Arg	Arg	Gln	Glu	Lys	
			615					620					625			
tgg	caa	cag	gaa	cag	gaa	cgt	ttg	ctc	cag	gag	aga	tac	cag	aag	gag	2096
Trp	Gln	Gln	Glu	Gln	Glu	Arg	Leu	Leu	Gln	Glu	Arg	Tyr	Gln	Lys	Glu	
			630					635				640				
cag	gac	aag	ctg	aaa	gaa	gag	tgg	gaa	aag	gcc	caa	aag	gag	gtg	gaa	2144
Gln	Asp	Lys	Leu	Lys	Glu	Glu	Trp	Glu	Lys	Ala	Gln	Lys	Glu	Val	Glu	
	645					650					655					
gag	gaa	gaa	cgc	aga	tac	tat	gag	gag	gag	cgt	aag	ata	att	gaa	gac	2192
Glu	Glu	Glu	Arg	Arg	Tyr	Tyr	Glu	Glu	Glu	Arg	Lys	Ile	Ile	Glu	Asp	
660					665					670					675	
act	gtg	gtt	cca	ttt	act	gtt	tct	tca	agt	tcc	gct	gac	cag	ctg	tct	2240
Thr	Val	Val	Pro	Phe	Thr	Val	Ser	Ser	Ser	Ser	Ala	Asp	Gln	Leu	Ser	
				680					685					690		
acc	tct	tcc	tcc	atg	act	gaa	ggc	agt	ggg	aca	atg	aat	aag	ata	gac	2288
Thr	Ser	Ser	Ser	Met	Thr	Glu	Gly	Ser	Gly	Thr	Met	Asn	Lys	Ile	Asp	
			695					700					705			
ctg	gga	aac	tgt	caa	gat	gaa	aaa	caa	gac	aga	aga	tgg	aag	aaa	tca	2336
Leu	Gly	Asn	Cys	Gln	Asp	Glu	Lys	Gln	Asp	Arg	Arg	Trp	Lys	Lys	Ser	
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ttc	cag	gga	gat	gac	agt	gac	tta	ttg	ctg	aag	act	agg	gaa	agt	gat	2384
Phe	Gln	Gly	Asp	Asp	Ser	Asp	Leu	Leu	Leu	Lys	Thr	Arg	Glu	Ser	Asp	
	725					730					735					
cga	ctg	gag	gag	aag	ggc	agc	cta	act	gaa	ggg	gcc	ttg	gct	cat	tct	2432
Arg	Leu	Glu	Glu	Lys	Gly	Ser	Leu	Thr	Glu	Gly	Ala	Leu	Ala	His	Ser	
740					745					750					755	
ggg	aac	cct	gta	tca	aaa	gga	gtc	cat	gaa	gac	cat	cag	ctg	gat	acc	2480
Gly	Asn	Pro	Val	Ser	Lys	Gly	Val	His	Glu	Asp	His	Gln	Leu	Asp	Thr	
				760					765					770		
gag	gct	ggg	gcc	cca	cac	tgt	gga	aca	aac	cca	cag	ctt	gct	cag	gat	2528
Glu	Ala	Gly	Ala	Pro	His	Cys	Gly	Thr	Asn	Pro	Gln	Leu	Ala	Gln	Asp	
			775					780					785			
cca	tcc	cag	aat	cag	cag	aca	tca	aat	cca	acg	cac	agt	tca	gaa	gat	2576
Pro	Ser	Gln	Asn	Gln	Gln	Thr	Ser	Asn	Pro	Thr	His	Ser	Ser	Glu	Asp	
		790						795				800				
gtg	aag	cca	aaa	acc	ctc	ccg	ctg	gat	aaa	agc	att	aac	cat	cag	atc	2624
Val	Lys	Pro	Lys	Thr	Leu	Pro	Leu	Asp	Lys	Ser	Ile	Asn	His	Gln	Ile	
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Arg Ser Leu Asn Pro His Lys Thr Lys His His Met Glu Cys Arg Val
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Ser	Gln	Pro	Pro	Pro	Val	Pro	Ala	Lys	Lys	Ser	Arg	Glu	Arg	Leu	Ala		
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att tgg gaa tat agt cgg cta aat ctc aac aac aca gtg cta tcc aaa Ile Trp Glu Tyr Ser Arg Leu Asn Leu Asn Asn Thr Val Leu Ser Lys			1470

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Arg Lys Leu Thr Trp Phe Val Asn Glu Gly Leu Val Asp Gly Trp Asp				
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Asp Pro Arg Phe Pro Thr Val Arg Gly Val Leu Arg Arg Gly Met Thr				
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Val Glu Gly Leu Lys Gln Phe Ile Ala Ala Gln Gly Ser Ser Arg Ser				
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Val Val Asn Met Glu Trp Asp Lys Ile Trp Ala Phe Asn Lys Lys Val				
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Ile Asp Pro Val Ala Pro Arg Tyr Val Ala Leu Leu Lys Lys Glu Val				
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Ile Pro Val Asn Val Pro Glu Ala Gln Glu Glu Met Lys Glu Val Ala				
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Lys His Pro Lys Asn Pro Glu Val Gly Leu Lys Pro Val Trp Tyr Ser				
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ccc aaa gtt ttc att gaa ggt gct gat gca gag act ttt tcg gag ggt				1854
Pro Lys Val Phe Ile Glu Gly Ala Asp Ala Glu Thr Phe Ser Glu Gly				
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Glu Met Val Thr Phe Ile Asn Trp Gly Asn Leu Asn Ile Thr Lys Ile				
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cac aaa aat gca gat gga aaa atc ata tct ctt gat gca aag ttg aat				1950
His Lys Asn Ala Asp Gly Lys Ile Ile Ser Leu Asp Ala Lys Leu Asn				
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Leu Glu Asn Lys Asp Tyr Lys Lys Thr Thr Lys Val Thr Trp Leu Ala				
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Glu Thr Thr His Ala Leu Pro Ile Pro Val Ile Cys Val Thr Tyr Glu				
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cac ttg atc aca aag cca gtg cta gga aaa gac gag gac ttt aag cag				2094
His Leu Ile Thr Lys Pro Val Leu Gly Lys Asp Glu Asp Phe Lys Gln				
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Tyr Val Asn Lys Asn Ser Lys His Glu Glu Leu Met Leu Gly Asp Pro				
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tgc ctt aag gat ttg aaa aaa gga gat att ata caa ctc cag aga aga				2190
Cys Leu Lys Asp Leu Lys Lys Gly Asp Ile Ile Gln Leu Gln Arg Arg				
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Gly Phe Phe Ile Cys Asp Gln Pro Tyr Glu Pro Val Ser Pro Tyr Ser				

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Cys	Lys	Glu	Ala	Pro	Cys	Val	Leu	Ile	Tyr	Ile	Pro	Asp	Gly	His	Thr	
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Lys	Glu	Met	Pro	Thr	Ser	Gly	Ser	Lys	Glu	Lys	Thr	Lys	Val	Glu	Ala	
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Thr	Lys	Asn	Glu	Thr	Ser	Ala	Pro	Phe	Lys	Glu	Arg	Pro	Thr	Pro	Ser	
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Leu	Asn	Asn	Asn	Cys	Thr	Thr	Ser	Glu	Asp	Ser	Leu	Val	Leu	Tyr	Asn	
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Arg	Val	Ala	Val	Gln	Gly	Asp	Val	Val	Arg	Glu	Leu	Lys	Ala	Lys	Lys	
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Ala	Pro	Lys	Glu	Asp	Val	Asp	Ala	Ala	Val	Lys	Gln	Leu	Leu	Ser	Leu	
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Pro	Pro	Ala	Glu	Ile	Gly	Gln	Asn	Ile	Ser	Ser	Asn	Ser	Ser	Ala	Ser	
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Ser Gly Cys Tyr Ile Leu Arg Pro Trp Ala Tyr Ala Ile Trp Glu Ala				
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Ile Lys Asp Phe Phe Asp Ala Glu Ile Lys Lys Leu Gly Val Glu Asn				
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Cys Tyr Phe Pro Met Phe Val Ser Gln Ser Ala Leu Glu Lys Glu Lys				
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Thr His Val Ala Asp Phe Ala Pro Glu Val Ala Trp Val Thr Arg Ser				
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Gly Lys Thr Glu Leu Ala Glu Pro Ile Ala Ile Arg Pro Thr Ser Glu				
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Thr Val Met Tyr Pro Ala Tyr Ala Lys Trp Val Gln Ser His Arg Asp				
1125	1130	1135		
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Leu Pro Ile Lys Leu Asn Gln Trp Cys Asn Val Val Arg Trp Glu Phe				
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Lys His Pro Gln Pro Phe Leu Arg Thr Arg Glu Phe Leu Trp Gln Glu				
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Gly His Ser Ala Phe Ala Thr Met Glu Glu Ala Ala Glu Glu Val Leu				
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Gln Ile Leu Asp Leu Tyr Ala Gln Val Tyr Glu Glu Leu Leu Ala Ile				

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gac tat aca act aca ata gaa gca ttt ata tct gct agt gga aga gct Asp Tyr Thr Thr Thr Ile Glu Ala Phe Ile Ser Ala Ser Gly Arg Ala 1220 1225 1230 1235			3870
atc cag gga gga aca tca cat cat tta ggg cag aat ttt tcc aaa atg Ile Gln Gly Gly Thr Ser His His Leu Gly Gln Asn Phe Ser Lys Met 1240 1245 1250			3918
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	Met Pro Phe Pro Val Thr
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Leu	Val	Lys	Glu	Trp	Ile	Arg	Glu	Ile	Ser	Glu	Ser	Lys	Asn	Leu	Pro		
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Tyr	Asn	Val	Ser	Val	Ser	Thr	Arg	Met	Val	Met	Val	Glu	Glu	Phe	Lys		
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Ser	Lys	Leu	Phe	Glu	Ala	Pro	Asn	Phe	Phe	Gln	Lys	Tyr	Lys	His	Tyr		
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Asp Ser Glu Tyr Leu Leu Gln Glu Asn Glu Pro Asp Gly Thr Leu Asp	
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caa aaa tta ttg gaa gat tta caa aag aaa aaa aat gac ctt cgg tat	691
Gln Lys Leu Leu Glu Asp Leu Gln Lys Lys Lys Asn Asp Leu Arg Tyr	
185 190 195	
att gaa atg cag cat ttc aga gaa aag ctg cct tcg tat gga atg caa	739
Ile Glu Met Gln His Phe Arg Glu Lys Leu Pro Ser Tyr Gly Met Gln	
200 205 210	
aag gaa ttg gta aat tta att gat aac cat cag gta aca gta ata agt	787
Lys Glu Leu Val Asn Leu Ile Asp Asn His Gln Val Thr Val Ile Ser	
215 220 225	
ggt gaa act ggt tgt ggc aaa acc act caa gtt act cag <sup>0</sup> ttc att ttg	835
Gly Glu Thr Gly Cys Gly Lys Thr Thr Gln Val Thr Gln Phe Ile Leu	
230 235 240 245	
gat aac tac att gaa aga gga aaa gga tct gct tgc aga ata gtt tgt	883
Asp Asn Tyr Ile Glu Arg Gly Lys Gly Ser Ala Cys Arg Ile Val Cys	
250 255 260	
act cag cca aga aga att agt gcc att tca gtt gcg gaa aga gta gct	931
Thr Gln Pro Arg Arg Ile Ser Ala Ile Ser Val Ala Glu Arg Val Ala	
265 270 275	
gca gaa agg gca gaa tct tgt ggc agt ggt aat agt act gga tat caa	979
Ala Glu Arg Ala Glu Ser Cys Gly Ser Gly Asn Ser Thr Gly Tyr Gln	
280 285 290	
att cgt ctc cag agt cgg ttg cca agg aaa cag ggt tct atc tta tac	1027
Ile Arg Leu Gln Ser Arg Leu Pro Arg Lys Gln Gly Ser Ile Leu Tyr	
295 300 305	

tgt aca aca gga atc atc ctt cag tgg ctc cag tca gac ccg tat ttg	1075
Cys Thr Thr Gly Ile Ile Leu Gln Trp Leu Gln Ser Asp Pro Tyr Leu	
310 315 320 325	
tcc agt gtt agt cat atc gta ctt gat gaa atc cat gaa aga aat ctg	1123
Ser Ser Val Ser His Ile Val Leu Asp Glu Ile His Glu Arg Asn Leu	
330 335 340	
cag tca gat gtt tta atg act gtt gtt aaa gac ctt ctc aat ttt cga	1171
Gln Ser Asp Val Leu Met Thr Val Val Lys Asp Leu Leu Asn Phe Arg	
345 350 355	
tct gac ttg aaa gta ata ttg atg agt gca aca ttg aat gca gaa aag	1219
Ser Asp Leu Lys Val Ile Leu Met Ser Ala Thr Leu Asn Ala Glu Lys	
360 365 370	
ttt tca gaa tat ttt ggt aac tgt cca atg ata cat ata cct ggt ttt	1267
Phe Ser Glu Tyr Phe Gly Asn Cys Pro Met Ile His Ile Pro Gly Phe	
375 380 385	
acc ttt ccg gtt gtg gaa tat ctt ttg gaa gat gta att gaa aaa ata	1315
Thr Phe Pro Val Val Glu Tyr Leu Leu Glu Asp Val Ile Glu Lys Ile	
390 395 400 405	
agg tat gtt cca gaa caa aaa gaa cac aga tcc cag ttt aag agg ggt	1363
Arg Tyr Val Pro Glu Gln Lys Glu His Arg Ser Gln Phe Lys Arg Gly	
410 415 420	
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Phe Met Gln Gly His Val Asn Arg Gln Lys Lys Lys Lys Lys Glu Ala	
425 430 435	
ata tat aaa gaa cgt tgg cca gat tat gta agg gaa ctg cga aga agg	1459
Ile Tyr Lys Glu Arg Trp Pro Asp Tyr Val Arg Glu Leu Arg Arg Arg	
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Tyr Ser Ala Ser Thr Val Asp Val Ile Glu Met Met Glu Asp Asp Lys	
455 460 465	
gtt gat ctg aat ttg att gtt gcc ctc atc cga tac att gtt ttg gaa	1555
Val Asp Leu Asn Leu Ile Val Ala Leu Ile Arg Tyr Ile Val Leu Glu	
470 475 480 485	
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Glu Glu Asp Gly Ala Ile Leu Val Phe Leu Pro Gly Trp Asp Asn Ile	
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Ser Thr Leu His Asp Leu Leu Met Ser Gln Val Met Phe Lys Ser Asp	
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Lys Phe Leu Ile Ile Pro Leu His Ser Leu Met Pro Thr Val Asn Gln	
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Thr Gln Val Phe Lys Arg Thr Pro Pro Gly Val Arg Lys Ile Val Ile	
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Ala Thr Asn Ile Ala Glu Thr Ser Ile Thr Ile Asp Asp Val Val Tyr	
550 555 560 565	

gtg ata gat gga gga aaa ata aaa gag acg cat ttt gat act cag aac	1843
Val Ile Asp Gly Gly Lys Ile Lys Glu Thr His Phe Asp Thr Gln Asn	
570 575 580	
aat atc agt aca atg tcc gct gag tgg gtt agt aaa gct aat gcc aaa	1891
Asn Ile Ser Thr Met Ser Ala Glu Trp Val Ser Lys Ala Asn Ala Lys	
585 590 595	
cag aga aaa ggt cga gct gga aga gtt caa cct ggt cat tgc tat cat	1939
Gln Arg Lys Gly Arg Ala Gly Arg Val Gln Pro Gly His Cys Tyr His	
600 605 610	
ctg tat aat ggt ctt aga gca agt ctt cta gat gac tat caa ctg cca	1987
Leu Tyr Asn Gly Leu Arg Ala Ser Leu Leu Asp Asp Tyr Gln Leu Pro	
615 620 625	
gaa att ttg aga act cct ttg gaa gaa ctt tgt tta caa ata aag att	2035
Glu Ile Leu Arg Thr Pro Leu Glu Glu Leu Cys Leu Gln Ile Lys Ile	
630 635 640 645	
tta agg cta ggt gga att gct tat ttt ctg agt aga tta atg gac cca	2083
Leu Arg Leu Gly Gly Ile Ala Tyr Phe Leu Ser Arg Leu Met Asp Pro	
650 655 660	
cca tca aat gag gca gtg tta ctc tcc ata aga cac ctg atg gag ctg	2131
Pro Ser Asn Glu Ala Val Leu Leu Ser Ile Arg His Leu Met Glu Leu	
665 670 675	
aac gct ttg gat aaa caa gaa gaa ttg aca cct ctt gga gtc cac ttg	2179
Asn Ala Leu Asp Lys Gln Glu Glu Leu Thr Pro Leu Gly Val His Leu	
680 685 690	
gca cga tta ccc gtt gag cca cat att gga aaa atg att ctt ttt gga	2227
Ala Arg Leu Pro Val Glu Pro His Ile Gly Lys Met Ile Leu Phe Gly	
695 700 705	
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Ala Leu Phe Cys Cys Leu Asp Pro Val Leu Thr Ile Ala Ala Ser Leu	
710 715 720 725	
agt ttc aaa gat cca ttt gtc att cca ctg gga aaa gaa aag att gca	2323
Ser Phe Lys Asp Pro Phe Val Ile Pro Leu Gly Lys Glu Lys Ile Ala	
730 735 740	
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Asp Ala Arg Arg Lys Glu Leu Ala Lys Asp Thr Arg Ser Asp His Leu	
745 750 755	
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Thr Val Val Asn Ala Phe Glu Gly Trp Glu Glu Ala Arg Arg Arg Gly	
760 765 770	
ttc aga tac gaa aag gac tat tgc tgg gaa tat ttt ctg tct tca aac	2467
Phe Arg Tyr Glu Lys Asp Tyr Cys Trp Glu Tyr Phe Leu Ser Ser Asn	
775 780 785	
aca ctg cag atg ctg cat aac atg aaa gga cag ttt gct gag cat ctt	2515
Thr Leu Gln Met Leu His Asn Met Lys Gly Gln Phe Ala Glu His Leu	
790 795 800 805	
ctt gga gct gga ttt gta agc agt aga aat cct aaa gat cca gaa tct	2563
Leu Gly Ala Gly Phe Val Ser Ser Arg Asn Pro Lys Asp Pro Glu Ser	
810 815 820	

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ggt tta tat ccc aaa gtt gct aaa att cga cta aat ttg ggt aaa aaa Gly Leu Tyr Pro Lys Val Ala Lys Ile Arg Leu Asn Leu Gly Lys Lys 840 845 850	2659
aga aaa atg gta aaa gtt tac aca aaa acc gat ggc ctg gtt gct gtt Arg Lys Met Val Lys Val Tyr Thr Lys Thr Asp Gly Leu Val Ala Val 855 860 865	2707
cat cct aaa tct gtt aat gtg gag caa aca gac ttt cac tac aac tgg His Pro Lys Ser Val Asn Val Glu Gln Thr Asp Phe His Tyr Asn Trp 870 875 880 885	2755
ctt atc tat cac cta aag atg aga aca agc agt ata tac ttg tat gac Leu Ile Tyr His Leu Lys Met Arg Thr Ser Ser Ile Tyr Leu Tyr Asp 890 895 900	2803
tgc aca gag gtt tcc cca tac tgt ctc ttg ttt ttt gga ggt gac att Cys Thr Glu Val Ser Pro Tyr Cys Leu Leu Phe Phe Gly Gly Asp Ile 905 910 915	2851
tcc atc cag aag gat aac gat cag gaa act att gct gta gat gag tgg Ser Ile Gln Lys Asp Asn Asp Gln Glu Thr Ile Ala Val Asp Glu Trp 920 925 930	2899
att gta ttt cag tct cca gca aga att gcc cat ctt gtt aag gaa tta Ile Val Phe Gln Ser Pro Ala Arg Ile Ala His Leu Val Lys Glu Leu 935 940 945	2947
aga aag gaa cta gat att ctt ctg caa gag aag att gaa agt cct cat Arg Lys Glu Leu Asp Ile Leu Leu Gln Glu Lys Ile Glu Ser Pro His 950 955 960 965	2995
cct gta gac tgg aat gac act aaa tcc aga gac tgt gca gta ctg tca Pro Val Asp Trp Asn Asp Thr Lys Ser Arg Asp Cys Ala Val Leu Ser 970 975 980	3043
gct att ata gac ttg atc aaa aca cag gaa aag gca act ccc agg aac Ala Ile Ile Asp Leu Ile Lys Thr Gln Glu Lys Ala Thr Pro Arg Asn 985 990 995	3091
ttt ccg cca cga ttc cag gat gga tat tac agc tga cagc ttttcagggg Phe Pro Pro Arg Phe Gln Asp Gly Tyr Tyr Ser *	3141
1000 1005	
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caaaccctgg gacatgaaca attttcatgt gtaaggtaga agccttcagt aggtagtaaa	3261
gacttaatgt gcatgacttg atgttatatg tagagatata tatatatata tatatatacc	3321
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accccaaaac aagtgtcaat taagaatttg aacacaacca catttttttaa aatgaaactt	3561
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3667

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 tccactctaa cacctcagag taaagaactg atgggcaggc atcggcttct gctgacaatt 180  
 gccaacccggc atgagattgc tgagctgagg tggactctcc agacactgga actggaactc 240  
 caggcccaat ggcctctggt aagaatgctg caacgtgaga cccttgagag agactgactt 300  
 gttgaag atg aag aga aaa cca aga gcc tcc agt cca gtt gtt gaa gag 349  
           Met Lys Arg Lys Pro Arg Ala Ser Ser Pro Val Val Glu Glu  
               1                  5                  10  
 caa cca cga gcc aac acc aag gag aca agg aag aag aag tcc ttc tct 397  
 Gln Pro Arg Ala Asn Thr Lys Glu Thr Arg Lys Lys Lys Ser Phe Ser  
       15                  20                  25                  30  
 caa ccg atg acc gca agc aca aag aag agt ccc aag ata gcg aag aaa 445  
 Gln Pro Met Thr Ala Ser Thr Lys Lys Ser Pro Lys Ile Ala Lys Lys  
               35                  40                  45  
 gga aaa taa ctcaagg gagagccagg aagaaaaatg ctccacaaaa atccatggct 501  
 Gly Lys \*  
 ttaagaatac ttgaggaagg gagcaggcca acaccctctg gccacagtga ccagctgaat 561  
 gaggaactct aacagaatga gctgcagttg gagcaacaga ggggacatag ctggaacaac 621  
 agagcgaggg gacacagccg gagcaacaga gtgggaggat gccaacatt tcaactctct 681  
 ccctgagcag cgagtaattt cagggcaagc ccagagacta ggatccatct gagaagtctt 741  
 cagaggtctg acccagagta ctcaacaaca ggatacgtcc catggtgatg aaaataaaat 801  
 gaatcttgtg ttcaccgttg tattcctcac gacttaagtt aaaaacctga tgaaaagtgg 861  
 ttaatctcca taatgggtgt tagctccatc gcagggagca tgaggttgga cagacagagt 921  
 cgggcaaggt tatggagaag acttaatcca tccacaagag gtccgagtat gttgatgaag 981  
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 Met Lys Ile Thr Arg Gln Lys His  
 1 5  
 gcc aag aag cat ctt ggc ttc ttc cgc aac aac ttc gga gtc cgc gag 160  
 Ala Lys Lys His Leu Gly Phe Phe Arg Asn Asn Phe Gly Val Arg Glu  
 10 15 20  
 ccg tac cag atc ctg ctg gac ggc acc ttc tgt cag gcg gcg ctg cgg 208  
 Pro Tyr Gln Ile Leu Leu Asp Gly Thr Phe Cys Gln Ala Ala Leu Arg  
 25 30 35 40  
 ggc cgc atc cag ctg cgg gag cag ctg ccc cgc tac ctc atg ggg gag 256  
 Gly Arg Ile Gln Leu Arg Glu Gln Leu Pro Arg Tyr Leu Met Gly Glu  
 45 50 55  
 acg cag ctg tgc acc aca aga tgt gtg tta aaa gag cta gaa aca ttg 304  
 Thr Gln Leu Cys Thr Thr Arg Cys Val Leu Lys Glu Leu Glu Thr Leu  
 60 65 70  
 gga aag gac tta tat ggg gca aaa ctg att gca caa aaa tgc caa gtt 352  
 Gly Lys Asp Leu Tyr Gly Ala Lys Leu Ile Ala Gln Lys Cys Gln Val  
 75 80 85  
 cga aat tgt cct cat ttc aag aat gca gtg agt gga tca gaa tgt ctg 400  
 Arg Asn Cys Pro His Phe Lys Asn Ala Val Ser Gly Ser Glu Cys Leu  
 90 95 100  
 ctt tcc atg gtt gaa gag gga aat cct cat cat tat ttt gtg gca aca 448  
 Leu Ser Met Val Glu Glu Gly Asn Pro His His Tyr Phe Val Ala Thr  
 105 110 115 120  
 cag gat cag aat ttg tct gtg aaa gta aaa aag aag cct gga gtt cct 496  
 Gln Asp Gln Asn Leu Ser Val Lys Val Lys Lys Lys Pro Gly Val Pro  
 125 130 135  
 ctc atg ttt att att cag aac act atg gtt ttg gac aaa cct tct ccc 544  
 Leu Met Phe Ile Ile Gln Asn Thr Met Val Leu Asp Lys Pro Ser Pro  
 140 145 150  
 aaa aca att gcc ttt gta aaa gca gtg gag tca ggt cag ctt gtc tca 592  
 Lys Thr Ile Ala Phe Val Lys Ala Val Glu Ser Gly Gln Leu Val Ser  
 155 160 165  
 gtg cat gag aaa gaa agt atc aaa cat ctc aaa gag gaa cag ggt tta 640  
 Val His Glu Lys Glu Ser Ile Lys His Leu Lys Glu Glu Gln Gly Leu  
 170 175 180  
 gtg aaa aac act gaa cag agt aga aga aaa aag cgc aag aaa ata agt 688  
 Val Lys Asn Thr Glu Gln Ser Arg Arg Lys Lys Arg Lys Lys Ile Ser  
 185 190 195 200

ggt ccc aat cct ctt agt tgt ttg aag aaa aag aaa aag gca ccg gac 736  
 Gly Pro Asn Pro Leu Ser Cys Leu Lys Lys Lys Lys Lys Ala Pro Asp  
 205 210 215  
  
 aca caa tca tct gct tct gaa aag aaa aga aaa aga aaa aga att cgg 784  
 Thr Gln Ser Ser Ala Ser Glu Lys Lys Arg Lys Arg Lys Arg Ile Arg  
 220 225 230  
  
 aac aga tct aac cca aaa gta ctt tct gag aag cag aat gca gaa gga 832  
 Asn Arg Ser Asn Pro Lys Val Leu Ser Glu Lys Gln Asn Ala Glu Gly  
 235 240 245  
  
 gaa tga atcctttgga tacttttcaag gacattcaaa tgtgaaaatg aatttttttac 888  
 Glu \*  
 250  
  
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 actaaaatta attataaaat aaaaacagtg accagtctag ccagcatgga aaaccccatc 1008  
 tctactaaaa tacaaaaatt agctgggcat gatgggtgcac agttgtaatt ccagctactc 1068  
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 agcg atg cgg gaa tgc ata tca gtc cac gtg ggc caa gcg gga gtt cag 169  
 Met Arg Glu Cys Ile Ser Val His Val Gly Gln Ala Gly Val Gln  
 1 5 10 15  
  
 att ggc aat gcc tgc tgg gag ctc ttc tgc ctg gaa cac ggc atc cag 217  
 Ile Gly Asn Ala Cys Trp Glu Leu Phe Cys Leu Glu His Gly Ile Gln  
 20 25 30  
  
 gca gac ggc act ttt gat gct caa gct agc aag atc aac gat gat gac 265  
 Ala Asp Gly Thr Phe Asp Ala Gln Ala Ser Lys Ile Asn Asp Asp Asp  
 35 40 45  
  
 tcc ttc acc acc ttt ttc agc gag act ggc aat ggg aag cat gtg ccc 313

Ser	Phe	Thr	Thr	Phe	Phe	Ser	Glu	Thr	Gly	Asn	Gly	Lys	His	Val	Pro	
		50					55					60				
cgg	gcc	gtc	atg	ata	gat	ctg	gag	cct	act	gta	gtg	gat	gag	gtt	cgg	361
Arg	Ala	Val	Met	Ile	Asp	Leu	Glu	Pro	Thr	Val	Val	Asp	Glu	Val	Arg	
	65					70				75						
gca	gga	acc	tac	cgc	cag	ctc	ttc	cat	cca	gag	cag	ctg	atc	aca	gga	409
Ala	Gly	Thr	Tyr	Arg	Gln	Leu	Phe	His	Pro	Glu	Gln	Leu	Ile	Thr	Gly	
	80				85				90						95	
aag	gag	gat	gca	gcc	aac	aac	tat	gcc	cgg	ggc	cac	tac	acg	gtg	ggc	457
Lys	Glu	Asp	Ala	Ala	Asn	Asn	Tyr	Ala	Arg	Gly	His	Tyr	Thr	Val	Gly	
				100				105						110		
aag	gag	agc	att	gac	ctg	gtg	ctg	gac	cgc	ata	cgg	aag	ctg	aca	gat	505
Lys	Glu	Ser	Ile	Asp	Leu	Val	Leu	Asp	Arg	Ile	Arg	Lys	Leu	Thr	Asp	
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gct	tgc	tct	ggc	ctg	cag	ggc	ttc	ctg	att	ttc	cac	agt	ttt	ggt	ggg	553
Ala	Cys	Ser	Gly	Leu	Gln	Gly	Phe	Leu	Ile	Phe	His	Ser	Phe	Gly	Gly	
		130					135					140				
ggc	act	ggc	tcc	ggc	ttc	act	tct	ctg	ctg	atg	gaa	cgc	ctc	tcc	ctg	601
Gly	Thr	Gly	Ser	Gly	Phe	Thr	Ser	Leu	Leu	Met	Glu	Arg	Leu	Ser	Leu	
	145					150					155					
gat	tat	ggc	aag	aaa	tcc	aag	ctg	gag	ttt	gcc	atc	tac	cca	gcc	ccc	649
Asp	Tyr	Gly	Lys	Lys	Ser	Lys	Leu	Glu	Phe	Ala	Ile	Tyr	Pro	Ala	Pro	
	160				165					170					175	
cag	gtc	tct	act	gca	gtg	gtg	gag	ccc	tac	aac	tcc	atc	ctg	acc	acc	697
Gln	Val	Ser	Thr	Ala	Val	Val	Glu	Pro	Tyr	Asn	Ser	Ile	Leu	Thr	Thr	
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cac	acc	aca	ctg	gaa	cat	tca	gat	tgt	gct	ttc	atg	gtg	gac	aac	gaa	745
His	Thr	Thr	Leu	Glu	His	Ser	Asp	Cys	Ala	Phe	Met	Val	Asp	Asn	Glu	
			195				200						205			
gcc	atc	tat	gac	atc	tgc	cgc	agg	aac	ctt	gac	att	gag	cgc	cct	acc	793
Ala	Ile	Tyr	Asp	Ile	Cys	Arg	Arg	Asn	Leu	Asp	Ile	Glu	Arg	Pro	Thr	
	210					215						220				
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Tyr	Thr	Asn	Leu	Asn	Arg	Leu	Ile	Ser	Gln	Ile	Val	Ser	Ser	Ile	Thr	
	225					230					235					
gct	tct	ctc	cgc	ttt	gac	ggg	gcc	ctc	aat	gtg	gac	ctc	act	gag	ttc	889
Ala	Ser	Leu	Arg	Phe	Asp	Gly	Ala	Leu	Asn	Val	Asp	Leu	Thr	Glu	Phe	
	240				245				250						255	
cag	acc	aac	ctg	gtg	ccc	tac	ccc	cgc	atc	cac	ttc	ccg	ctg	gtc	acc	937
Gln	Thr	Asn	Leu	Val	Pro	Tyr	Pro	Arg	Ile	His	Phe	Pro	Leu	Val	Thr	
				260				265					270			
tac	gcg	ccc	atc	atc	tct	gcc	gag	aaa	gcc	tat	cac	gaa	cag	ctc	tct	985
Tyr	Ala	Pro	Ile	Ile	Ser	Ala	Glu	Lys	Ala	Tyr	His	Glu	Gln	Leu	Ser	
			275				280						285			
gtg	gcc	gag	ata	acc	agc	tcc	tgc	ttt	gag	ccc	aac	agc	cag	atg	gtg	1033
Val	Ala	Glu	Ile	Thr	Ser	Ser	Cys	Phe	Glu	Pro	Asn	Ser	Gln	Met	Val	
	290					295					300					
aag	tgc	gac	ccg	aga	cat	ggc	aag	tac	atg	gcc	tgc	tgc	atg	ctc	tac	1081

Lys	Cys	Asp	Pro	Arg	His	Gly	Lys	Tyr	Met	Ala	Cys	Cys	Met	Leu	Tyr	
305						310					315					
cgg	ggc	gac	gtg	gtg	ccc	aag	gat	gtg	aat	gtc	gct	att	gct	gcc	atc	1129
Arg	Gly	Asp	Val	Val	Pro	Lys	Asp	Val	Asn	Val	Ala	Ile	Ala	Ala	Ile	
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gccgcccgcg	gtgcc	atg	ggg	ttc	ccg	gcc	gcg	gcg	ctg	ctc	tgc	gcg	ctg	231		
	Met	Gly	Phe	Pro	Ala	Ala	Ala	Leu	Leu	Cys	Ala	Leu				
	1				5					10						
tgc	tgc	ggc	ctc	ctg	gcc	ccg	gct	gcc	cgc	gcc	ggc	tac	tcc	gag	gag	279
Cys	Cys	Gly	Leu	Leu	Ala	Pro	Ala	Ala	Arg	Ala	Gly	Tyr	Ser	Glu	Glu	
		15				20						25				
cgc	tgc	agc	tgg	agg	ggc	agc	ggc	ctc	acc	cag	gag	ccc	ggc	agc	gtg	327
Arg	Cys	Ser	Trp	Arg	Gly	Ser	Gly	Leu	Thr	Gln	Glu	Pro	Gly	Ser	Val	
	30				35						40					
ggg	cag	ctg	gcc	ctg	gcc	tgt	gcg	gag	ggc	gcg	gtt	gag	tgg	ctg	tac	375
Gly	Gln	Leu	Ala	Leu	Ala	Cys	Ala	Glu	Gly	Ala	Val	Glu	Trp	Leu	Tyr	
	45				50				55					60		
ccg	gct	ggg	gcg	ctg	cgc	ctg	acc	ctg	ggc	ggc	ccc	gat	ccc	aga	gcg	423
Pro	Ala	Gly	Ala	Leu	Arg	Leu	Thr	Leu	Gly	Gly	Pro	Asp	Pro	Arg	Ala	
				65				70						75		
cgg	ccc	ggc	atc	gcc	tgt	ctg	cgg	ccg	gtg	cgg	ccc	ttc	gcg	ggc	gcc	471
Arg	Pro	Gly	Ile	Ala	Cys	Leu	Arg	Pro	Val	Arg	Pro	Phe	Ala	Gly	Ala	
			80				85						90			
cag	gtc	ttc	gcg	gag	cgc	gca	ggg	ggc	gcc	ctg	gag	ctg	ctg	ctg	gct	519
Gln	Val	Phe	Ala	Glu	Arg	Ala	Gly	Gly	Ala	Leu	Glu	Leu	Leu	Leu	Ala	
		95					100					105				
gag	ggc	ccg	ggc	ccg	gca	ggg	ggc	cgc	tgc	gtg	cgc	tgg	ggc	ccc	cgc	567
Glu	Gly	Pro	Gly	Pro	Ala	Gly	Gly	Arg	Cys	Val	Arg	Trp	Gly	Pro	Arg	
	110					115					120					
gag	cgc	cgg	gcc	ctc	ttc	ctg	cag	gcc	acg	ccg	cac	cag	gac	atc	agc	615
Glu	Arg	Arg	Ala	Leu	Phe	Leu	Gln	Ala	Thr	Pro	His	Gln	Asp	Ile	Ser	
	125				130				135					140		
cgc	cgc	gtg	gcc	gcc	ttc	cgc	ttt	gag	ctg	cgc	gag	gac	ggg	cgc	ccc	663
Arg	Arg	Val	Ala	Ala	Phe	Arg	Phe	Glu	Leu	Arg	Glu	Asp	Gly	Arg	Pro	
			145					150					155			
gag	ctg	ccc	ccg	cag	gcc	cac	ggt	ctc	ggc	gta	gac	ggt	gcc	tgc	agg	711
Glu	Leu	Pro	Pro	Gln	Ala	His	Gly	Leu	Gly	Val	Asp	Gly	Ala	Cys	Arg	
			160				165						170			
ccc	tgc	agc	gac	gct	gag	ctg	ctc	ctg	gcc	gca	tgc	acc	agc	gac	ttc	759
Pro	Cys	Ser	Asp	Ala	Glu	Leu	Leu	Leu	Ala	Ala	Cys	Thr	Ser	Asp	Phe	
		175				180						185				
gta	att	cac	ggg	atc	atc	cat	ggg	gtc	acc	cat	gac	gtg	gag	ctg	cag	807
Val	Ile	His	Gly	Ile	Ile	His	Gly	Val	Thr	His	Asp	Val	Glu	Leu	Gln	
	190					195					200					
gag	tct	gtc	atc	act	gtg	gtg	gcc	gcc	cgt	gtc	ctc	cgc	cag	aca	ccg	855
Glu	Ser	Val	Ile	Thr	Val	Val	Ala	Ala	Arg	Val	Leu	Arg	Gln	Thr	Pro	
	205				210				215					220		
ccg	ctg	ttc	cag	gcg	ggg	cga	tcc	ggg	gac	cag	ggg	ctg	acc	tcc	att	903
Pro	Leu	Phe	Gln	Ala	Gly	Arg	Ser	Gly	Asp	Gln	Gly	Leu	Thr	Ser	Ile	
			225					230					235			
cgt	acc	cca	ctg	cgc	tgt	ggc	gtc	cac	ccg	ggc	cca	ggc	acc	ttc	ctc	951
Arg	Thr	Pro	Leu	Arg	Cys	Gly	Val	His	Pro	Gly	Pro	Gly	Thr	Phe	Leu	
			240				245						250			

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ttc atg ggc tgg agc cgc ttt ggg gag gcc cgg ctg ggc tgt gcc cca      999
Phe Met Gly Trp Ser Arg Phe Gly Glu Ala Arg Leu Gly Cys Ala Pro
      255                260                265

cga ttc cag gag ttc cgc cgt gcc tac gag gct gcc cgt gct gcc cac      1047
Arg Phe Gln Glu Phe Arg Arg Ala Tyr Glu Ala Ala Arg Ala Ala His
      270                275                280

ctc cac ccc tgc gag gtg gcg ctg cac tga g gggctgggtg ctggggaggg      1098
Leu His Pro Cys Glu Val Ala Leu His *
      285                290

gctggttagga gggaggggtgg gccactgct ttggaggtga tgggactatc aataagaact      1158

ctgttcacgc aaaaaaaaaa aa                                             1180

```

```

<210> 418
<211> 1540
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (210)..(1322)

```

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<220>
<221> misc_feature
<222> (1)...(1540)
<223> n = a,t,c or g

```

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<400> 418
agggtccccc cnntttgacg actgagagca tgatgatata actatctatt cgatgatgaa      60
gatacccccac caaacccaaa aaaagagatc tctcgaggat ccgaattcgc ggccgcgtcg      120
accgacacga ccatcatttg tcgacgccgc tgccaccgcc tgcctgagag aagtcgtcgc      180
ggccgacccc gtcgcctccg ccggctacc  atg tcc gcc cag gcg cag atg cgg      233
                               Met Ser Ala Gln Ala Gln Met Arg
                               1                5

gcc ctg ctg gac cag ctc atg ggc acg gct cgg gac gac gaa acc aga      281
Ala Leu Leu Asp Gln Leu Met Gly Thr Ala Arg Asp Asp Glu Thr Arg
      10                15                20

cag agg gtc aag ttt aca gat gac cgt gtc tgc aag agt cac ctt ctg      329
Gln Arg Val Lys Phe Thr Asp Asp Arg Val Cys Lys Ser His Leu Leu
      25                30                35                40

gac tgc tgc ccc cat gac atc ctg gct ggg acg cgc atg gat tta gga      377
Asp Cys Cys Pro His Asp Ile Leu Ala Gly Thr Arg Met Asp Leu Gly
      45                50                55

gaa tgt acc aaa atc cac gac ttg gcc ctc cga gca gat tat gag att      425
Glu Cys Thr Lys Ile His Asp Leu Ala Leu Arg Ala Asp Tyr Glu Ile
      60                65                70

gca agt aaa gaa aga gac ctg ttt ttt gaa tta gat gca atg gat cac      473
Ala Ser Lys Glu Arg Asp Leu Phe Phe Glu Leu Asp Ala Met Asp His
      75                80                85

```

ttg gag tcc ttt att gct gaa tgt gat cgg aga act gag ctc gcc aag	521
Leu Glu Ser Phe Ile Ala Glu Cys Asp Arg Arg Thr Glu Leu Ala Lys	
90 95 100	
aag cgg ctg gca gaa aca cag gag gaa atc agt gcg gaa gtt tct gca	569
Lys Arg Leu Ala Glu Thr Gln Glu Glu Ile Ser Ala Glu Val Ser Ala	
105 110 115 120	
aag gca gaa aaa gta cat gag tta aat gaa gaa ata gga aaa ctc ctt	617
Lys Ala Glu Lys Val His Glu Leu Asn Glu Glu Ile Gly Lys Leu Leu	
125 130 135	
gct aaa gcc gaa cag cta ggg gct gaa ggt aat gtg gat gaa tcc cag	665
Ala Lys Ala Glu Gln Leu Gly Ala Glu Gly Asn Val Asp Glu Ser Gln	
140 145 150	
aag att ctt atg gaa gtg gaa aaa gtt cgt gcg aag aaa aaa gaa gct	713
Lys Ile Leu Met Glu Val Glu Lys Val Arg Ala Lys Lys Lys Glu Ala	
155 160 165	
gag gaa gaa tac aga aat tcc atg cct gca tcc agt ttt cag cag caa	761
Glu Glu Glu Tyr Arg Asn Ser Met Pro Ala Ser Ser Phe Gln Gln Gln	
170 175 180	
aag ctg cgt gtc tgc gag gtc tgt tca gcc tac ctt ggt ctc cat gac	809
Lys Leu Arg Val Cys Glu Val Cys Ser Ala Tyr Leu Gly Leu His Asp	
185 190 195 200	
aat gac cgt cgc ctg gca gac cac ttc ggt ggc aag tta cac ttg ggg	857
Asn Asp Arg Arg Leu Ala Asp His Phe Gly Gly Lys Leu His Leu Gly	
205 210 215	
ttc att cag atc cga gag aag ctt gat cag ttg agg aaa act gtc gct	905
Phe Ile Gln Ile Arg Glu Lys Leu Asp Gln Leu Arg Lys Thr Val Ala	
220 225 230	
gaa aag cag gag aag aga aat cag gat cgc ttg agg agg aga gag gag	953
Glu Lys Gln Glu Lys Arg Asn Gln Asp Arg Leu Arg Arg Arg Glu Glu	
235 240 245	
agg gaa cgg gag gag cgt ctg agc agg agg tcg gga tca aga acc aga	1001
Arg Glu Arg Glu Glu Arg Leu Ser Arg Arg Ser Gly Ser Arg Thr Arg	
250 255 260	
gat cgc agg agg tca cgc tcc cgg gat cgg cgt cgg agg cgg tca aga	1049
Asp Arg Arg Arg Ser Arg Ser Arg Asp Arg Arg Arg Arg Ser Arg	
265 270 275 280	
tct acc tcc cga gag cga cgg aaa ttg tcc cgg tcc cgg tcc cga gat	1097
Ser Thr Ser Arg Glu Arg Arg Lys Leu Ser Arg Ser Arg Ser Arg Asp	
285 290 295	
aga cat cgg cgc cac cgc agc cgt tcc cgg agc cac agc cgg gga cat	1145
Arg His Arg Arg His Arg Ser Arg Ser Arg Ser His Ser Arg Gly His	
300 305 310	
cgt cgg gct tcc cgg gac cga agt gcg aaa tac aag ttc tcc aga gag	1193
Arg Arg Ala Ser Arg Asp Arg Ser Ala Lys Tyr Lys Phe Ser Arg Glu	
315 320 325	
cgg gca tcc aga gag gag tcc tgg gag agc ggg cgg agc gag cga ggg	1241
Arg Ala Ser Arg Glu Glu Ser Trp Glu Ser Gly Arg Ser Glu Arg Gly	
330 335 340	



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ccc ccg gac tgg agg ctt gag agc tcc aac ggg aag atg gct tca cgg      1289
Pro Pro Asp Trp Arg Leu Glu Ser Ser Asn Gly Lys Met Ala Ser Arg
345                      350                      355                      360

agg tca gaa gag aag gag gcc ggc gag atc tga acccgtct cccgggtgct      1340
Arg Ser Glu Glu Lys Glu Ala Gly Glu Ile *
                      365                      370

gtaaatagtc tgataaacgt tcacacagtc taaaattacc ctttatatatt gctgaataca      1400

actcatcttt tgtagtttaa aatttctatt gttttggagc tagctgtgag tttctagaag      1460

tgtacagagt tgctcctgtg ttcccgggctc atgttgagta ggaataaata aatctgatgc      1520

tgctcctga aaaaaaaaaa                                              1540

```

```

<210> 419
<211> 1363
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (210) .. (1145)

```

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<220>
<221> misc_feature
<222> (1) ... (1363)
<223> n = a,t,c or g

```

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<400> 419
aggttcccc cnntttgacg actgagagca tgatgatata actatctatt cgatgatgaa      60
gatacccccac caaacccaaa aaaagagatc tctcgaggat ccgaattcgc ggccgcgtcg      120
accgacacga ccatcatttg tcgacgccgc tgccaccgcc tgccctgagag aagtcgtcgc      180
ggccgacccc gtcgcctccg ccggctacc  atg tcc gcc cag gcg cag atg cgg      233
                               Met Ser Ala Gln Ala Gln Met Arg
                               1                      5

gcc ctg ctg gac cag ctc atg ggc acg gct cgg gac gac gaa acc aga      281
Ala Leu Leu Asp Gln Leu Met Gly Thr Ala Arg Asp Asp Glu Thr Arg
    10                      15                      20

cag agg gtc aag ttt aca gat gac cgt gtc tgc aag agt cac ctt ctg      329
Gln Arg Val Lys Phe Thr Asp Asp Arg Val Cys Lys Ser His Leu Leu
    25                      30                      35                      40

gac tgc tgc ccc cat gac atc ctg gct ggg acg cgc atg gat tta gga      377
Asp Cys Cys Pro His Asp Ile Leu Ala Gly Thr Arg Met Asp Leu Gly
                      45                      50                      55

gaa tgt acc aaa atc cac gac ttg gcc ctc cga gca gat tat gag att      425
Glu Cys Thr Lys Ile His Asp Leu Ala Leu Arg Ala Asp Tyr Glu Ile
                      60                      65                      70

gca agt aaa gaa aga gac ctg ttt ttt gaa tta gat gca atg gat cac      473
Ala Ser Lys Glu Arg Asp Leu Phe Phe Glu Leu Asp Ala Met Asp His
    75                      80                      85

```

ttg gag tcc ttt att gct gaa tgt gat cgg aga act gag ctc gcc aag	521
Leu Glu Ser Phe Ile Ala Glu Cys Asp Arg Arg Thr Glu Leu Ala Lys	
90 95 100	
aag cgg ctg gca gaa aca cag gag gaa atc agt gcg gaa gtt tct gca	569
Lys Arg Leu Ala Glu Thr Gln Glu Glu Ile Ser Ala Glu Val Ser Ala	
105 110 115 120	
aag gca gaa aaa gta cat gag tta aat gaa gaa ata gga aaa ctc ctt	617
Lys Ala Glu Lys Val His Glu Leu Asn Glu Glu Ile Gly Lys Leu Leu	
125 130 135	
gct aaa gcc gaa cag cta ggg gct gaa ggt aat gtg gat gaa tcc cag	665
Ala Lys Ala Glu Gln Leu Gly Ala Glu Gly Asn Val Asp Glu Ser Gln	
140 145 150	
aag att ctt atg gaa gtg gaa aaa gtt cgt gcg aag aaa aaa gaa gct	713
Lys Ile Leu Met Glu Val Glu Lys Val Arg Ala Lys Lys Lys Glu Ala	
155 160 165	
gag aaa act gtc gct gaa aag cag gag aag aga aat cag gat cgc ttg	761
Glu Lys Thr Val Ala Glu Lys Gln Glu Lys Arg Asn Gln Asp Arg Leu	
170 175 180	
agg agg aga gag gag agg gaa cgg gag gag cgt ctg agc agg agg tcg	809
Arg Arg Arg Glu Glu Arg Glu Arg Glu Glu Arg Leu Ser Arg Arg Ser	
185 190 195 200	
gga tca aga acc aga gat cgc agg agg tca cgc tcc cgg gat cgg cgt	857
Gly Ser Arg Thr Arg Asp Arg Arg Arg Ser Arg Ser Arg Asp Arg Arg	
205 210 215	
cgg agg cgg tca aga tct acc tcc cga gag cga cgg aaa ttg tcc cgg	905
Arg Arg Arg Ser Arg Ser Thr Ser Arg Glu Arg Arg Lys Leu Ser Arg	
220 225 230	
tcc cgg tcc cga gat aga cat cgg cgc cac cgc agc cgt tcc cgg agc	953
Ser Arg Ser Arg Asp Arg His Arg Arg His Arg Ser Arg Ser Arg Ser	
235 240 245	
cac agc cgg gga cat cgt cgg gct tcc cgg gac cga agt gcg aaa tac	1001
His Ser Arg Gly His Arg Arg Ala Ser Arg Asp Arg Ser Ala Lys Tyr	
250 255 260	
aag ttc tcc aga gag cgg gca tcc aga gag gag tcc tgg gag agc ggg	1049
Lys Phe Ser Arg Glu Arg Ala Ser Arg Glu Glu Ser Trp Glu Ser Gly	
265 270 275 280	
cgg agc gag cga ggg ccc ccg gac tgg agg ctt gag agc tcc aac ggg	1097
Arg Ser Glu Arg Gly Pro Pro Asp Trp Arg Leu Glu Ser Ser Asn Gly	
285 290 295	
aag atg gct tca cgg agg tca gaa gag aag gag gcc ggc gag atc tga	1145
Lys Met Ala Ser Arg Arg Ser Glu Glu Lys Glu Ala Gly Glu Ile *	
300 305 310	
acccgtctcc cgggtgctgt aaatagtctg ataaacgttc acacagtcta aaattaccct	1205
ttatatattgc tgaatacaac tcatcttttg tagtttaaaa tttctattgt tttggagcta	1265
gctgtgagtt tctagaagtg tacagagttg ctctgtgtt cccgggtcat gttgagtagg	1325
aataaataaa tctgatgctg cctcctgaaa aaaaaaaaa	1363

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<220>
<221> CDS      .
<222> (30) .. (3218)
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1086

gac agc cca tgg gtg aag ccg tct cgg aaa cgg cgc aag cgg gag cct Asp Ser Pro Trp Val Lys Pro Ser Arg Lys Arg Arg Lys Arg Glu Pro 205 210 215	677
ccg cgg gcc aag gag cca cga gga gtg aat ggt gtg ggc tcc tca ggc Pro Arg Ala Lys Glu Pro Arg Gly Val Asn Gly Val Gly Ser Ser Gly 220 225 230	725
ccc agt gag tac atg gag gtc cct ctg ggg tcc ctg gag ctg ccc agc Pro Ser Glu Tyr Met Glu Val Pro Leu Gly Ser Leu Glu Leu Pro Ser 235 240 245	773
gag ggg acc ctc tcc ccc aac cac gct ggg gtg tcc aat gac aca tct Glu Gly Thr Leu Ser Pro Asn His Ala Gly Val Ser Asn Asp Thr Ser 250 255 260	821
tgc ctg gag aca gag cga ggg ttt gag gag ttg ccc ctg tgc agc tgc Ser Leu Glu Thr Glu Arg Gly Phe Glu Glu Leu Pro Leu Cys Ser Cys 265 270 275 280	869
cgc atg gag gca ccc aag att gac cgc atc agc gag agg gcg ggg cac Arg Met Glu Ala Pro Lys Ile Asp Arg Ile Ser Glu Arg Ala Gly His 285 290 295	917
aag tgc atg gcc act gag agt gtg gac gga gag ctg tca ggc tgc aat Lys Cys Met Ala Thr Glu Ser Val Asp Gly Glu Leu Ser Gly Cys Asn 300 305 310	965
gcc gcc atc ctc aag cgg gag acc atg agg cca tcc agc cgt gtg gcc Ala Ala Ile Leu Lys Arg Glu Thr Met Arg Pro Ser Ser Arg Val Ala 315 320 325	1013
ctg atg gtg ctc tgt gag acc cac cgc gcc cgc atg gtc aaa cac cac Leu Met Val Leu Cys Glu Thr His Arg Ala Arg Met Val Lys His His 330 335 340	1061
tgc tgc ccg ggc tgc ggc tac ttc tgc acg gcg ggc acc ttc ctg gag Cys Cys Pro Gly Cys Gly Tyr Phe Cys Thr Ala Gly Thr Phe Leu Glu 345 350 355 360	1109
tgc cac cct gac ttc cgt gtg gcc cac cgc ttc cac aag gcc tgt gtg Cys His Pro Asp Phe Arg Val Ala His Arg Phe His Lys Ala Cys Val 365 370 375	1157
tct cag ctg aat ggg atg gtc ttc tgt ccc cac tgt ggg gag gat gct Ser Gln Leu Asn Gly Met Val Phe Cys Pro His Cys Gly Glu Asp Ala 380 385 390	1205
tct gaa gct caa gag gtg acc atc ccc cgg ggt gac ggg gtg acc cca Ser Glu Ala Gln Glu Val Thr Ile Pro Arg Gly Asp Gly Val Thr Pro 395 400 405	1253
ccg gcc ggc act gca gct cct gca ccc cca ccc ctg tcc cag gat gtc Pro Ala Gly Thr Ala Ala Pro Ala Pro Pro Pro Leu Ser Gln Asp Val 410 415 420	1301
ccc ggg aga gca gac act tct cag ccc agt gcc cgg atg cga ggg cat Pro Gly Arg Ala Asp Thr Ser Gln Pro Ser Ala Arg Met Arg Gly His 425 430 435 440	1349
ggg gaa ccc cgg cgc ccg ccc tgc gat ccc ctg gct gac acc att gac Gly Glu Pro Arg Arg Pro Pro Cys Asp Pro Leu Ala Asp Thr Ile Asp 445 450 455	1397

agc tca ggg ccc tcc ctg acc ctg ccc aat ggg ggc tgc ctt tca gcc Ser Ser Gly Pro Ser Leu Thr Leu Pro Asn Gly Gly Cys Leu Ser Ala 460 465 470	1445
gtg ggg ctg cca ctg ggg cca ggc cgg gag gcc ctg gaa aag gcc ctg Val Gly Leu Pro Leu Gly Pro Gly Arg Glu Ala Leu Glu Lys Ala Leu 475 480 485	1493
gtc atc cag gag tca gag agg cgg aag aag ctc cgt ttc cac cct cgg Val Ile Gln Glu Ser Glu Arg Arg Lys Lys Leu Arg Phe His Pro Arg 490 495 500	1541
cag ttg tac ctg tcc gtg aag cag ggc gag ctg cag aag gtg atc ctg Gln Leu Tyr Leu Ser Val Lys Gln Gly Glu Leu Gln Lys Val Ile Leu 505 510 515 520	1589
atg ctg ttg gac aac ctg gac ccc aac ttc cag agc gac cag cag agc Met Leu Leu Asp Asn Leu Asp Pro Asn Phe Gln Ser Asp Gln Gln Ser 525 530 535	1637
aag cgc acg ccc ctg cat gca gcc gcc cag aag ggc tcc gtg gag atc Lys Arg Thr Pro Leu His Ala Ala Ala Gln Lys Gly Ser Val Glu Ile 540 545 550	1685
tgc cat gtg ctg ctg cag gct gga gcc aac ata aat gca gtg gac aaa Cys His Val Leu Leu Gln Ala Gly Ala Asn Ile Asn Ala Val Asp Lys 555 560 565	1733
cag cag cgg acg cca ctg atg gag gcc gtg gtg aac aac cac ctg gag Gln Gln Arg Thr Pro Leu Met Glu Ala Val Val Asn Asn His Leu Glu 570 575 580	1781
gta gcc cgt tac atg gtg cag cgt ggt ggc tgt gtc tat agc aag gag Val Ala Arg Tyr Met Val Gln Arg Gly Gly Cys Val Tyr Ser Lys Glu 585 590 595 600	1829
gag gac ggt tcc acc tgc ctc cac cac gca gcc aaa atc ggg aac ttg Glu Asp Gly Ser Thr Cys Leu His His Ala Ala Lys Ile Gly Asn Leu 605 610 615	1877
gag atg gtc agc ctg ctg ctg agc aca gga cag gtg gac gtc aac gcc Glu Met Val Ser Leu Leu Leu Ser Thr Gly Gln Val Asp Val Asn Ala 620 625 630	1925
cag gac agt ggg ggg tgg acg ccc atc atc tgg gct gca gag cac aag Gln Asp Ser Gly Gly Trp Thr Pro Ile Ile Trp Ala Ala Glu His Lys 635 640 645	1973
cac atc gag gtg atc cgc atg cta ctg acg cgg ggc gcc gac gtc acc His Ile Glu Val Ile Arg Met Leu Leu Thr Arg Gly Ala Asp Val Thr 650 655 660	2021
ctc act gac aac gag gag aac atc tgc ctg cac tgg gcc tcc ttc acg Leu Thr Asp Asn Glu Glu Asn Ile Cys Leu His Trp Ala Ser Phe Thr 665 670 675 680	2069
ggc agc gcc gcc atc gcc gaa gtc ctt ctg aat gcg cgc tgt gac ctc Gly Ser Ala Ala Ile Ala Glu Val Leu Leu Asn Ala Arg Cys Asp Leu 685 690 695	2117
cat gct gtc aac tac cat ggg gac acc ccc ctg cac atc gca gct cgg His Ala Val Asn Tyr His Gly Asp Thr Pro Leu His Ile Ala Ala Arg 700 705 710	2165

gag agc tac cat gac tgc gtg ctg tta ttc ctg tca cgt ggg gcc aac Glu Ser Tyr His Asp Cys Val Leu Leu Phe Leu Ser Arg Gly Ala Asn 715 720 725	2213
cct gag ctg cgg aac aaa gag ggg gac aca gca tgg gac ctg act ccc Pro Glu Leu Arg Asn Lys Glu Gly Asp Thr Ala Trp Asp Leu Thr Pro 730 735 740	2261
gag cgc tcc gac gtg tgg ttt gcg ctt caa ctc aac cgc aag ctc cga Glu Arg Ser Asp Val Trp Phe Ala Leu Gln Leu Asn Arg Lys Leu Arg 745 750 755 760	2309
ctt ggg gtg gga aat cgg gcc atc cgc aca gag aag atc atc tgc cgg Leu Gly Val Gly Asn Arg Ala Ile Arg Thr Glu Lys Ile Ile Cys Arg 765 770 775	2357
gac gtg gct cgg ggc tat gag aac gtg ccc att ccc tgt gtc aac ggt Asp Val Ala Arg Gly Tyr Glu Asn Val Pro Ile Pro Cys Val Asn Gly 780 785 790	2405
gtg gat ggg gag ccc tgc cct gag gat tac aag tac atc tca gag aac Val Asp Gly Glu Pro Cys Pro Glu Asp Tyr Lys Tyr Ile Ser Glu Asn 795 800 805	2453
tgc gag acg tcc acc atg aac atc gat cgc aac atc acc cac ctg cag Cys Glu Thr Ser Thr Met Asn Ile Asp Arg Asn Ile Thr His Leu Gln 810 815 820	2501
cac tgc acg tgt gtg gac gac tgc tct agc tcc aac tgc ctg tgc ggc His Cys Thr Cys Val Asp Asp Cys Ser Ser Ser Asn Cys Leu Cys Gly 825 830 835 840	2549
cag ctc agc atc cgg tgc tgg tat gac aag gat ggg cga ttg ctc cag Gln Leu Ser Ile Arg Cys Trp Tyr Asp Lys Asp Gly Arg Leu Leu Gln 845 850 855	2597
gaa ttt aac aag att gag cct ccg ctg att ttc gag tgt aac cag gcg Glu Phe Asn Lys Ile Glu Pro Pro Leu Ile Phe Glu Cys Asn Gln Ala 860 865 870	2645
tgc tca tgc tgg aga aac tgc aag aac cgg gtc gta cag agt ggc atc Cys Ser Cys Trp Arg Asn Cys Lys Asn Arg Val Val Gln Ser Gly Ile 875 880 885	2693
aag gtg cgg cta cag ctc tac cga aca gcc aag atg ggc tgg ggg gtc Lys Val Arg Leu Gln Leu Tyr Arg Thr Ala Lys Met Gly Trp Gly Val 890 895 900	2741
cgc gcc ctg cag acc atc cca cag ggg acc ttc atc tgc gag tat gtc Arg Ala Leu Gln Thr Ile Pro Gln Gly Thr Phe Ile Cys Glu Tyr Val 905 910 915 920	2789
ggg gag ctg atc tct gat gct gag gct gat gtg aga gag gat gat tct Gly Glu Leu Ile Ser Asp Ala Glu Ala Asp Val Arg Glu Asp Asp Ser 925 930 935	2837
tac ctc ttc gac tta gac aac aag gat gga gag gtg tac tgc ata gat Tyr Leu Phe Asp Leu Asp Asn Lys Asp Gly Glu Val Tyr Cys Ile Asp 940 945 950	2885
gcc cgt tac tat ggc aac atc agc cgc ctc ctc tgc cac ctg tgt gac Ala Arg Tyr Tyr Gly Asn Ile Ser Arg Leu Leu Cys His Leu Cys Asp 955 960 965	2933



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ccc aac atc att ccc gtc cgg gtc ttc atg ctg cac caa gac ctg cga      2981
Pro Asn Ile Ile Pro Val Arg Val Phe Met Leu His Gln Asp Leu Arg
      970                      975                      980

ttt cca cgc atc gcc ttc ttc agt tcc cga gac atc cgg act ggg gag      3029
Phe Pro Arg Ile Ala Phe Phe Ser Ser Arg Asp Ile Arg Thr Gly Glu
985                      990                      995                      1000

gag cta ggg ttt gac tat ggc gac cgc ttc tgg gac atc aaa agc aaa      3077
Glu Leu Gly Phe Asp Tyr Gly Asp Arg Phe Trp Asp Ile Lys Ser Lys
      1005                      1010                      1015

tat ttc acc tgc caa tgt ggc tct gag aag tgc aag cac tca gcc gaa      3125
Tyr Phe Thr Cys Gln Cys Gly Ser Glu Lys Cys Lys His Ser Ala Glu
      1020                      1025                      1030

gcc att gcc ctg gag cag agc cgt ctg gcc cgc ctg gac cca cac cct      3173
Ala Ile Ala Leu Glu Gln Ser Arg Leu Ala Arg Leu Asp Pro His Pro
      1035                      1040                      1045

gag ctg ctg ccc gag ctc ggc tcc ctg ccc cct gtc aac aca tga gaa      3221
Glu Leu Leu Pro Glu Leu Gly Ser Leu Pro Pro Val Asn Thr *
      1050                      1055                      1060

cggaccacac cctctctccc cagcatggat ggccacagct cagccgcctc ctctgccacc      3281

agctgctcgc agcccatgcc tgggggtgct gccatcttct ctccccacca ccctttcaca      3341

cattcctgac cagagatccc agccaggccc tggagggtctg acagcccctc cctcccagag      3401

ctggttcctc cctgggaggg caacttcagg gctggccacc ccccggtgttc cccatcctca      3461

gttgaagttt gatgaattga agtcgggcct ctatgccaac tggttccttt tgttctcaat      3521

aaatgttggg tttggttaata aaaaaaaaaa a      3552

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<210> 421
<211> 1925
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (510)..(1562)

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<220>
<221> misc_feature
<222> (1)...(1925)
<223> n = a,t,c or g

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<400> 421
atttggccct cgaggccaag aattcggcac gaggggagcc gcacgggtccc ctctccttcc      60

ccatcctctc cctccccctc tccgggttcc cccaccacaa ggagccttgg gccgaccact      120

cccccgatgg cctcagccac ggaggacccc gttctggagc gttatttcaa aggccacaaa      180

gctgcgatca cctccttggg cctcagcccc aacggcaagc aacttgctac tgcttcttgg      240

gatacctttc tcatgctatg gaatttcaag ccacatgcta gagcttacag atatgtgggt      300

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1091

Ile	Asn	Pro	Lys	Leu	Glu	Val	Ile	Asp	Leu	Gln	Ile	Ser	Thr	Pro	Pro		
			220					225					230				
gtt	atg	gat	atc	ctt	tct	ttt	gat	tct	acc	aca	aca	aca	gaa	acc	agt	1253	
Val	Met	Asp	Ile	Leu	Ser	Phe	Asp	Ser	Thr	Thr	Thr	Thr	Glu	Thr	Ser		
		235					240					245					
ggt	agg	act	ctg	cca	gac	aag	ggt	gaa	gag	gcc	tgt	gga	tat	ttc	ttg	1301	
Gly	Arg	Thr	Leu	Pro	Asp	Lys	Gly	Glu	Glu	Ala	Cys	Gly	Tyr	Phe	Leu		
	250					255					260						
aac	cct	tcc	tta	atg	tca	cca	gaa	tgt	ttg	cca	aca	acc	acg	aaa	aag	1349	
Asn	Pro	Ser	Leu	Met	Ser	Pro	Glu	Cys	Leu	Pro	Thr	Thr	Thr	Lys	Lys		
265					270					275					280		
aaa	aca	gaa	gac	atg	agt	gac	ctc	ccc	tgt	gaa	agt	caa	agg	agc	ata	1397	
Lys	Thr	Glu	Asp	Met	Ser	Asp	Leu	Pro	Cys	Glu	Ser	Gln	Arg	Ser	Ile		
			285					290					295				
cct	ctc	gct	gtg	act	gat	gct	tta	gag	cat	att	atg	gaa	caa	ctc	aat	1445	
Pro	Leu	Ala	Val	Thr	Asp	Ala	Leu	Glu	His	Ile	Met	Glu	Gln	Leu	Asn		
		300					305						310				
gtt	ttg	aca	cag	act	gtt	tca	atc	ttg	gag	cag	cga	ctg	act	ttg	aca	1493	
Val	Leu	Thr	Gln	Thr	Val	Ser	Ile	Leu	Glu	Gln	Arg	Leu	Thr	Leu	Thr		
	315					320					325						
gag	gat	aag	ctg	aaa	gac	tgc	ctt	gaa	aat	cag	caa	aag	ctt	ttc	agt	1541	
Glu	Asp	Lys	Leu	Lys	Asp	Cys	Leu	Glu	Asn	Gln	Gln	Lys	Leu	Phe	Ser		
	330				335					340							
gct	gtc	caa	cag	aaa	agc	tga	at	aaaaaattca	ttttcatttg	ttgggcagag	1594						
Ala	Val	Gln	Gln	Lys	Ser	*											
345				350													
gccaataaaa	tgaacaaatg	tacatacact	caggaaggta	gtacaagata	ctccatacaa	1654											
cacaaccatg	tgctatztat	catggcattt	cttaaaaggg	tgagcaacag	aacaaaaggc	1714											
agaaaaggca	tacctaagga	ctaatttaaa	cacatatcaa	tgtgaaggac	taatttaa	1774											
tactatcatt	tatgattgca	gtaataaagt	gataagcatt	caagcaactc	tgtattttcc	1834											
ccatattaat	ttaa	atgtcc	attntcattt	ataggccana	tcctgccaa	aaaagaaccc	1894										
agatctctgg	atttcactgt	taagtcattt	a	1925													

<210> 422  
 <211> 956  
 <212> DNA  
 <213> Homo sapiens

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 <221> CDS  
 <222> (484)..(837)

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gctccccggg	aagcgttttg	gccccaccg	gaatggtgtc	atctgggttaa	gaagcgcaag	120											

tggcgctttg gagaaaccaa ccaagacccc gggggggggg tgggcccacaa tcctaattac 180  
 ccttctgtcc ccaacttcca gttagccaaa atataaagaa ggcaaatcct gtactgttgg 240  
 caaaaacagc caccctaaaag ttgttaaaaa gcaaaaacaaa acacctcaag cttaaatttt 300  
 tgaaaaacaa tcctcacaca aagatactat caacaaatca cacaccaatt tatcttagaa 360  
 ggatcaagag atgaaaaaca gcaagagata ttttcgtaat atgctagaat ctttgaatat 420  
 aatactgaag ttggcaacca aaagcaattc agaagttcaa cttagaacta atggctgtat 480  
 ccg atg gca ctg tct att tta gat att aaa atg tca cca tct tgg tat 528  
 Met Ala Leu Ser Ile Leu Asp Ile Lys Met Ser Pro Ser Trp Tyr  
 1 5 10 15  
 ttt cac atg gct ata ggc att ata aac tgg aac act act gcg ggt tta 576  
 Phe His Met Ala Ile Gly Ile Ile Asn Trp Asn Thr Thr Ala Gly Leu  
 20 25 30  
 tct ggc act ctg tat cca aaa gtc ccc caa aag tac ata ctc ttt gac 624  
 Ser Gly Thr Leu Tyr Pro Lys Val Pro Gln Lys Tyr Ile Leu Phe Asp  
 35 40 45  
 tct gta att ctg ctt cta ggc atg tta aga aaa ata cgt cag gta tgc 672  
 Ser Val Ile Leu Leu Leu Gly Met Leu Arg Lys Ile Arg Gln Val Cys  
 50 55 60  
 caa aat gta tac atg aaa ggg tgt tca cca ata aca tta ttt aaa ata 720  
 Gln Asn Val Tyr Met Lys Gly Cys Ser Pro Ile Thr Leu Phe Lys Ile  
 65 70 75  
 gtt cac tac tgg cca ggc gca gta gct cat gcc tat aat cct agc act 768  
 Val His Tyr Trp Pro Gly Ala Val Ala His Ala Tyr Asn Pro Ser Thr  
 80 85 90 95  
 ttg gga ggc caa gtt ggg ggc aaa tca cct gag gtc agg agt tcg aga 816  
 Leu Gly Gly Gln Val Gly Gly Lys Ser Pro Glu Val Arg Ser Ser Arg  
 100 105 110  
 cca gcc tgg act aca tgg tga aa ccccatctct actaaaagaa caaaaattag 869  
 Pro Ala Trp Thr Thr Trp \*  
 115  
 gtcgacgcgg ccgcgaattc ggatcctcga gagatctctt tttttgggtt tgggtggggta 929  
 tcttcatcgt cgaatcgtaa gttatat 956

<210> 423  
 <211> 1615  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (215)..(1507)

<400> 423  
 agttcggaaat tcccggcacg acccagcga tcgcggacgc gtgggccgga atgttaccta 60  
 tgatgaagca ggtggacccc gtgaggctgt cagcaaactt caagaattat gtcacatctatg 120

1094

Val	Ile	Ser	Lys	Lys	Ala	Lys	Val	Lys	Val	Pro	Gln	Lys	Thr	Ala	Gly		
				235					240					245			
aaa	gaa	aat	cat	ttt	gat	atg	cac	aga	gtg	gga	aaa	tgg	cac	caa	gat		1000
Lys	Glu	Asn	His	Phe	Asp	Met	His	Arg	Val	Gly	Lys	Trp	His	Gln	Asp		
			250					255					260				
ttt	cca	gtg	aag	aaa	aga	aag	aaa	ctt	tca	acc	tgg	aaa	caa	gag	ctg		1048
Phe	Pro	Val	Lys	Lys	Arg	Lys	Lys	Leu	Ser	Thr	Trp	Lys	Gln	Glu	Leu		
			265					270					275				
ctc	aaa	ctt	atg	gat	cgt	cac	aag	aaa	gat	tgt	gca	aga	gag	aag	cct		1096
Leu	Lys	Leu	Met	Asp	Arg	His	Lys	Lys	Asp	Cys	Ala	Arg	Glu	Lys	Pro		
			280				285					290					
ttt	aaa	tgt	cag	gaa	tgt	ggg	aaa	acc	ttc	aga	gtt	agc	tct	gac	ctt		1144
Phe	Lys	Cys	Gln	Glu	Cys	Gly	Lys	Thr	Phe	Arg	Val	Ser	Ser	Asp	Leu		
					300					305					310		
att	aag	cac	caa	aga	att	cac	act	gaa	gag	aaa	ccc	tat	aaa	tgt	caa		1192
Ile	Lys	His	Gln	Arg	Ile	His	Thr	Glu	Glu	Lys	Pro	Tyr	Lys	Cys	Gln		
				315						320					325		
cag	tgt	gat	aag	agg	ttt	aga	tgg	agt	tca	gat	ctt	aat	aag	cac	tta		1240
Gln	Cys	Asp	Lys	Arg	Phe	Arg	Trp	Ser	Ser	Asp	Leu	Asn	Lys	His	Leu		
			330					335						340			
aca	aca	cac	caa	gga	ata	aaa	cca	tat	aaa	tgt	tca	tgg	tgt	ggg	aaa		1288
Thr	Thr	His	Gln	Gly	Ile	Lys	Pro	Tyr	Lys	Cys	Ser	Trp	Cys	Gly	Lys		
			345				350						355				
agc	ttc	agt	caa	aat	aca	aat	tta	cat	aca	cac	caa	aga	act	cat	aca		1336
Ser	Phe	Ser	Gln	Asn	Thr	Asn	Leu	His	Thr	His	Gln	Arg	Thr	His	Thr		
			360				365					370					
gga	gaa	aag	ccc	ttc	aca	tgt	cat	gaa	tgt	gga	aaa	aaa	ttc	agt	cag		1384
Gly	Glu	Lys	Pro	Phe	Thr	Cys	His	Glu	Cys	Gly	Lys	Lys	Phe	Ser	Gln		
					380					385					390		
aac	tcc	cac	ctt	att	aaa	cac	cgg	aga	acc	cac	aca	ggt	gag	cag	cca		1432
Asn	Ser	His	Leu	Ile	Lys	His	Arg	Arg	Thr	His	Thr	Gly	Glu	Gln	Pro		
				395					400						405		
tat	act	tgt	agc	ata	tgc	agg	aga	aac	ttc	agc	agg	cgg	tca	agc	ctt		1480
Tyr	Thr	Cys	Ser	Ile	Cys	Arg	Arg	Asn	Phe	Ser	Arg	Arg	Ser	Ser	Leu		
			410					415							420		
ctt	aga	cac	cag	aaa	ctc	cac	ctg	tga	agaga	agctt	gtcca	gtgtc	ctcat				1532
Leu	Arg	His	Gln	Lys	Leu	His	Leu	*									
			425				430										
tctgaagaca	ttcaccaa	aat	ggagctt	ggc	actaaa	at	atgtaa	agaa	aatcacaaa								1592
cctttgaaaa	ttttacat	ca	gaa														1615

<210> 424  
 <211> 2531  
 <212> DNA  
 <213> Homo sapiens

<220>



&lt;221&gt; CDS

&lt;222&gt; (221) .. (2314)

&lt;400&gt; 424

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aatttccggt tgcacgatcc cgtcccctgg cggagccggc gcgcccgggg tgccgctccc      60
tgccctggcgc gctccgcacc tggaggtgcc ttgcccctct cctgcccacc tcggaatttc      120
cctgtggctc ctttgatcct tgcagtctcc agctcctctc ccttccacct gtttccccca      180
agaaaggcag gatcctggtc cctgctacgt ttctggggcc  atg gct ggt ctg ggc      235
                                         Met Ala Gly Leu Gly
                                         1                               5

ccc ggc gta ggc gat tca gag ggg gga ccc cgg ccc ctg ttt tgc aga      283
Pro Gly Val Gly Asp Ser Glu Gly Gly Pro Arg Pro Leu Phe Cys Arg
                               10                               15                               20

aag ggg gct ctg agg cag aag gtg gtc cac gaa gtc aag agc cac aag      331
Lys Gly Ala Leu Arg Gln Lys Val Val His Glu Val Lys Ser His Lys
                               25                               30                               35

ttc acc gct cgc ttc ttc aag cag ccc acc ttc tgc agc cac tgc acc      379
Phe Thr Ala Arg Phe Phe Lys Gln Pro Thr Phe Cys Ser His Cys Thr
                               40                               45                               50

gac ttc atc tgg ggt atc gga aag cag ggc ctg caa tgt caa gtc tgc      427
Asp Phe Ile Trp Gly Ile Gly Lys Gln Gly Leu Gln Cys Gln Val Cys
                               55                               60                               65

agc ttt gtg gtt cat cga cga tgc cac gaa ttt gtg acc ttc gag tgt      475
Ser Phe Val Val His Arg Arg Cys His Glu Phe Val Thr Phe Glu Cys
                               70                               75                               80                               85

cca ggc gct ggg aag ggc ccc cag acg gac gac ccc cgg aac aaa cac      523
Pro Gly Ala Gly Lys Gly Pro Gln Thr Asp Asp Pro Arg Asn Lys His
                               90                               95                               100

aag ttc cgc ctg cat agc tac agc agc ccc acc ttc tgc gac cac tgt      571
Lys Phe Arg Leu His Ser Tyr Ser Ser Pro Thr Phe Cys Asp His Cys
                               105                               110                               115

ggc tcc ctc ctc tac ggg ctt gtg cac cag ggc atg aaa tgc tcc tgc      619
Gly Ser Leu Leu Tyr Gly Leu Val His Gln Gly Met Lys Cys Ser Cys
                               120                               125                               130

tgc gag atg aac gtg cac cgg cgc tgt gtg cgt agc gtg ccc tcc ctg      667
Cys Glu Met Asn Val His Arg Arg Cys Val Arg Ser Val Pro Ser Leu
                               135                               140                               145

tgc ggt gtg gac cac acc gag cgc cgc ggg cgc ctg cag ctg gag atc      715
Cys Gly Val Asp His Thr Glu Arg Arg Gly Arg Leu Gln Leu Glu Ile
                               150                               155                               160                               165

cgg gct ccc aca gca gat gag atc cac gta act gtt ggc gag gcc cgt      763
Arg Ala Pro Thr Ala Asp Glu Ile His Val Thr Val Gly Glu Ala Arg
                               170                               175                               180

aac cta att cct atg gac ccc aat ggt ctc tct gat ccc tat gtg aaa      811
Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser Asp Pro Tyr Val Lys
                               185                               190                               195

ctg aag ctc atc cca gac cct cgg aac ctg acg aaa cag aag acc cga      859
Leu Lys Leu Ile Pro Asp Pro Arg Asn Leu Thr Lys Gln Lys Thr Arg

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200	205	210	
acg gtg aaa gcc acg cta aac cct gtg tgg aat gag acc ttt gtg ttc Thr Val Lys Ala Thr Leu Asn Pro Val Trp Asn Glu Thr Phe Val Phe 215 220 225			907
aac ctg aag cca ggg gat gtg gag cgc cgg ctc agc gtg gag gtg tgg Asn Leu Lys Pro Gly Asp Val Glu Arg Arg Leu Ser Val Glu Val Trp 230 235 240 245			955
gac tgg gac cgg acc tcc cgc aac gac ttc atg ggg gcc atg tcc ttt Asp Trp Asp Arg Thr Ser Arg Asn Asp Phe Met Gly Ala Met Ser Phe 250 255 260			1003
ggc gtc tcg gag ctg ctc aag gcg ccc gtg gat ggc tgg tac aag tta Gly Val Ser Glu Leu Leu Lys Ala Pro Val Asp Gly Trp Tyr Lys Leu 265 270 275			1051
ctg aac cag gag gag ggc gag tat tac aat gtg ccg gtg gcc gat gct Leu Asn Gln Glu Glu Gly Glu Tyr Tyr Asn Val Pro Val Ala Asp Ala 280 285 290			1099
gac aac tgc agc ctc ctc cag aag ttt gag gct tgt aac tac ccc ctg Asp Asn Cys Ser Leu Leu Gln Lys Phe Glu Ala Cys Asn Tyr Pro Leu 295 300 305			1147
gaa ttg tat gag cgg gtg cgg atg ggc ccc tct tcc tct ccc atc ccc Glu Leu Tyr Glu Arg Val Arg Met Gly Pro Ser Ser Ser Pro Ile Pro 310 315 320 325			1195
tcc cct tcc cct agt ccc acc gac ccc aag cgc tgc ttc ttc ggg gcg Ser Pro Ser Pro Ser Pro Thr Asp Pro Lys Arg Cys Phe Phe Gly Ala 330 335 340			1243
agt cca gga cgc ctg cac atc tcc gac ttc agc ttc ctc atg gtt cta Ser Pro Gly Arg Leu His Ile Ser Asp Phe Ser Phe Leu Met Val Leu 345 350 355			1291
gga aaa ggc agt ttt ggg aag gtg atg ctg gcc gag cgc agg ggc tct Gly Lys Gly Ser Phe Gly Lys Val Met Leu Ala Glu Arg Arg Gly Ser 360 365 370			1339
gat gag ctc tac gcc atc aag atc ttg aaa aag gac gtg atc gtc cag Asp Glu Leu Tyr Ala Ile Lys Ile Leu Lys Lys Asp Val Ile Val Gln 375 380 385			1387
gac gac gat gtg gac tgc acg ctg gtg gag aaa cgt gtg ctg gcg ctg Asp Asp Asp Val Asp Cys Thr Leu Val Glu Lys Arg Val Leu Ala Leu 390 395 400 405			1435
ggg ggc cgg ggt cct ggc ggc cgg ccc cac ttc ctc acc cag ctc cac Gly Gly Arg Gly Pro Gly Gly Arg Pro His Phe Leu Thr Gln Leu His 410 415 420			1483
tcc acc ttc cag acc ccg gac cgc ctg tat ttc gtg atg gag tac gtc Ser Thr Phe Gln Thr Pro Asp Arg Leu Tyr Phe Val Met Glu Tyr Val 425 430 435			1531
acc ggg gga gac ttg atg tac cac att caa cag ctg ggc aag ttt aag Thr Gly Gly Asp Leu Met Tyr His Ile Gln Gln Leu Gly Lys Phe Lys 440 445 450			1579
gag ccc cat gca gcg ttc tac gcg gca gaa atc gct atc ggc ctc ttc Glu Pro His Ala Ala Phe Tyr Ala Ala Glu Ile Ala Ile Gly Leu Phe 460 465 470			1627

455	460	465	
ttc ctt cac aat cag ggc atc atc tac agg gac ctg aag ctg gac aat			1675
Phe Leu His Asn Gln Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn			
470	475	480	485
gtg atg ctg gat gct gag gga cac atc aag atc act gac ttt ggc atg			1723
Val Met Leu Asp Ala Glu Gly His Ile Lys Ile Thr Asp Phe Gly Met			
	490	495	500
tgt aag gag aac gtc ttc ccc ggg acg aca acc cgc acc ttc tgc ggg			1771
Cys Lys Glu Asn Val Phe Pro Gly Thr Thr Thr Arg Thr Phe Cys Gly			
	505	510	515
acc ccg gac tac ata gcc ccg gag atc att gcc tac cag ccc tat ggg			1819
Thr Pro Asp Tyr Ile Ala Pro Glu Ile Ile Ala Tyr Gln Pro Tyr Gly			
	520	525	530
aag tct gtc gat tgg tgg tcc ttt gga gtt ctg ctg tat gag atg ttg			1867
Lys Ser Val Asp Trp Trp Ser Phe Gly Val Leu Leu Tyr Glu Met Leu			
	535	540	545
gca gga cag cct ccc ttc gat ggg gag gac gag gag gag ctg ttt cag			1915
Ala Gly Gln Pro Pro Phe Asp Gly Glu Asp Glu Glu Glu Leu Phe Gln			
550	555	560	565
gcc atc atg gaa caa act gtc acc tac ccc aag tcg ctt tcc cgg gaa			1963
Ala Ile Met Glu Gln Thr Val Thr Tyr Pro Lys Ser Leu Ser Arg Glu			
	570	575	580
gcc gtg gcc atc tgc aag ggg ttc ctg acc aag cac cca ggg aag cgc			2011
Ala Val Ala Ile Cys Lys Gly Phe Leu Thr Lys His Pro Gly Lys Arg			
	585	590	595
ctg ggc tca ggg cct gat ggg gaa cct acc atc cgt gca cat ggc ttt			2059
Leu Gly Ser Gly Pro Asp Gly Glu Pro Thr Ile Arg Ala His Gly Phe			
	600	605	610
ttc cgc tgg att gac tgg gag cgg ctg gaa cga ttg gag atc ccg cct			2107
Phe Arg Trp Ile Asp Trp Glu Arg Leu Glu Arg Leu Glu Ile Pro Pro			
	615	620	625
cct ttc aga ccc cgc ccg tgt ggc cgc agc ggc gag aac ttt gac aag			2155
Pro Phe Arg Pro Arg Pro Cys Gly Arg Ser Gly Glu Asn Phe Asp Lys			
630	635	640	645
ttc ttc acg cgg gcg gcg cca gcg ctg acc cct cca gac cgc cta gtc			2203
Phe Phe Thr Arg Ala Ala Pro Ala Leu Thr Pro Pro Asp Arg Leu Val			
	650	655	660
ctg gcc agc atc gac cag gcc gat ttc cag ggc ttc acc tac gtg aac			2251
Leu Ala Ser Ile Asp Gln Ala Asp Phe Gln Gly Phe Thr Tyr Val Asn			
	665	670	675
ccc gac ttc gtg cac ccg gat gcc cgc agc ccc acc agc cca gtg cct			2299
Pro Asp Phe Val His Pro Asp Ala Arg Ser Pro Thr Ser Pro Val Pro			
	680	685	690
gtg ccc gtc atg taa tctcaaccgc cgccactagg tgtccccaac gtcccctccg			2354
Val Pro Val Met *			
695			
ccgtgcccgc ggcagcccca cttcaccccc aacttcacca ccccctgtcc cattctagat			2414

cctgcacccc agcattccag ctctgcccc gggggttcta gacgcccctc ccaagcggtc 2474  
ctggccttct gaactccata cagcctctac agccgtcccc cggtcaagac ttgagcg 2531

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<213> Homo sapiens

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<222> (4556) .. (4729)

<400> 425  
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atgagagaag aaaaagtagt ttgaagctat ggagtaaggg actttgagta tcccaggctc 180  
aaaaagttgg gacttgaaca gtacgggggt gctgctgaaa acgtttgagg gaggtaatga 240  
catgatcgaa gctatacttg agaaagggtga atctgataaa gtatgagtga aaaagagact 300  
gaaggctctag aaattagatt gaggctaatt acaaaatcca cataaatagg aggacttgaa 360  
cgaaggggca cttagaagag gacaggagat agtaaaaggc attcaatgat gagagcacac 420  
actacagggg agcatgaggg aggttggaag agataatgaa aggattaccg agcttcactg 480  
acgatgtgtt tgaaatgagc aggaatcttg tagtgatcct aatccgtggg tttctggagc 540  
atttcacagc ctaggaacat acaagggggg catctccctg gaatgtaaat tgactaagag 600  
gaattcaata atggtcaaat gaatgcagaa ttttagagtc ttgcttagta ttctcaccac 660  
atttcgttta atctactcat actctttttc tcttactgct gacactagat ggaaaaactc 720  
ttaattaaaa gtatttcaca aaatgtgctc gttttcagtc attccgtttc cactccagcc 780  
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 Met Lys  
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 Thr Phe Ile Ile Gly Ile Ser Gly Val Thr Asn Ser Gly Lys Thr Thr  
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 Gly Phe Leu Gln Tyr Asp Val Leu Glu Ala Leu Asn Met Glu Lys Met  
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 70 75 80  
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 Ser Thr Asp Gln Glu Ser Ala Glu Glu Ile Pro Ile Leu Ile Ile Glu

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agc tat ttc ctg act att cca tat gaa gaa tgt aaa agg agg agg agt			680
Ser Tyr Phe Leu Thr Ile Pro Tyr Glu Glu Cys Lys Arg Arg Arg Ser			
115	120	125 130	
aca agg gtc tat cag cct cca gac tct ccg gga tac ttt gat ggc cat			728
Thr Arg Val Tyr Gln Pro Pro Asp Ser Pro Gly Tyr Phe Asp Gly His			
	135	140 145	
gtg tgg ccc atg tat cta aag tac aga caa gaa atg cag gac atc aca			776
Val Trp Pro Met Tyr Leu Lys Tyr Arg Gln Glu Met Gln Asp Ile Thr			
	150	155 160	
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Trp Glu Val Val Tyr Leu Asp Gly Thr Lys Ser Glu Glu Asp Leu Phe			
	165	170 175	
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Leu Gln Val Tyr Glu Asp Leu Ile Gln Glu Leu Ala Lys Gln Lys Cys			
	180	185 190	
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Met Lys  
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tca aca gac cag gaa agt gct gag gaa att ccc att tta atc atc gaa 584  
 Ser Thr Asp Gln Glu Ser Ala Glu Glu Ile Pro Ile Leu Ile Ile Glu  
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tct ccg gga tac ttt gat ggc cat gtg tgg ccc atg tat cta aag tac 680  
 Ser Pro Gly Tyr Phe Asp Gly His Val Trp Pro Met Tyr Leu Lys Tyr  
           115                          120                          125                          130

aga caa gaa atg cag gac atc aca tgg gaa gtt gtg tac ctg gat gga 728  
 Arg Gln Glu Met Gln Asp Ile Thr Trp Glu Val Val Tyr Leu Asp Gly  
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aca aaa tct gaa gag gac ctc ttt ttg caa gta tat gaa gat cta ata 776  
 Thr Lys Ser Glu Glu Asp Leu Phe Leu Gln Val Tyr Glu Asp Leu Ile  
                           150                          155                          160

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ccttccca atg tcc tcg gcc atc gaa agg aag agc ctg gac cct tca gag      710
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gaa cca gtg gat gag gtg ctg cag atc ccc cca tcc ctg ctg aca tgc      758
Glu Pro Val Asp Glu Val Leu Gln Ile Pro Pro Ser Leu Leu Thr Cys
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ggc ggc tgc cag cag aac atc ggg gac cgc tac ttc ctg aag gcc atc      806
Gly Gly Cys Gln Gln Asn Ile Gly Asp Arg Tyr Phe Leu Lys Ala Ile
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gac cag tac tgg cac gag gac tgc ctg agc tgc gac ctc tgt ggc tgc      854
Asp Gln Tyr Trp His Glu Asp Cys Leu Ser Cys Asp Leu Cys Gly Cys
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cgg ctg ggt gag gtg ggg cgg cgc ctc tac tac aaa ctg ggc cgg aag      902
Arg Leu Gly Glu Val Gly Arg Arg Leu Tyr Tyr Lys Leu Gly Arg Lys
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ctc tgc cgg aga gac tat ctc agg ctt ttt ggg caa gac ggt ctc tgc      950
Leu Cys Arg Arg Asp Tyr Leu Arg Leu Phe Gly Gln Asp Gly Leu Cys
              80              85              90

gca tcc tgt gac aag cgg att cgt gcc tat gag atg aca atg cgg gtg      998
Ala Ser Cys Asp Lys Arg Ile Arg Ala Tyr Glu Met Thr Met Arg Val
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aaa gac aaa gtg tat cac ctg gaa tgt ttc aag tgc gcc gcc tgt cag     1046
Lys Asp Lys Val Tyr His Leu Glu Cys Phe Lys Cys Ala Ala Cys Gln
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aag cat ttc tgt gta ggt gac aga tac ctc ctc atc aac tct gac ata     1094
Lys His Phe Cys Val Gly Asp Arg Tyr Leu Leu Ile Asn Ser Asp Ile

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ggggccccag gag atg ttg acc cag cag ggc atg gcg ctg cag aac tac	169
Met Leu Thr Gln Gln Gly Met Ala Leu Gln Asn Tyr	
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gac aac aag ctg gtc aaa tgc ata gag gag cta tgc cag aag cag gag	217
Asp Asn Lys Leu Val Lys Cys Ile Glu Glu Leu Cys Gln Lys Gln Glu	
15 20 25	

gag ctg tgc tgg cag atc cag cag gag gag gac aag aaa cag cgg ctg 265  
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cag aat gag gtg agg cag ctg aca gag aag ctg gcc tgc gtc aac gag 313  
 Gln Asn Glu Val Arg Gln Leu Thr Glu Lys Leu Ala Cys Val Asn Glu  
 45 50 55 60

aag ctg gcc cgc gtc aac gag aac ctg gca cgc aag att gcc tct tgc 361  
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agt aag ttc tac cag acc atc gcg gag acg gag gcc gcc tac ctc aag 409  
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 95 100 105

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 Arg Asp Ser \*  
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1108

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His Leu Ser Val Asn Leu Glu Tyr Ala Pro Thr Glu Gly Thr Leu Asp	
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Ile Lys Glu Asp Met Ser Glu Pro Gln Glu Lys Lys Leu Ser Glu Asn	
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Thr Asp Phe Leu Ala Pro Gly Val Ser Ser Phe Thr Asp Ser Asn Gln	
140 145 150	
caa gaa agt atc aca aag aga gag gaa aac caa gaa caa cct aga aat	830
Gln Glu Ser Ile Thr Lys Arg Glu Glu Asn Gln Glu Gln Pro Arg Asn	
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tat tca cat cat cag ttg aac agg agc agt aaa cat agc caa ggc cta	878
Tyr Ser His His Gln Leu Asn Arg Ser Ser Lys His Ser Gln Gly Leu	
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Arg Asp Gln Gly Asn Gln Glu Gln Asp Pro Asn Ile Ser Asn Gly Glu	
190 195 200	
gag gaa gaa gaa aaa gag cca ggt gaa gtt ggt acc cac aat gat aac	974
Glu Glu Glu Glu Lys Glu Pro Gly Glu Val Gly Thr His Asn Asp Asn	
205 210 215	
caa gaa aga aag aca gaa ttg ccc agg gag cat gct aac agc aag cag	1022
Gln Glu Arg Lys Thr Glu Leu Pro Arg Glu His Ala Asn Ser Lys Gln	
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Glu Glu Asp Asn Thr Gln Ser Asp Asp Ile Leu Glu Glu Ser Asp Gln	
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cca act caa gta agc aag atg cag gag gat gaa ttt gat cag ggt aac	1118
Pro Thr Gln Val Ser Lys Met Gln Glu Asp Glu Phe Asp Gln Gly Asn	
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Gln Glu Gln Glu Asp Asn Ser Asn Ala Glu Met Glu Glu Glu Asn Ala	
270 275 280	
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Ser Asn Val Asn Lys His Ile Gln Glu Thr Glu Trp Gln Ser Gln Glu	
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Gly Lys Thr Gly Leu Glu Ala Ile Ser Asn His Lys Glu Thr Glu Glu	
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Lys Thr Val Ser Glu Ala Leu Leu Met Glu Pro Thr Asp Asp Gly Asn	
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Thr Thr Pro Arg Asn His Gly Val Asp Asp Asp Gly Asp Asp Asp Gly	
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Asp Asp Gly Gly Thr Asp Gly Pro Arg His Ser Ala Ser Asp Asp Tyr	
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Phe Ile Pro Ser Gln Ala Phe Leu Glu Ala Glu Arg Ala Gln Ser Ile	
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Ala Tyr His Leu Lys Ile Glu Glu Gln Arg Glu Lys Val His Glu Asn	
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gaa aat ata ggt acc act gag cct gga gag cac caa gag gcc aag aaa	1550
Glu Asn Ile Gly Thr Thr Glu Pro Gly Glu His Gln Glu Ala Lys Lys	
395 400 405	
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Ala Glu Asn Ser Ser Asn Glu Glu Glu Thr Ser Ser Glu Gly Asn Met	
410 415 420 425	
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Arg Val His Ala Val Asp Ser Cys Met Ser Phe Gln Cys Lys Arg Gly	
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cac atc tgt aag gca gac caa cag gga aaa cct cac tgt gtc tgc cag	1694
His Ile Cys Lys Ala Asp Gln Gln Gly Lys Pro His Cys Val Cys Gln	
445 450 455	
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Asp Pro Val Thr Cys Pro Pro Thr Lys Pro Leu Asp Gln Val Cys Gly	
460 465 470	
act gac aat cag acc tat gct agt tcc tgt cat cta ttc gct act aaa	1790
Thr Asp Asn Gln Thr Tyr Ala Ser Ser Cys His Leu Phe Ala Thr Lys	
475 480 485	
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Cys Arg Leu Glu Gly Thr Lys Lys Gly His Gln Leu Gln Leu Asp Tyr	
490 495 500 505	
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Phe Gly Ala Cys Lys Ser Ile Pro Thr Cys Thr Asp Phe Glu Val Ile	
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Gln Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Ile Leu Met Gln	
525 530 535	
ctt tat gaa gcc aac tct gaa cac gct ggt tat cta aat gag aag cag	1982
Leu Tyr Glu Ala Asn Ser Glu His Ala Gly Tyr Leu Asn Glu Lys Gln	
540 545 550	
aga aat aaa gtc aag aaa att tac ctg gat gaa aag agg ctt ttg gct	2030
Arg Asn Lys Val Lys Lys Ile Tyr Leu Asp Glu Lys Arg Leu Leu Ala	
555 560 565	
ggg gac cat ccc att gat ctt ctc tta agg gac ttt aag aaa aac tac	2078
Gly Asp His Pro Ile Asp Leu Leu Leu Arg Asp Phe Lys Lys Asn Tyr	
570 575 580 585	
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His Met Tyr Val Tyr Pro Val His Trp Gln Phe Ser Glu Leu Asp Gln	
590 595 600	

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 His Pro Met Asp Arg Val Leu Thr His Ser Glu Leu Ala Pro Leu Arg  
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 Ala Ser Leu Val Pro Met Glu His Cys Ile Thr Arg Phe Phe Glu Glu  
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 ctatgcttca gtaattccca taagctggcg gtcgcctctg ggtctaaact cccaaggcct 180  
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 Phe Arg Arg Glu Arg Pro Glu Asp Leu Glu Leu Leu Pro Gly Asp Val  
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 Leu Val Val Ser Arg Ala Ala Leu Gln Ala Leu Gly Val Ala Glu Gly  
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 Arg Thr Arg Gln Arg Gly Asp Phe Pro Gly Thr Tyr Val Glu Phe Leu  
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 Gly Pro Val Ala Leu Ala Arg Pro Gly Pro Arg Pro Arg Gly Pro Arg  
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 Pro Leu Pro Ala Arg Pro Arg Asp Gly Ala Pro Glu Pro Gly Leu Thr  
 95 100 105 110  
 ctc ccc gac ttg ccc gag cag ttc tcc cca cct gat gtg gct ccc cct 1464  
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 115 120 125  
 ctt ctg gtg aag ctt gtg gag gcc att gaa agg aca ggg ctg gac agc 1512  
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 160 165 170



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Lys Ser Phe Leu Leu Ala Leu Pro Ala Pro Leu Val Thr Pro Glu Ala	
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Ser Ala Glu Ala Arg Arg Ala Leu Arg Glu Ala Ala Gly Pro Val Gly	
195 200 205	
ccg gcg ctg gag cca ccg acg ctg ccg ctg cac cgc gcg ctc acg ctg	1752
Pro Ala Leu Glu Pro Pro Thr Leu Pro Leu His Arg Ala Leu Thr Leu	
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225 230 235	
ctg ggt ccc gcg gtc cgg gcc ctg ggc gcc acc ttt ggg ccg ctg ctg	1848
Leu Gly Pro Ala Val Arg Ala Leu Gly Ala Thr Phe Gly Pro Leu Leu	
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Leu Arg Ala Pro Pro Pro Pro Ser Ser Pro Pro Pro Gly Gly Ala Pro	
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Asp Gly Ser Glu Pro Ser Pro Asp Phe Pro Ala Leu Leu Val Glu Lys	
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Pro Pro Lys Pro Pro Lys Ala Lys Pro Ala Ser Thr Val Leu Ala Asn	
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Gly Gly Ser Pro Pro Ser Leu Gln Asp Ala Glu Trp Tyr Trp Gly Asp	
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Ile Ser Arg Glu Glu Val Asn Glu Lys Leu Arg Asp Thr Pro Asp Gly	
335 340 345 350	
acc ttc cta gtc cga gat gct tct agc aag atc cag ggc gag tac acg	2184
Thr Phe Leu Val Arg Asp Ala Ser Ser Lys Ile Gln Gly Glu Tyr Thr	
355 360 365	
ctg acc ctc agg aaa ggc ggg aac aat aag ctg atc aag gtc ttc cac	2232
Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu Ile Lys Val Phe His	
370 375 380	
cga gat ggg cac tat ggc ttc tca gag cca ctc acc ttc tgc tcc gtt	2280
Arg Asp Gly His Tyr Gly Phe Ser Glu Pro Leu Thr Phe Cys Ser Val	
385 390 395	
gtg gac ctc atc aat cac tac cgc cac gag tct ctg gcc cag tac aat	2328
Val Asp Leu Ile Asn His Tyr Arg His Glu Ser Leu Ala Gln Tyr Asn	
400 405 410	
gcc aag ctg gac aca cgg ctc ctc tac cct gtg tcc aaa tac cag cag	2376
Ala Lys Leu Asp Thr Arg Leu Leu Tyr Pro Val Ser Lys Tyr Gln Gln	
415 420 425 430	

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aag gtc tat cac cag cag tac cag gac aag agc cgc gag tat gac cag Lys Val Tyr His Gln Gln Tyr Gln Asp Lys Ser Arg Glu Tyr Asp Gln 450 455 460	2472
ctt tat gaa gag tac aca cgg acc tcc cag gag ctg cag atg aag cgt Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu Leu Gln Met Lys Arg 465 470 475	2520
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agc cag act caa gag aaa tgc agc aag gaa tac ctg gag cgc ttc cgg Ser Gln Thr Gln Glu Lys Cys Ser Lys Glu Tyr Leu Glu Arg Phe Arg 495 500 505 510	2616
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ctc atg gag gac gag gac gat ctc ccg cac cac gag gaa cgc act tgg Leu Met Glu Asp Glu Asp Asp Leu Pro His His Glu Glu Arg Thr Trp 610 615 620	2952
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tac gcc tgc tcc gtg gta gtg gac ggc gac acc aag cac tgc gtc atc Tyr Ala Cys Ser Val Val Val Asp Gly Asp Thr Lys His Cys Val Ile 655 660 665 670	3096
tac cgc acg gcc acc ggc ttc ggc ttc gcg gag ccc tac aac ctg tac Tyr Arg Thr Ala Thr Gly Phe Gly Phe Ala Glu Pro Tyr Asn Leu Tyr 675 680 685	3144

ggg tcg ctg aag gag ctg gtg ctg cac tac cag cac gcc tcg ctg gtg 3192  
 Gly Ser Leu Lys Glu Leu Val Leu His Tyr Gln His Ala Ser Leu Val  
                   690                                  695                                  700

cag cac aac gac gcg ctc acc gtc acc ctg gcg cac cca gtg cgc gcc 3240  
 Gln His Asn Asp Ala Leu Thr Val Thr Leu Ala His Pro Val Arg Ala  
                   705                                  710                                  715

ccg ggc ccc ggc ccg ccg cct gcc gcc cgc tga gcaccgag gacccgcccc 3291  
 Pro Gly Pro Gly Pro Pro Pro Ala Ala Arg \*  
                   720                                  725

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 taattaaact cgcaggccag gcacggtggc tcatgcctgt aatcccagca ctttgggagg 3951  
 ccaagacggg cggatctttt gaggtcggga gttggaggcc agcctggcca aaatggcaaa 4011  
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 ggcaaccaag taatcttaaa tctggggaaa gaaagatgcc agctgagaga aacaggactc 240  
 aagctttact tacctggg atg gac tct gcc aga cac cat ata agc cac tct 291  
                   Met Asp Ser Ala Arg His His Ile Ser His Ser

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Thr Ser Ala Gly Pro Ile Pro Ser Gln Lys Glu Glu Glu Met Thr Glu				
	15	20	25	
tcc cag gga aca gta aca ttc aaa gat gtg gct atc gac ttc act cag				387
Ser Gln Gly Thr Val Thr Phe Lys Asp Val Ala Ile Asp Phe Thr Gln				
	30	35	40	
gag gag tgg aag aga ttg gat cct gct cag aga aaa ctg tac cgg aat				435
Glu Glu Trp Lys Arg Leu Asp Pro Ala Gln Arg Lys Leu Tyr Arg Asn				
	45	50	55	
gtg atg cta gaa aac tat aac aac tta atc aca gta ggc tat ccg ttc				483
Val Met Leu Glu Asn Tyr Asn Asn Leu Ile Thr Val Gly Tyr Pro Phe				
	60	65	70	75
acc aaa cct gat gtg att ttc aaa ttg gag caa gaa gaa gaa cca tgg				531
Thr Lys Pro Asp Val Ile Phe Lys Leu Glu Gln Glu Glu Glu Pro Trp				
	80	85	90	
gtg atg gag gaa gaa gta tta agg aga cac tgg caa gga gaa ata tgg				579
Val Met Glu Glu Glu Val Leu Arg Arg His Trp Gln Gly Glu Ile Trp				
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gga gtt gat gag cat cag aaa aac cag gac aga ctt ttg aga caa gtt				627
Gly Val Asp Glu His Gln Lys Asn Gln Asp Arg Leu Leu Arg Gln Val				
	110	115	120	
gaa gtt aaa ttc cag aaa aca ctg act gaa gaa aaa ggc aat gaa tgt				675
Glu Val Lys Phe Gln Lys Thr Leu Thr Glu Glu Lys Gly Asn Glu Cys				
	125	130	135	
caa aag aaa ttt gca aat gta ttt cct ctg aac tct gat ttt ttc cct				723
Gln Lys Lys Phe Ala Asn Val Phe Pro Leu Asn Ser Asp Phe Phe Pro				
	140	145	150	155
tcc aga cac aat ctc tat gag tat gac tta ttt gga aag tgt tta gaa				771
Ser Arg His Asn Leu Tyr Glu Tyr Asp Leu Phe Gly Lys Cys Leu Glu				
	160	165	170	
cat aat ttt gac tgt cat aat aat gtg aaa tgc ctt atg aga aag gag				819
His Asn Phe Asp Cys His Asn Asn Val Lys Cys Leu Met Arg Lys Glu				
	175	180	185	
cat tgt gaa tat aat gaa cct gtg aaa tca tat ggt aat agc tca tcc				867
His Cys Glu Tyr Asn Glu Pro Val Lys Ser Tyr Gly Asn Ser Ser Ser				
	190	195	200	
cat ttt gtc att acc ccc ttt aag tgt aat cat tgt gga aaa ggc ttc				915
His Phe Val Ile Thr Pro Phe Lys Cys Asn His Cys Gly Lys Gly Phe				
	205	210	215	
aat cag act ttg gac ctc atc aga cat ctg aga att cat act gga gag				963
Asn Gln Thr Leu Asp Leu Ile Arg His Leu Arg Ile His Thr Gly Glu				
	220	225	230	235
aag ccc tat gaa tgt agt aac tgt aga aaa gcc ttc agt cac aag gaa				1011
Lys Pro Tyr Glu Cys Ser Asn Cys Arg Lys Ala Phe Ser His Lys Glu				
	240	245	250	
aaa ctt att aaa cat tat aaa att cac agt agg gag cag tct tac aaa				1059
Lys Leu Ile Lys His Tyr Lys Ile His Ser Arg Glu Gln Ser Tyr Lys				

255					260					265						
tgt	aat	gaa	tgt	ggt	aaa	gct	ttc	att	aaa	atg	tca	aat	ctc	att	aga	1107
Cys	Asn	Glu	Cys	Gly	Lys	Ala	Phe	Ile	Lys	Met	Ser	Asn	Leu	Ile	Arg	
270					275					280						
cat	caa	aga	att	cat	act	gga	gag	aag	ccc	tat	gca	tgt	aag	gaa	tgt	1155
His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Ala	Cys	Lys	Glu	Cys	
285					290					295						
gag	aag	tcc	ttc	agc	cag	aaa	tca	aat	ctt	att	gat	cat	gaa	aaa	att	1203
Glu	Lys	Ser	Phe	Ser	Gln	Lys	Ser	Asn	Leu	Ile	Asp	His	Glu	Lys	Ile	
300					305					310					315	
cat	act	gga	gag	aaa	cct	tat	gaa	tgt	aat	gag	tgt	gga	aaa	gca	ttc	1251
His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Asn	Glu	Cys	Gly	Lys	Ala	Phe	
320					325					330						
agc	cag	aag	caa	agc	ctc	att	gca	cat	cag	aaa	gtt	cat	act	ggg	gag	1299
Ser	Gln	Lys	Gln	Ser	Leu	Ile	Ala	His	Gln	Lys	Val	His	Thr	Gly	Glu	
335					340					345						
aaa	cct	tat	gca	tgt	aat	gaa	tgt	ggt	aaa	gcc	ttc	cct	cga	att	gca	1347
Lys	Pro	Tyr	Ala	Cys	Asn	Glu	Cys	Gly	Lys	Ala	Phe	Pro	Arg	Ile	Ala	
350					355					360						
tcc	ctt	gct	ctt	cat	atg	aga	agt	cat	aca	gga	gaa	aaa	cct	tat	aaa	1395
Ser	Leu	Ala	Leu	His	Met	Arg	Ser	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	
365					370					375						
tgt	gat	aaa	tgt	ggt	aaa	gcc	ttc	tct	cag	ttt	tcc	atg	ctt	att	ata	1443
Cys	Asp	Lys	Cys	Gly	Lys	Ala	Phe	Ser	Gln	Phe	Ser	Met	Leu	Ile	Ile	
380					385					390					395	
cat	gtt	aga	att	cat	aca	ggt	gaa	aaa	ccc	tat	gaa	tgt	aat	gag	tgt	1491
His	Val	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Asn	Glu	Cys	
400					405					410						
gga	aaa	gcc	ttc	tct	caa	agc	tca	gcc	ctt	act	gta	cat	atg	aga	agt	1539
Gly	Lys	Ala	Phe	Ser	Gln	Ser	Ser	Ala	Leu	Thr	Val	His	Met	Arg	Ser	
415					420					425						
cac	act	ggt	gag	aaa	ccc	tat	gaa	tgt	aag	gaa	tgc	aga	aaa	gcc	ttc	1587
His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Glu	Cys	Arg	Lys	Ala	Phe	
430					435					440						
agc	cac	aag	aaa	aac	ttc	att	aca	cac	cag	aaa	att	cat	act	aga	gag	1635
Ser	His	Lys	Lys	Asn	Phe	Ile	Thr	His	Gln	Lys	Ile	His	Thr	Arg	Glu	
445					450					455						
aaa	cct	tat	gag	tgt	aat	gaa	tgt	ggg	aaa	gct	ttt	ata	cag	atg	tca	1683
Lys	Pro	Tyr	Glu	Cys	Asn	Glu	Cys	Gly	Lys	Ala	Phe	Ile	Gln	Met	Ser	
460					465					470					475	
aat	ctt	gtt	aga	cac	cag	aga	att	cat	act	ggg	gaa	aaa	ccc	tat	ata	1731
Asn	Leu	Val	Arg	His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Ile	
480					485					490						
tgt	aag	gaa	tgt	ggg	aaa	gcc	ttt	agc	cag	aat	tca	aat	ctc	att	gct	1779
Cys	Lys	Glu	Cys	Gly	Lys	Ala	Phe	Ser	Gln	Asn	Ser	Asn	Leu	Ile	Ala	
495					500					505						
cat	gaa	aaa	att	cat	tct	gga	gag	aaa	ccc	tat	gaa	tgc	aat	gaa	tgt	1827
His	Glu	Lys	Ile	His	Ser	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Asn	Glu	Cys	

510	515	520	
ggt aaa gcc ttc agc caa aag caa aac ttc att aca cat caa aaa gtt Gly Lys Ala Phe Ser Gln Lys Gln Asn Phe Ile Thr His Gln Lys Val 525 530 535			1875
cat act gga gag aaa cct tat gat tgt aat gaa tgt ggt aaa gcc ttc His Thr Gly Glu Lys Pro Tyr Asp Cys Asn Glu Cys Gly Lys Ala Phe 540 545 550 555			1923
tct caa att gca tcc ctt acc ctt cat ttg aga agt cat aca ggg gaa Ser Gln Ile Ala Ser Leu Thr Leu His Leu Arg Ser His Thr Gly Glu 560 565 570			1971
aag cct tat gaa tgt gat aaa tgt ggt aaa gcc ttc tct cag tgc tca Lys Pro Tyr Glu Cys Asp Lys Cys Gly Lys Ala Phe Ser Gln Cys Ser 575 580 585			2019
ctg ctt aat tta cat atg aga agt cac aca ggt gag aag ccc tat gta Leu Leu Asn Leu His Met Arg Ser His Thr Gly Glu Lys Pro Tyr Val 590 595 600			2067
tgt aat gaa tgt ggg aaa gcc ttc tct caa aga act tcc ctt att gtg Cys Asn Glu Cys Gly Lys Ala Phe Ser Gln Arg Thr Ser Leu Ile Val 605 610 615			2115
cac atg aga ggc cat aca ggt gaa aaa ccc tat gaa tgt aat aaa tgt His Met Arg Gly His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Lys Cys 620 625 630 635			2163
gga aaa gcc ttc tcc caa agc tca tcc ctt act ata cat ata cga gga Gly Lys Ala Phe Ser Gln Ser Ser Ser Leu Thr Ile His Ile Arg Gly 640 645 650			2211
cat aca ggt gag aaa ccc tat gaa tgt aag gaa tgc aga aaa gcc ttc His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Arg Lys Ala Phe 655 660 665			2259
agc cac aag aaa aac ttc att aca cac cag aaa att cat act aga gag Ser His Lys Lys Asn Phe Ile Thr His Gln Lys Ile His Thr Arg Glu 670 675 680			2307
aaa cct tta agt gta atc att gtg gaa aag gct tca atc aga ctt tgg Lys Pro Leu Ser Val Ile Ile Val Glu Lys Ala Ser Ile Arg Leu Trp 685 690 695			2355
acc tca tca gac atc tga gaattc atactggaga gaagccctat gaatgtagta Thr Ser Ser Asp Ile * 700 705			2409
actgtagaaa agccttcagt cacaaggaaa aacttattaa acattataaa gtcgacgcgg			2469
ccgcgaattc ggatcctcga gagatctctt tttttggggtt tgggtggggta tcttcatcat			2529
cgaatagata gttatgccat cagcattcag aggggggctg t			2570

&lt;210&gt; 434

&lt;211&gt; 1698

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (419) .. (1195)

&lt;400&gt; 434

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ggtacctgtc cggaattccc gggctcgacgt ttcgtggggc ggcgggagtg cgggtgggcg      60
tttaaagggg ccttcggcac ccaggctcggg tcgccgccgg gactgctgac ggggagggct      120
aggtagccct gggagtcggg atctagaagg tagaggagaa gcggggctgt ctgacccccg      180
gaggtgacaa ggggagaggg gctgtgtgaa taccctccat gggcagtaat gggatgacta      240
tccccagggg gcattgcgaa ggagagaggc ggctgaggga ctgcactttc tggggccccc      300
cgggagagtc agagggcagt taagagggat cacaggcccc gcttggtact gtcactcccc      360

ttcccactcc ctgctctcag cattctgtca cctccctacc ccgtcgcggg gccccagcc      418
atg gcc aga cct ccc gtg ccc ggt tcg gtg gtt gtc cca aac tgg cac      466
Met Ala Arg Pro Pro Val Pro Gly Ser Val Val Val Pro Asn Trp His
  1             5             10             15

gag agt gcc gag ggc aag gag tac ctg gct tgc att ctg cgc aag aac      514
Glu Ser Ala Glu Gly Lys Glu Tyr Leu Ala Cys Ile Leu Arg Lys Asn
          20             25             30

cgc cgg cgg gtg ttt ggg ctg ctt gag cgg cca gtg ctg ctg ccg cct      562
Arg Arg Arg Val Phe Gly Leu Leu Glu Arg Pro Val Leu Leu Pro Pro
          35             40             45

gtg tcc att gac act gcc agc tac aag atc ttt gtg tcc ggg aag agt      610
Val Ser Ile Asp Thr Ala Ser Tyr Lys Ile Phe Val Ser Gly Lys Ser
          50             55             60

ggg gtg ggc aag acg gcg ctg gtg gcc aag ctg gct ggc ctg gag gtg      658
Gly Val Gly Lys Thr Ala Leu Val Ala Lys Leu Ala Gly Leu Glu Val
          65             70             75             80

cct gtg gtg cac cac gag acc acc ggc atc cag acc acc gtg gta ttt      706
Pro Val Val His His Glu Thr Thr Gly Ile Gln Thr Thr Val Val Phe
          85             90             95

tgg cca gcc aag ctg cag gcc agc agc cgt gtc gtc atg ttt cgt ttt      754
Trp Pro Ala Lys Leu Gln Ala Ser Ser Arg Val Val Met Phe Arg Phe
          100             105             110

gag ttc tgg gac tgt gga gag tct gca ctc aaa aag ttc gat cat atg      802
Glu Phe Trp Asp Cys Gly Glu Ser Ala Leu Lys Lys Phe Asp His Met
          115             120             125

ctg ctg gct tgc atg gag aac aca gat gcc ttc ctc ttc ctc ttc tcc      850
Leu Leu Ala Cys Met Glu Asn Thr Asp Ala Phe Leu Phe Leu Phe Ser
          130             135             140

ttc act gac cgt gcc tcc ttt gaa gac ctc cct gga cag ctg gcc cgc      898
Phe Thr Asp Arg Ala Ser Phe Glu Asp Leu Pro Gly Gln Leu Ala Arg
          145             150             155             160

ata gca ggt gag gcc cct ggt gtc gtc agg atg gtc atc ggc tcc aaa      946
Ile Ala Gly Glu Ala Pro Gly Val Val Arg Met Val Ile Gly Ser Lys
          165             170             175

ttt gac cag tac atg cac acg gac gtg ccc gag cgg gac ctc aca gcc      994
Phe Asp Gln Tyr Met His Thr Asp Val Pro Glu Arg Asp Leu Thr Ala

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180	185	190	
ttc cgg cag gcc tgg gag ctg ccc ctg cta cgg gtg aag agt gtg ccg			1042
Phe Arg Gln Ala Trp Glu Leu Pro Leu Leu Arg Val Lys Ser Val Pro			
195	200	205	
ggg cgg cgg ctg gct gat ggg cgc aca ctg gac ggg cgg gct ggg ctg			1090
Gly Arg Arg Leu Ala Asp Gly Arg Thr Leu Asp Gly Arg Ala Gly Leu			
210	215	220	
gcc gac gtt gcc cac ata ctc aat ggc ctt gct gag cag ctg tgg cac			1138
Ala Asp Val Ala His Ile Leu Asn Gly Leu Ala Glu Gln Leu Trp His			
225	230	235	240
cag gac cag gtg gcg gct ggc ctg ctt ccc aac ccc cca gag agt gct			1186
Gln Asp Gln Val Ala Ala Gly Leu Leu Pro Asn Pro Pro Glu Ser Ala			
245	250	255	
cct gaa tga gtcacga gtggttgct gtgatccac cccaaccct caggctctga			1242
Pro Glu *			
catagggctg gaggtggtggg caggaacatg gatcctatct ggaggactgg ccagcatggc			1302
ctgatcaggg aggatgtggc cagagaaggc ccacccgcga gcagcgcttt ccttgcagaa			1362
ttcatggcag ggaggtggtgg accaaggccc tgagctcgaa catctcccgt ggcctttccc			1422
cctttggcag caccgatgga ggatgactgg gagaggggggt gcctctcaag ttacttcaat			1482
caagaacctg tattggttga ggtgacacca tctgttgtaa cagataaacc ccgaaatccc			1542
agtgtgaac tccagagacg tggtcgttct cacgtaggcc tcagctcggg aggaggtgac			1602
agtgggcgtg gggctctgct ccaggcgctc ctgcagagac ccagccccag agaccctacc			1662
ctgcccagtt gccctagggg gtcagcacc agtcag			1698

&lt;210&gt; 435

&lt;211&gt; 2188

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (349) .. (1425)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (2188)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 435

gctggtcacc tgtggtaccg gaccggaatt cccgggtcga cccacgcgctc cgggtccagca	60
agttgggggaa atgcaacagc ttgaagtggc tctagtggcc cagagtcaga gctggaatag	120
gaattggcat ctgctggctg tgtggcccct gcttgcccta gtgagttacc atttctctgt	180
ccctacggng gagcctttgg gggtattgtg agttcatggg aggagcgtgt aagcaccggc	240

acagcatcag cccatgagag tgctcctggc ctgagagggg aaggggtcagg gcagctcagg 300

agaccctaga cctgcatagt gatcccccca ccaggaaggc cccacaag atg ctc acc 357  
Met Leu Thr  
1

tgc cct ccc tat ccc tgt ccc cag ctg gag gag cac cgg aat tca cag 405  
Cys Pro Pro Tyr Pro Cys Pro Gln Leu Glu Glu His Arg Asn Ser Gln  
5 10 15

aag cag atg aag ctc cta cag aaa aag cag agc cag ctg gtg caa gag 453  
Lys Gln Met Lys Leu Leu Gln Lys Lys Gln Ser Gln Leu Val Gln Glu  
20 25 30 35

aag gac cac ctg cgc ggt gag cac agc aag gcc gtc ctg gcc cgc agc 501  
Lys Asp His Leu Arg Gly Glu His Ser Lys Ala Val Leu Ala Arg Ser  
40 45 50

aag ctt gag agc cta tgc cgt gag ctg cag cgg cac aac cgc tcc ctc 549  
Lys Leu Glu Ser Leu Cys Arg Glu Leu Gln Arg His Asn Arg Ser Leu  
55 60 65

aag gaa gaa ggt gtg cag cgg gcc cgg gag gag gag gag aag cgc aag 597  
Lys Glu Glu Gly Val Gln Arg Ala Arg Glu Glu Glu Glu Lys Arg Lys  
70 75 80

gag gtg acc tcg cac ttc cag gtg aca ctg aat gac att cag ctg cag 645  
Glu Val Thr Ser His Phe Gln Val Thr Leu Asn Asp Ile Gln Leu Gln  
85 90 95

atg gaa cag cac aat gag cgc aac tcc aag ctg cgc caa gag aac atg 693  
Met Glu Gln His Asn Glu Arg Asn Ser Lys Leu Arg Gln Glu Asn Met  
100 105 110 115

gag ctg gct gag agg ctc aag aag ctg att gag cag tat gag ctg cgc 741  
Glu Leu Ala Glu Arg Leu Lys Lys Leu Ile Glu Gln Tyr Glu Leu Arg  
120 125 130

gag gag cat atc gac aaa gtc ttc aaa cac aag gac cta caa cag cag 789  
Glu Glu His Ile Asp Lys Val Phe Lys His Lys Asp Leu Gln Gln Gln  
135 140 145

ctg gtg gat gcc aag ctc cag cag gcc cag gag atg cta aag gag gca 837  
Leu Val Asp Ala Lys Leu Gln Gln Ala Gln Glu Met Leu Lys Glu Ala  
150 155 160

gaa gag cgg cac cag cgg gag aag gat ttt ctc ctg aaa gag gca gta 885  
Glu Glu Arg His Gln Arg Glu Lys Asp Phe Leu Leu Lys Glu Ala Val  
165 170 175

gag tcc cag agg atg tgt gag ctg atg aag cag caa gag acc cac ctg 933  
Glu Ser Gln Arg Met Cys Glu Leu Met Lys Gln Gln Glu Thr His Leu  
180 185 190 195

aag caa cag ctt gcc cta tac aca gag aag ttt gag gag ttc cag aac 981  
Lys Gln Gln Leu Ala Leu Tyr Thr Glu Lys Phe Glu Glu Phe Gln Asn  
200 205 210

aca ctt tcc aaa agc agc gag gta ttc acc aca ttc aag cag gag atg 1029  
Thr Leu Ser Lys Ser Ser Glu Val Phe Thr Thr Phe Lys Gln Glu Met  
215 220 225

gaa aag atg act aag aag atc aag aag ctg gag aaa gaa acc acc atg 1077  
Glu Lys Met Thr Lys Lys Ile Lys Lys Leu Glu Lys Glu Thr Thr Met

230	235	240	
tac cgg tcc cgg tgg gag agc agc aac aag gcc ctg ctt gag atg gct			1125
Tyr Arg Ser Arg Trp Glu Ser Ser Asn Lys Ala Leu Leu Glu Met Ala			
245	250	255	
gag gag aaa aca gtc cgg gat aaa gaa ctg gag ggc ctg cag gta aaa			1173
Glu Glu Lys Thr Val Arg Asp Lys Glu Leu Glu Gly Leu Gln Val Lys			
260	265	270	275
atc caa cgg ctg gag aag ctg tgc cgg gca ctg cag aca gag cgc aat			1221
Ile Gln Arg Leu Glu Lys Leu Cys Arg Ala Leu Gln Thr Glu Arg Asn			
280	285	290	
gac ctg aac aag agg gta cag gac ctg agt gct ggt ggc cag ggc tcc			1269
Asp Leu Asn Lys Arg Val Gln Asp Leu Ser Ala Gly Gly Gln Gly Ser			
295	300	305	
ctc act gac agt ggc cct gag agg agg cca gag ggg cct ggg gct caa			1317
Leu Thr Asp Ser Gly Pro Glu Arg Arg Pro Glu Gly Pro Gly Ala Gln			
310	315	320	
gca ccc agc tcc ccc agg gtc aca gaa gcg cct tgc tac cca gga gca			1365
Ala Pro Ser Ser Pro Arg Val Thr Glu Ala Pro Cys Tyr Pro Gly Ala			
325	330	335	
ccg agc aca gaa gca tca ggc cag act ggg cct caa gag ccc acc tcc			1413
Pro Ser Thr Glu Ala Ser Gly Gln Thr Gly Pro Gln Glu Pro Thr Ser			
340	345	350	355
gcc agg gcc tag aga gcctggtgtt gggatcatgct gggaaggag cggcagccca			1468
Ala Arg Ala *			
gccaggcctg gcccataaaa ggctcccatg ctgagcagcc cattgctgaa gccaggatgt			1528
tctgacctgg ctggcatctg gcacttgcaa ttttggattt tgtgggtcag ttttacgtac			1588
atagggcatt ttgcaaggcc ttgcaaatgc atttatacct gtaagtgtac agtgggcttg			1648
cattggggat gggggtgtgt acagatgaag tcagtggctt gtctgtgagc tgaagagtct			1708
tgagaggggc tgtcatctgt agctgccatc acagtgagtt ggcagaagtg acttaagcat			1768
ttctctgtct ggtgtgaggc tcagaccctt ccctgccctt cagagctcaa gacaagtaat			1828
gcacccaggt cttgactgca tttgtcttgt gagcagggct tgcttggtca gctcaggccc			1888
tcctagctgc tctggaggct cctttgatct tctagacctg gaaaagggtgt ccctaggcag			1948
agccctggca gggcgctcag agctggggat ttctgcctg gaacaaggga cctggagaat			2008
gtttttgcgt gggatgatgt gctgggtcagg agcccttgg gcacgccttc ccctgccctt			2068
tggtagtgcc aggaccaggc caatgatgct tctcagtagc cttatcattc acaggtgcct			2128
ctctagcctg cacaaatgat tgacaagaga tcacccaaag gattatttct gaagggtgtg			2188

&lt;210&gt; 436

&lt;211&gt; 2903

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (118) .. (2667)

&lt;400&gt; 436

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agaccacacg ggccggaatt cccgggtcga cgatttcgtc cagcccaagc ctgagcctga      60

gcccgccccg aggtccccgc cccgcccgcc tggtctcttc gccgcggagc cgccaag      117
atg ggg gac aag aaa gat gac aag gac tca ccc aag aag aac aag ggc      165
Met Gly Asp Lys Lys Asp Asp Lys Asp Ser Pro Lys Lys Asn Lys Gly
   1             5             10             15

aag gag cgc cgg gac ctg gat gac ctc aag aag gag gtg gct atg aca      213
Lys Glu Arg Arg Asp Leu Asp Asp Leu Lys Lys Glu Val Ala Met Thr
           20             25             30

gag cac aag atg tca gtg gaa gag gtc tgc cgg aaa tac aac aca gac      261
Glu His Lys Met Ser Val Glu Glu Val Cys Arg Lys Tyr Asn Thr Asp
           35             40             45

tgt gtg cag ggt ttg acc cac agc aaa gcc cag gag atc ctg gcc cgg      309
Cys Val Gln Gly Leu Thr His Ser Lys Ala Gln Glu Ile Leu Ala Arg
           50             55             60

gat ggg cct aac gca ctc acg cca ccg cct acc acc cca gag tgg gtc      357
Asp Gly Pro Asn Ala Leu Thr Pro Pro Pro Thr Thr Pro Glu Trp Val
           65             70             75             80

aag ttt tgc cgg cag ctc ttc ggg ggc ttc tcc atc ctg ctg tgg atc      405
Lys Phe Cys Arg Gln Leu Phe Gly Gly Phe Ser Ile Leu Leu Trp Ile
           85             90             95

ggg gct atc ctc tgc ttc ctg gcc tac ggt atc cag gcg ggc acc gag      453
Gly Ala Ile Leu Cys Phe Leu Ala Tyr Gly Ile Gln Ala Gly Thr Glu
           100            105            110

gac gac ccc tct ggt gac aac ctg tac ctg ggc atc gtg ctg gcg gcc      501
Asp Asp Pro Ser Gly Asp Asn Leu Tyr Leu Gly Ile Val Leu Ala Ala
           115            120            125

gtg gtg atc atc act ggc tgc ttc tcc tac tac cag gag gcc aag agc      549
Val Val Ile Ile Thr Gly Cys Phe Ser Tyr Tyr Gln Glu Ala Lys Ser
           130            135            140

tcc aag atc atg gag tcc ttc aag aac atg gtg ccc cag caa gcc ctg      597
Ser Lys Ile Met Glu Ser Phe Lys Asn Met Val Pro Gln Gln Ala Leu
           145            150            155            160

gtg atc cgg gaa ggt gag aag atg cag gtg aac gct gag gag gtg gtg      645
Val Ile Arg Glu Gly Glu Lys Met Gln Val Asn Ala Glu Glu Val Val
           165            170            175

gtc ggg gac ctg gtg gag atc aag ggt gga gac cga gtg cca gct gac      693
Val Gly Asp Leu Val Glu Ile Lys Gly Gly Asp Arg Val Pro Ala Asp
           180            185            190

ctg cgg atc atc tca gcc cac ggc tgc aag gtg gac aac tcc tcc ctg      741
Leu Arg Ile Ile Ser Ala His Gly Cys Lys Val Asp Asn Ser Ser Leu
           195            200            205

act ggc gaa tcc gag ccc cag act cgc tct ccc gac tgc act cac gac      789
Thr Gly Glu Ser Glu Pro Gln Thr Arg Ser Pro Asp Cys Thr His Asp

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210	215	220	
aac ccc ttg gag act cgg aac atc acc ttc ttt tcc acc aac tgt gtg Asn Pro Leu Glu Thr Arg Asn Ile Thr Phe Phe Ser Thr Asn Cys Val 225 230 235 240			837
gaa ggc acg gct cgg ggc gtg gtg gtg gcc acg ggc gac cgc act gtc Glu Gly Thr Ala Arg Gly Val Val Val Ala Thr Gly Asp Arg Thr Val 245 250 255			885
atg ggc cgt atc gcc acc ctg gca tca ggg ctg gag gtg ggc aag acg Met Gly Arg Ile Ala Thr Leu Ala Ser Gly Leu Glu Val Gly Lys Thr 260 265 270			933
ccc atc gcc atc gag att gag cac ttc atc cag ctc atc acc ggc gtg Pro Ile Ala Ile Glu Ile Glu His Phe Ile Gln Leu Ile Thr Gly Val 275 280 285			981
gct gtc ttc ctg ggt gtc tcc ttc ttc atc ctc tcc ctc att ctc gga Ala Val Phe Leu Gly Val Ser Phe Phe Ile Leu Ser Leu Ile Leu Gly 290 295 300			1029
tac acc tgg ctt gag gct gtc atc ttc ctc atc ggc atc atc gtg gcc Tyr Thr Trp Leu Glu Ala Val Ile Phe Leu Ile Gly Ile Ile Val Ala 305 310 315 320			1077
aat gtc cca gag ggt ctg ctg gcc act gtc act gtg tgt ctg acg ctg Asn Val Pro Glu Gly Leu Leu Ala Thr Val Thr Val Cys Leu Thr Leu 325 330 335			1125
acc gcc aag cgc atg gcc cgg aag aac tgc ctg gtg aag aac ctg gag Thr Ala Lys Arg Met Ala Arg Lys Asn Cys Leu Val Lys Asn Leu Glu 340 345 350			1173
gct gta gaa acc ctg ggc tcc acg tcc acc atc tgc tca gat aag aca Ala Val Glu Thr Leu Gly Ser Thr Ser Thr Ile Cys Ser Asp Lys Thr 355 360 365			1221
ggg acc ctc act cag aac cgc atg aca gtc gcc cac atg tgg ttt gac Gly Thr Leu Thr Gln Asn Arg Met Thr Val Ala His Met Trp Phe Asp 370 375 380			1269
aac cag atc cac gag gct gac acc act gag gac cag tca ggg acc tca Asn Gln Ile His Glu Ala Asp Thr Thr Glu Asp Gln Ser Gly Thr Ser 385 390 395 400			1317
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ctc tgc aat cgc gct gtc ttc aag ggt ggt cag gac aac atc cct gtg Leu Cys Asn Arg Ala Val Phe Lys Gly Gly Gln Asp Asn Ile Pro Val 420 425 430			1413
ctc aag agg gat gtg gct ggg gat gcg tct gag tct gcc ctg ctc aag Leu Lys Arg Asp Val Ala Gly Asp Ala Ser Glu Ser Ala Leu Leu Lys 435 440 445			1461
tgc atc gag ctg tcc tct ggc tcc gtg aag ctg atg cgt gaa cgc aac Cys Ile Glu Leu Ser Ser Gly Ser Val Lys Leu Met Arg Glu Arg Asn 450 455 460			1509
aag aaa gtg gct gag att ccc ttc aat tcc acc aac aaa tac cag ctc Lys Lys Val Ala Glu Ile Pro Phe Asn Ser Thr Asn Lys Tyr Gln Leu			1557



465	470	475	480	
tcc atc cat gag acc gag gac ccc aac gac aac cga tac ctg ctg gtg				1605
Ser Ile His Glu Thr Glu Asp Pro Asn Asp Asn Arg Tyr Leu Leu Val	485	490	495	
atg aag ggt gcc ccc gag cgc atc ctg gac cgc tgc tcc acc atc ctg				1653
Met Lys Gly Ala Pro Glu Arg Ile Leu Asp Arg Cys Ser Thr Ile Leu	500	505	510	
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Leu Gln Gly Lys Glu Gln Pro Leu Asp Glu Glu Met Lys Glu Ala Phe	515	520	525	
cag aat gcc tac ctt gag ctc ggt ggc ctg ggc gag cgc gtg ctt ggt				1749
Gln Asn Ala Tyr Leu Glu Leu Gly Gly Leu Gly Glu Arg Val Leu Gly	530	535	540	
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Phe Cys His Tyr Tyr Leu Pro Glu Glu Gln Phe Pro Lys Gly Phe Ala	545	550	555	560
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Phe Asp Cys Asp Asp Val Asn Phe Thr Thr Asp Asn Leu Cys Phe Val	565	570	575	
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Gly Leu Met Ser Met Ile Asp Pro Pro Arg Ala Ala Val Pro Asp Ala	580	585	590	
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Val Gly Lys Cys Arg Ser Ala Gly Ile Lys Val Ile Met Val Thr Gly	595	600	605	
gat cac ccc atc acg gcc aag gcc att gcc aag ggt gtg ggc atc atc				1989
Asp His Pro Ile Thr Ala Lys Ala Ile Ala Lys Gly Val Gly Ile Ile	610	615	620	
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Phe Glu Gly Asn Glu Thr Val Glu Asp Ile Ala Ala Arg Leu Asn Ile	625	630	635	640
ccc gtc agc cag gtt aac ccc cgg gat gcc aag gcc tgc gtg atc cac				2085
Pro Val Ser Gln Val Asn Pro Arg Asp Ala Lys Ala Cys Val Ile His	645	650	655	
ggc acc gac ctc aag gac ttc acc tcc gag caa atc gac gag atc ctg				2133
Gly Thr Asp Leu Lys Asp Phe Thr Ser Glu Gln Ile Asp Glu Ile Leu	660	665	670	
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Gln Asn His Thr Glu Ile Val Phe Ala Arg Thr Ser Pro Gln Gln Lys	675	680	685	
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Leu Ile Ile Val Glu Gly Cys Gln Arg Gln Gly Ala Ile Val Ala Val	690	695	700	
acc ggg gat ggt gtg aac gac tcc ccc gct ctg aag aag gcc gac att				2277
Thr Gly Asp Gly Val Asn Asp Ser Pro Ala Leu Lys Lys Ala Asp Ile	705	710	715	720
ggg gtg gcc atg ggc atc gct ggc tct gac gtc tcc aag cag gca gct				2325
Gly Val Ala Met Gly Ile Ala Gly Ser Asp Val Ser Lys Gln Ala Ala				

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Asp Met Ile Leu Leu Asp Asp Asn Phe Ala Ser Ile Val Thr Gly Val			
740	745	750	
gag gag ggc cgc ctg atc ttc gac aac cta aag aag tcc att gcc tac			2421
Glu Glu Gly Arg Leu Ile Phe Asp Asn Leu Lys Lys Ser Ile Ala Tyr			
755	760	765	
acc ctg acc agc aat atc ccg gag atc acg ccc ttc ctg ctg ttc atc			2469
Thr Leu Thr Ser Asn Ile Pro Glu Ile Thr Pro Phe Leu Leu Phe Ile			
770	775	780	
atg gcc aac atc ccg ctg ccc ctg ggc acc atc acc atc ctc tgc atc			2517
Met Ala Asn Ile Pro Leu Pro Leu Gly Thr Ile Thr Ile Leu Cys Ile			
785	790	795	800
gat ctg ggc act gac atg gtc cct gcc atc tca ctg gcg tac gag gct			2565
Asp Leu Gly Thr Asp Met Val Pro Ala Ile Ser Leu Ala Tyr Glu Ala			
805	810	815	
gcc gaa agc gac atc atg aag aga cag ccc agg aac ccg cgg acg gac			2613
Ala Glu Ser Asp Ile Met Lys Arg Gln Pro Arg Asn Pro Arg Thr Asp			
820	825	830	
aaa ttg gct gag gag cca atg ggg cga agc tac cat ctg tgg gat tat			2661
Lys Leu Ala Glu Glu Pro Met Gly Arg Ser Tyr His Leu Trp Asp Tyr			
835	840	845	
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Asp *			
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cggaattcaa aacggacctg gagg atg ttg atc tcc aag aac atg ccc tgg	171
Met Leu Ile Ser Lys Asn Met Pro Trp	
1 5	
cgg cgg ctg cag ggc att tcc ttc ggg atg tat tcg gct gaa gag ctc	219

Arg	Arg	Leu	Gln	Gly	Ile	Ser	Phe	Gly	Met	Tyr	Ser	Ala	Glu	Glu	Leu	
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Lys	Lys	Leu	Ser	Val	Lys	Ser	Ile	Thr	Asn	Pro	Arg	Tyr	Leu	Asp	Ser	
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Leu	Gly	Asn	Pro	Ser	Ala	Asn	Gly	Leu	Tyr	Asp	Leu	Ala	Leu	Gly	Pro	
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gca	gat	tcc	aaa	gag	gtg	tgc	tcc	acc	tgc	gtg	cag	gac	ttc	agc	aac	363
Ala	Asp	Ser	Lys	Glu	Val	Cys	Ser	Thr	Cys	Val	Gln	Asp	Phe	Ser	Asn	
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Cys	Ser	Gly	His	Leu	Gly	His	Ile	Glu	Leu	Pro	Leu	Thr	Val	Tyr	Asn	
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cct	ctc	ctc	ttc	gat	aag	ctg	tac	ctg	ctg	ctt	cgg	ggc	tct	tgt	tta	459
Pro	Leu	Leu	Phe	Asp	Lys	Leu	Tyr	Leu	Leu	Leu	Arg	Gly	Ser	Cys	Leu	
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aac	tgc	cac	atg	ctg	act	tgt	ccc	cgg	gcc	gtg	att	cac	ctc	tta	ctc	507
Asn	Cys	His	Met	Leu	Thr	Cys	Pro	Arg	Ala	Val	Ile	His	Leu	Leu	Leu	
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Cys	Gln	Leu	Arg	Val	Leu	Glu	Val	Gly	Ala	Leu	Gln	Ala	Val	Tyr	Glu	
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Leu	Glu	Arg	Ile	Leu	Asn	Arg	Phe	Leu	Glu	Glu	Asn	Ala	Asp	Pro	Ser	
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Ala	Ser	Glu	Ile	Arg	Glu	Glu	Leu	Glu	Gln	Tyr	Thr	Thr	Glu	Ile	Val	
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Glu	Ser	Lys	Ser	Lys	Leu	Ile	Ala	Leu	Phe	Trp	Lys	Ala	His	Met	Asn	
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Ala	Lys	Arg	Cys	Pro	His	Cys	Lys	Thr	Gly	Arg	Ser	Val	Val	Arg	Lys	
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Glu	His	Asn	Ser	Lys	Leu	Thr	Ile	Thr	Phe	Pro	Ala	Met	Val	His	Arg	
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Thr	Ala	Gly	Gln	Lys	Asp	Ser	Glu	Pro	Leu	Gly	Ile	Glu	Glu	Ala	Gln	
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ata	gga	aaa	cga	gga	tac	tta	aca	ccc	acc	agt	gcc	cgc	gaa	cac	ctt	939
Ile	Gly	Lys	Arg	Gly	Tyr	Leu	Thr	Pro	Thr	Ser	Ala	Arg	Glu	His	Leu	
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tct	gcc	ctg	tgg	aag	aat	gaa	gga	ttc	ttt	ctg	aac	tac	ctt	ttt	tcg	987

Ser	Ala	Leu	Trp	Lys	Asn	Glu	Gly	Phe	Phe	Leu	Asn	Tyr	Leu	Phe	Ser	
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Gly	Met	Asp	Asp	Asp	Gly	Met	Glu	Ser	Arg	Phe	Asn	Pro	Ser	Val	Phe	
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Phe	Leu	Asp	Phe	Leu	Val	Val	Pro	Pro	Ser	Arg	Tyr	Arg	Pro	Val	Ser	
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cgc	cta	gga	gac	cag	atg	ttt	act	aat	ggc	cag	acg	gtg	aac	ttg	cag	1131
Arg	Leu	Gly	Asp	Gln	Met	Phe	Thr	Asn	Gly	Gln	Thr	Val	Asn	Leu	Gln	
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Ala	Val	Met	Lys	Asp	Val	Val	Leu	Ile	Arg	Lys	Leu	Leu	Ala	Leu	Met	
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Ala	Gln	Glu	Gln	Lys	Leu	Pro	Glu	Glu	Val	Ala	Thr	Pro	Thr	Thr	Asp	
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Glu	Glu	Lys	Asp	Ser	Leu	Ile	Ala	Ile	Asp	Arg	Ser	Phe	Leu	Ser	Thr	
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Leu	Pro	Gly	Gln	Ser	Leu	Ile	Asp	Lys	Leu	Tyr	Asn	Ile	Trp	Ile	Arg	
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Gly	Leu	Phe	Arg	Lys	His	Met	Met	Gly	Lys	Arg	Val	Asp	Tyr	Ala	Ala	
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Ile	Pro	Met	Val	Phe	Ala	Thr	Lys	Leu	Thr	Tyr	Pro	Gln	Pro	Val	Thr	
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Pro	Trp	Asn	Val	Gln	Glu	Leu	Arg	Gln	Ala	Val	Ile	Asn	Gly	Pro	Asn	
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Val	His	Pro	Gly	Ala	Ser	Met	Val	Ile	Asn	Glu	Asp	Gly	Ser	Arg	Thr	
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Gln	Tyr	Asp	Leu	Thr	Val	Arg	Asp	Ser	Asp	Gly	Ser	Val	Val	Gln	Phe		
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Leu	Tyr	Gly	Glu	Asp	Gly	Leu	Asp	Ile	Pro	Lys	Thr	Gln	Phe	Leu	Gln		
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Pro Lys Gln Phe Pro Phe Leu Ala Ser Asn Tyr Glu Val Ile Met Lys 1035	1040	1045	
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ctc cac cac ttc aga gct atc aaa aaa tgg caa agc aag cac ccc aac Leu His His Phe Arg Ala Ile Lys Lys Trp Gln Ser Lys His Pro Asn 1070	1075	1080	3387
acc ctg ctg aga aga ggc gcc ttc ttg agt tat tcc cag aaa att cag Thr Leu Leu Arg Arg Gly Ala Phe Leu Ser Tyr Ser Gln Lys Ile Gln 1085	1090	1095	3435
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aga ccc tgg gac tca ggg agg atg ctg agg atg tgg tat gag ttg gat Arg Pro Trp Asp Ser Gly Arg Met Leu Arg Met Trp Tyr Glu Leu Asp 1115	1120	1125	3531
gag gaa agc cga agg aaa tac cag aag aag gcg gcc gct tgt cct gac Glu Glu Ser Arg Arg Lys Tyr Gln Lys Lys Ala Ala Ala Cys Pro Asp 1130	1135	1140	3579
ccc agt ctg tct gtc tgg cgt cct gac atc tac ttt gca tca gtg tca Pro Ser Leu Ser Val Trp Arg Pro Asp Ile Tyr Phe Ala Ser Val Ser 1150	1155	1160	3627
gaa aca ttt gaa aca aag gtt gat gac tac agt caa gag tgg gca gct Glu Thr Phe Glu Thr Lys Val Asp Asp Tyr Ser Gln Glu Trp Ala Ala 1165	1170	1175	3675
caa aca gag aag agt tat gag aaa tca gag ctt tct ctc gac agg ttg Gln Thr Glu Lys Ser Tyr Glu Lys Ser Glu Leu Ser Leu Asp Arg Leu 1180	1185	1190	3723
agg acc ttg ctg cag ctg aag tgg cag cgc tca ctg tgt gag ccg ggc Arg Thr Leu Leu Gln Leu Lys Trp Gln Arg Ser Leu Cys Glu Pro Gly 1195	1200	1205	3771
gag gct gtg ggc ctg ctg gct gcc cag agc atc gga gag ccc tcc acc Glu Ala Val Gly Leu Leu Ala Ala Gln Ser Ile Gly Glu Pro Ser Thr 1210	1215	1220	3819
cag atg acc ctc aac acc ttc cac ttt gca ggc aga ggc gag atg aac Gln Met Thr Leu Asn Thr Phe His Phe Ala Gly Arg Gly Glu Met Asn 1230	1235	1240	3867
gtc acc ctg ggc att cca agg ttg cgg gag att ctc atg gtg gcc agc Val Thr Leu Gly Ile Pro Arg Leu Arg Glu Ile Leu Met Val Ala Ser 1245	1250	1255	3915
gcc aac atc aag aca ccc atg atg agc gtg ccc gtg ctc aac acc aag Ala Asn Ile Lys Thr Pro Met Met Ser Val Pro Val Leu Asn Thr Lys 1260	1265	1270	3963
aaa gcc ctg aag aga gtg aaa agc ctg aag aag caa ctc acc agg gtg Lys Ala Leu Lys Arg Val Lys Ser Leu Lys Lys Gln Leu Thr Arg Val 1275	1280	1285	4011
tgc ttg ggg gag gtg ttg cag aaa att gac gtc cag gag tcc ttc tgt			4059

Cys	Leu	Gly	Glu	Val	Leu	Gln	Lys	Ile	Asp	Val	Gln	Glu	Ser	Phe	Cys	
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Met	Glu	Glu	Lys	Gln	Asn	Lys	Phe	Gln	Val	Tyr	Gln	Leu	Arg	Phe	Gln	
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Phe	Leu	Pro	His	Ala	Tyr	Tyr	Gln	Gln	Glu	Lys	Cys	Leu	Arg	Pro	Glu	
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Asp	Ile	Leu	Arg	Phe	Met	Glu	Thr	Arg	Phe	Phe	Lys	Leu	Leu	Met	Glu	
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Arg	Ser	Arg	Gly	Glu	Gln	Glu	Gly	Asp	Glu	Glu	Glu	Glu	Gly	His	Ile	
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Glu	Glu	Arg	Glu	Gly	Glu	Glu	Asn	Asp	Asp	Glu	Asp	Met	Gln	Glu	Glu	
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Ala	Met	Glu	Arg	Arg	Val	Gln	Ala	Val	Arg	Glu	Ile	His	Pro	Phe	Ile	
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Asp	Asp	Tyr	Gln	Tyr	Asp	Thr	Glu	Glu	Ser	Leu	Trp	Cys	Gln	Val	Thr	
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Val	Lys	Leu	Pro	Leu	Met	Lys	Ile	Asn	Phe	Asp	Met	Ser	Ser	Leu	Val	
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Ile Lys Asp Val Phe Ala Val Tyr Gly Ile Ala Val Asp Pro Arg His	
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Leu Ser Leu Val Ala Asp Tyr Met Cys Phe Glu Gly Val Tyr Lys Pro	
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Ser His Asp Glu Leu Arg Ser Pro Ser Ala Cys Leu Val Val Gly Lys	
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Ile	Ser	Ser	Asp	Asn	Ser	Asp	Thr	Thr	Asp	Ser	His	Ala	Thr	Ser	Thr	
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Tyr	Tyr	Ile	Leu	Ala	Asp	Pro	Trp	Arg	Gln	Glu	Trp	Glu	Lys	Gly	Val	
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Gln	Val	Pro	Ala	Gly	Ala	Glu	Ala	Ile	Pro	Glu	Pro	Val	Val	Arg	Ile	
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Leu	Pro	Pro	Leu	Glu	Gly	Pro	Pro	Ala	Gln	Ala	Ser	Pro	Ser	Ser	Thr	
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&lt;222&gt; (990) .. (1340)

&lt;400&gt; 439

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aagagagttc aagtgaagga aggaggaggt tcctggatgt ggatgtcatc atttctggga      180
acactcttaa atggagactc agattttctta gccaaaattt agggaggatc cagaagaaac      240
caaagacgaa gcatcccagt tcttgggtat ttcttgaaac agaagaaa atg aca aag      297
                                   Met Thr Lys
                                   1

gcc cag gaa tca ctg acc ctg gag gat gtg gct gtg gac ttc acc tgg      345
Ala Gln Glu Ser Leu Thr Leu Glu Asp Val Ala Val Asp Phe Thr Trp
      5                      10                      15

gag gag tgg cag ttc ctg agc cct gct cag aag gac ctg tac cgg gat      393
Glu Glu Trp Gln Phe Leu Ser Pro Ala Gln Lys Asp Leu Tyr Arg Asp
      20                      25                      30                      35

gtg atg ttg gag aac tac agc aac ctt gtg tca gtg ggg tat caa gcc      441
Val Met Leu Glu Asn Tyr Ser Asn Leu Val Ser Val Gly Tyr Gln Ala
                        40                      45                      50

ggc aaa cct gat gcc ctc acc aag ttg gaa caa gga gaa cca cta tgg      489
Gly Lys Pro Asp Ala Leu Thr Lys Leu Glu Gln Gly Glu Pro Leu Trp
                        55                      60                      65

aca cta gaa gat gaa atc cac agt cca gcc cac cca gaa att gag aaa      537
Thr Leu Glu Asp Glu Ile His Ser Pro Ala His Pro Glu Ile Glu Lys
      70                      75                      80

gct gat gat cat ctg cag cag ccc ttg caa aac caa aaa ata ctg aag      585
Ala Asp Asp His Leu Gln Gln Pro Leu Gln Asn Gln Lys Ile Leu Lys
      85                      90                      95

agg acg gga caa cgc tat gaa cac gga aga act ttg aaa tca tat tta      633
Arg Thr Gly Gln Arg Tyr Glu His Gly Arg Thr Leu Lys Ser Tyr Leu
     100                      105                      110                      115

ggt tta acc aac cag agc aga aga tac aac aga aag gag cct gct gag      681
Gly Leu Thr Asn Gln Ser Arg Arg Tyr Asn Arg Lys Glu Pro Ala Glu
                        120                      125                      130

ttt aat gga gat gga gct ttt ctc cat gat aat cat gaa caa atg cct      729
Phe Asn Gly Asp Gly Ala Phe Leu His Asp Asn His Glu Gln Met Pro
                        135                      140                      145

acg gaa att gaa ttc cct gaa agt aga aaa ccc atc agc acc aag tca      777
Thr Glu Ile Glu Phe Pro Glu Ser Arg Lys Pro Ile Ser Thr Lys Ser
                        150                      155                      160

caa ttc ctt aaa cat cag caa aca cac aac ata gag aaa gcc cat gaa      825
Gln Phe Leu Lys His Gln Gln Thr His Asn Ile Glu Lys Ala His Glu
     165                      170                      175

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tgc act gac tgt ggg aaa gct ttc ctc aag aag tct cag ctc act gag Cys Thr Asp Cys Gly Lys Ala Phe Leu Lys Lys Ser Gln Leu Thr Glu 180 185 190 195	873
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ggg aaa gcc ttc tac aag aag tac agg ctc act gaa cac gag aga gct Gly Lys Ala Phe Tyr Lys Lys Tyr Arg Leu Thr Glu His Glu Arg Ala 215 220 225	969
cac aga gga gag aaa ccc cac ggg tgt agc ttg tgt ggg aaa gcc ttc His Arg Gly Glu Lys Pro His Gly Cys Ser Leu Cys Gly Lys Ala Phe 230 235 240	1017
tac aag agg tac agg ctc act gaa cac gag aga gct cac aaa gga gag Tyr Lys Arg Tyr Arg Leu Thr Glu His Glu Arg Ala His Lys Gly Glu 245 250 255	1065
aaa cca tac ggg tgc agt gaa tgt ggg aaa gcc ttc ccc agg aaa tct Lys Pro Tyr Gly Cys Ser Glu Cys Gly Lys Ala Phe Pro Arg Lys Ser 260 265 270 275	1113
gag ctt act gaa cat caa agg att cac acg gga att aag ccc cat caa Glu Leu Thr Glu His Gln Arg Ile His Thr Gly Ile Lys Pro His Gln 280 285 290	1161
tgc agc gaa tgt ggg aga gct ttc tcc aga aaa tca cta ctc gtt gta Cys Ser Glu Cys Gly Arg Ala Phe Ser Arg Lys Ser Leu Leu Val Val 295 300 305	1209
cat cag cga act cat aca gga gag aag cct cat aca tgc agt gaa tgt His Gln Arg Thr His Thr Gly Glu Lys Pro His Thr Cys Ser Glu Cys 310 315 320	1257
gga aaa ggc ttc att cag aag ggc aat ctc aac ata cat caa cga act Gly Lys Gly Phe Ile Gln Lys Gly Asn Leu Asn Ile His Gln Arg Thr 325 330 335	1305
cac act gga gag aaa cct tat gga tgc att gac tgt ggc aag gcc ttc His Thr Gly Glu Lys Pro Tyr Gly Cys Ile Asp Cys Gly Lys Ala Phe 340 345 350 355	1353
agc cag aag tct tgc ctt gta gca cat cag aga tat cat aca gga aag Ser Gln Lys Ser Cys Leu Val Ala His Gln Arg Tyr His Thr Gly Lys 360 365 370	1401
act ccc ttt gta tgt cct gaa tgt ggg caa ccc tgt tca cag aag tca Thr Pro Phe Val Cys Pro Glu Cys Gly Gln Pro Cys Ser Gln Lys Ser 375 380 385	1449
gga ctc att aga cat cag aaa att cac tca gga gag aaa ccc tat aaa Gly Leu Ile Arg His Gln Lys Ile His Ser Gly Glu Lys Pro Tyr Lys 390 395 400	1497
tgc agt gac tgt ggg aaa gcc ttc ctt aca aag aca atg ctc att gta Cys Ser Asp Cys Gly Lys Ala Phe Leu Thr Lys Thr Met Leu Ile Val 405 410 415	1545
cat cac aga act cac acg gga gag aga ccc tat ggc tgt gat gag tgt His His Arg Thr His Thr Gly Glu Arg Pro Tyr Gly Cys Asp Glu Cys 420 425 430 435	1593



gag aaa gct tac ttc tat atg tct tgc ctt gtt aaa cat aag aga ata 1641  
 Glu Lys Ala Tyr Phe Tyr Met Ser Cys Leu Val Lys His Lys Arg Ile  
 440 445 450  
  
 cac tca agg gag aaa cgg ggg gat tca gtg aag gtg gaa aat cct tcc 1689  
 His Ser Arg Glu Lys Arg Gly Asp Ser Val Lys Val Glu Asn Pro Ser  
 455 460 465  
  
 aca gca agt cac agc tta agt cct agt gaa cat gtg cag ggg aaa agc 1737  
 Thr Ala Ser His Ser Leu Ser Pro Ser Glu His Val Gln Gly Lys Ser  
 470 475 480  
  
 cct gtt aat atg gta act gtg gca atg gtg gca ggg cag tgt gag ttt 1785  
 Pro Val Asn Met Val Thr Val Ala Met Val Ala Gly Gln Cys Glu Phe  
 485 490 495  
  
 gcc cac atc ctg cat tca tga ta aacagtttgc tgtttgatca tatagcctcc 1838  
 Ala His Ile Leu His Ser \*  
 500 505  
  
 agcggaatgc tgagtttgtc atgtcccatg ggcctttggc tccctgcact aatatgtata 1898  
  
 gtagggttta caagatatga aatatatttt acttttttat atcttataaa cctcactacc 1958  
  
 cctcccacaa tattgttttt catttactat cttgatcata gagtttggct ggggaggggg 2018  
  
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 Met Ala  
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 gcc agc ggg aag acc agc aag tcc gaa ccg aac cat gtt atc ttc aag 345  
 Ala Ser Gly Lys Thr Ser Lys Ser Glu Pro Asn His Val Ile Phe Lys  
 5 10 15  
  
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 Lys Ile Ser Arg Asp Lys Ser Val Thr Ile Tyr Leu Gly Asn Arg Asp  
 20 25 30

tac ata gac cat gtc agc caa gtc cag cct gtg gat ggt gtc gtg ttg	441
Tyr Ile Asp His Val Ser Gln Val Gln Pro Val Asp Gly Val Val Leu	
35 40 45 50	
ggt gat cct gat ctt gtg aag gga aag aaa gtg tat gtc act ctg acc	489
Val Asp Pro Asp Leu Val Lys Gly Lys Lys Val Tyr Val Thr Leu Thr	
55 60 65	
tgc gcc ttc cgc tat ggc caa gag gac att gac gtg atc ggc ttg acc	537
Cys Ala Phe Arg Tyr Gly Gln Glu Asp Ile Asp Val Ile Gly Leu Thr	
70 75 80	
ttc cgc agg gac ctg tac ttc tcc cgg gtc cag gtg tat cct cct gtg	585
Phe Arg Arg Asp Leu Tyr Phe Ser Arg Val Gln Val Tyr Pro Pro Val	
85 90 95	
ggg gcc gcg agc acc ccc aca aaa ctg caa gag agc ctg ctt aaa aag	633
Gly Ala Ala Ser Thr Pro Thr Lys Leu Gln Glu Ser Leu Leu Lys Lys	
100 105 110	
ctg ggg agc aac acg tac ccc ttt ctc ctg acg ttt cct gac tac ttg	681
Leu Gly Ser Asn Thr Tyr Pro Phe Leu Leu Thr Phe Pro Asp Tyr Leu	
115 120 125 130	
ccc tgt tca gtg atg ttg cag cca gct cca caa gat tca ggg aag tcc	729
Pro Cys Ser Val Met Leu Gln Pro Ala Pro Gln Asp Ser Gly Lys Ser	
135 140 145	
tgt ggg gtt gac ttt gag gtc aaa gca ttc gcc aca gac agc acc gat	777
Cys Gly Val Asp Phe Glu Val Lys Ala Phe Ala Thr Asp Ser Thr Asp	
150 155 160	
gcc gaa gag gac aaa atc ccc aag aag agc tcc gtg cga tta ctg atc	825
Ala Glu Glu Asp Lys Ile Pro Lys Lys Ser Ser Val Arg Leu Leu Ile	
165 170 175	
cgc aaa gta cag cat gcc cca ctt gag atg ggt ccc cag ccc cga gct	873
Arg Lys Val Gln His Ala Pro Leu Glu Met Gly Pro Gln Pro Arg Ala	
180 185 190	
gag gcg gcc tgg cag ttc ttc atg tct gac aag ccc ctg cac ctt gcg	921
Glu Ala Ala Trp Gln Phe Phe Met Ser Asp Lys Pro Leu His Leu Ala	
195 200 205 210	
gtc tct ctc aac aaa gag atc tat ttc cat ggg gag ccc atc cct gtg	969
Val Ser Leu Asn Lys Glu Ile Tyr Phe His Gly Glu Pro Ile Pro Val	
215 220 225	
acc gtg act gtc acc aat aac aca gag aag acc gtg aag aag att aaa	1017
Thr Val Thr Val Thr Asn Asn Thr Glu Lys Thr Val Lys Lys Ile Lys	
230 235 240	
gca ttc gtg gaa cag gtg gcc aat gtg gtt ctc tac tcg agt gat tat	1065
Ala Phe Val Glu Gln Val Ala Asn Val Val Leu Tyr Ser Ser Asp Tyr	
245 250 255	
tac gtc aag ccc gtg gct atg gag gaa gcg caa gaa aaa gtg cca cca	1113
Tyr Val Lys Pro Val Ala Met Glu Glu Ala Gln Glu Lys Val Pro Pro	
260 265 270	
aac agc act ttg acc aag acg ctg acg ctg ctg ccc ttg ctg gct aac	1161
Asn Ser Thr Leu Thr Lys Thr Leu Thr Leu Leu Pro Leu Leu Ala Asn	
275 280 285 290	

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aat cga gaa agg aga ggc att gcc ctg gat ggg aaa atc aag cac gag      1209
Asn Arg Glu Arg Arg Gly Ile Ala Leu Asp Gly Lys Ile Lys His Glu
                               295                               300                               305

gac aca aac ctt gcc tcc agc acc atc att aag gag ggc ata gac cgg      1257
Asp Thr Asn Leu Ala Ser Ser Thr Ile Ile Lys Glu Gly Ile Asp Arg
                               310                               315                               320

acc gtc ctg gga atc ctg gtg tct tac cag atc aag gtg aag ctc aca      1305
Thr Val Leu Gly Ile Leu Val Ser Tyr Gln Ile Lys Val Lys Leu Thr
                               325                               330                               335

gtg tca ggc ttt ctg gga gag ctc acc tcc agt gaa gtc gcc act gag      1353
Val Ser Gly Phe Leu Gly Glu Leu Thr Ser Ser Glu Val Ala Thr Glu
                               340                               345                               350

gtc cca ttc cgc ctc atg cac cct cag cct gag gac cca gct aag gaa      1401
Val Pro Phe Arg Leu Met His Pro Gln Pro Glu Asp Pro Ala Lys Glu
                               355                               360                               365                               370

agt tat cag gat gca aat tta gtt ttt gag gag ttt gct cgc cat aat      1449
Ser Tyr Gln Asp Ala Asn Leu Val Phe Glu Glu Phe Ala Arg His Asn
                               375                               380                               385

ctg aaa gat gca gga gaa gct gag gag ggg aag aga gac aag aat gac      1497
Leu Lys Asp Ala Gly Glu Ala Glu Glu Gly Lys Arg Asp Lys Asn Asp
                               390                               395                               400

att gat gag tga aga tgtcggctca ggatgccgga aaatgacctg tagttaccag      1552
Ile Asp Glu *
                               405

tgcaacgagc aaagccccac agtttagtcc tttggagtta tgctgcgtat gaaaggatga      1612

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<210> 442  
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<220>  
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 <222> (259) .. (1611)

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ggagcggggc cttggaggcc cagcccgcgc ggcgacgtct ccgctggcg tcacggcacc      240
gactgacggc caccacc atg gcc gca gac cag cgc ccg aag gcc gac acg      291
                Met Ala Ala Asp Gln Arg Pro Lys Ala Asp Thr
                  1                5                10

ctg gcc ctg agg caa cgg ctc atc agc tct tcc tgc aga ctc ttt ttt      339
Leu Ala Leu Arg Gln Arg Leu Ile Ser Ser Ser Cys Arg Leu Phe Phe

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15	20	25	
ccc gag gat cct gtt aag att gtc cgg gcc caa ggg cag tac atg tac Pro Glu Asp Pro Val Lys Ile Val Arg Ala Gln Gly Gln Tyr Met Tyr 30 35 40			387
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gtt ggg cac tgc cac cct ctc gtg gtc caa gca gca cat gag cag aac Val Gly His Cys His Pro Leu Val Val Gln Ala Ala His Glu Gln Asn 60 65 70 75			483
cag gtg ctc aac acc aac agc cgg tac ctg cat gac aac atc gtg gac Gln Val Leu Asn Thr Asn Ser Arg Tyr Leu His Asp Asn Ile Val Asp 80 85 90			531
tat gcg cag agg ctg tca gag acc ctg ccg gag cag ctc tgt gtg ttc Tyr Ala Gln Arg Leu Ser Glu Thr Leu Pro Glu Gln Leu Cys Val Phe 95 100 105			579
tat ttc ctg aat tct ggg tca gaa gcc aat gac ctg gcc ctg agg ctg Tyr Phe Leu Asn Ser Gly Ser Glu Ala Asn Asp Leu Ala Leu Arg Leu 110 115 120			627
gct cgc cac tac acg gga cac cag gac gtg gtg gta tta gat cat gcg Ala Arg His Tyr Thr Gly His Gln Asp Val Val Val Leu Asp His Ala 125 130 135			675
tat cac ggc cac ctg agc tcc ctg att gac atc agt ccc tac aag ttc Tyr His Gly His Leu Ser Ser Leu Ile Asp Ile Ser Pro Tyr Lys Phe 140 145 150 155			723
cgc aac ctg gat ggc cag aag gag tgg gtc cac gtg gca cct ctc cca Arg Asn Leu Asp Gly Gln Lys Glu Trp Val His Val Ala Pro Leu Pro 160 165 170			771
gac acc tac cgg ggc ccc tac cgg gag gac cac ccc aac cca gct atg Asp Thr Tyr Arg Gly Pro Tyr Arg Glu Asp His Pro Asn Pro Ala Met 175 180 185			819
gcc tat gcc aac gag gtg aaa cgt gtg gtc agc agt gca cag gag aag Ala Tyr Ala Asn Glu Val Lys Arg Val Val Ser Ser Ala Gln Glu Lys 190 195 200			867
ggc agg aag att gca gcc ttc ttc gct gag tct ctg ccc agt gtg gga Gly Arg Lys Ile Ala Ala Phe Phe Ala Glu Ser Leu Pro Ser Val Gly 205 210 215			915
ggg cag atc att ccc cct gct ggc tac ttc tcc caa gtg gca gag cac Gly Gln Ile Ile Pro Pro Ala Gly Tyr Phe Ser Gln Val Ala Glu His 220 225 230 235			963
atc cgc aag gcc gga ggg gtc ttt gtt gca aat gag atc cag gtt ggc Ile Arg Lys Ala Gly Gly Val Phe Val Ala Asn Glu Ile Gln Val Gly 240 245 250			1011
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gac ttc gtc cct gac atc gtc acc atg ggc aag tcc att ggc aac ggc Asp Phe Val Pro Asp Ile Val Thr Met Gly Lys Ser Ile Gly Asn Gly 270 275 280 285 290 295			1107

270	275	280	
cac cct gtt gcc tgc gtg gcc gca acc cag cct gtg gcg agg gca ttt His Pro Val Ala Cys Val Ala Ala Thr Gln Pro Val Ala Arg Ala Phe 285 290 295			1155
gaa gcc acc ggc gtt gag tac ttc aac acg ttt ggg ggc agc cca gtg Glu Ala Thr Gly Val Glu Tyr Phe Asn Thr Phe Gly Gly Ser Pro Val 300 305 310 315			1203
tcc tgc gct gtg ggg ctg gcc gtc ctg aat gtc ttg gag aag gag cag Ser Cys Ala Val Gly Leu Ala Val Leu Asn Val Leu Glu Lys Glu Gln 320 325 330			1251
ctc cag gat cat gcc acc agt gta ggc agc ttc ctg atg cag ctc ctc Leu Gln Asp His Ala Thr Ser Val Gly Ser Phe Leu Met Gln Leu Leu 335 340 345			1299
ggg cag caa aaa atc aaa cat ccc atc gtc ggg gat gtc agg ggt gtt Gly Gln Gln Lys Ile Lys His Pro Ile Val Gly Asp Val Arg Gly Val 350 355 360			1347
ggg ctc ttc att ggt gtg gat ctg atc aaa gat gag gcc aca agg aca Gly Leu Phe Ile Gly Val Asp Leu Ile Lys Asp Glu Ala Thr Arg Thr 365 370 375			1395
cca gca act gaa gag gct gcc tac ttg gta tca agg ctg aag gag aac Pro Ala Thr Glu Glu Ala Ala Tyr Leu Val Ser Arg Leu Lys Glu Asn 380 385 390 395			1443
tac gtt ttg ctg agc act gat ggc cct ggg agg aac atc ctg aag ttt Tyr Val Leu Leu Ser Thr Asp Gly Pro Gly Arg Asn Ile Leu Lys Phe 400 405 410			1491
aag ccc cca atg tgc ttc agc ctg gac aat gca cgg cag gtg gtg gca Lys Pro Pro Met Cys Phe Ser Leu Asp Asn Ala Arg Gln Val Val Ala 415 420 425			1539
aag ctg gat gcc att ctg act gac atg gaa gag aag gtg aga agt tgt Lys Leu Asp Ala Ile Leu Thr Asp Met Glu Glu Lys Val Arg Ser Cys 430 435 440			1587
gaa acg ctg agg ctc cag ccc taa gccagccctg ctctgcctaa gtgtactcca Glu Thr Leu Arg Leu Gln Pro *			1641
445 450			
gaagaaactc atctcatcca aatacacgct attgagaagg cgagcctgac ctccctctta			1701
cagataaagt cagcttttcag aggctcaggg tggggggggcc tgcccagaggc cataatgcta			1761
cccacccct cctcctaacc actggtctgt tggaataacc cagatgtctg catccctca			1821
agtcagtcaa tttcctttct gtccactggg ggtggaatgg ggtagggtgg gatactttaa			1881
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&lt;220&gt;

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&lt;222&gt; (73) .. (1245)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (1570)

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&lt;400&gt; 443

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gggtgcggctg ca      atg ctg agc tcc cgg gcc gag gcg gcg atg acc gcg      108
                    Met Leu Ser Ser Arg Ala Glu Ala Ala Met Thr Ala
                      1              5              10

gcc gac agg gcc atc cag cgc ttc ctg cgg acc ggg gcg gcc gtc aga      156
Ala Asp Arg Ala Ile Gln Arg Phe Leu Arg Thr Gly Ala Ala Val Arg
                15              20              25

tat aaa gtc atg aag aac tgg gga gtt ata ggt gga att gct gct gct      204
Tyr Lys Val Met Lys Asn Trp Gly Val Ile Gly Gly Ile Ala Ala Ala
                30              35              40

ctt gca gca gga ata tat gtt att tgg ggt ccc att aca gaa aga aag      252
Leu Ala Ala Gly Ile Tyr Val Ile Trp Gly Pro Ile Thr Glu Arg Lys
                45              50              55              60

aag cgt aga aaa ggg ctt gtg cct ggc ctt gtt aat tta ggg aac acc      300
Lys Arg Arg Lys Gly Leu Val Pro Gly Leu Val Asn Leu Gly Asn Thr
                65              70              75

tgc ttc atg aac tcc ctg cta caa ggc ctg tct gcc tgt cct gct ttc      348
Cys Phe Met Asn Ser Leu Leu Gln Gly Leu Ser Ala Cys Pro Ala Phe
                80              85              90

atc ggg tgg ctg gaa gag ttc acc tcc cag tac tcc agg gat cag aag      396
Ile Gly Trp Leu Glu Glu Phe Thr Ser Gln Tyr Ser Arg Asp Gln Lys
                95              100              105

gag ccc ccc tca cac cag tat tta tcc tta aca ctc ttg cac ctt ctg      444
Glu Pro Pro Ser His Gln Tyr Leu Ser Leu Thr Leu Leu His Leu Leu
                110              115              120

aaa gcc ttg tcc tgc caa gaa gtt act gat gat gag gtc tta cat gca      492
Lys Ala Leu Ser Cys Gln Glu Val Thr Asp Asp Glu Val Leu His Ala
                125              130              135              140

agc tgc ttg ttg gat gtc tta aga atg tac aga tgg cag atc tca tca      540
Ser Cys Leu Leu Asp Val Leu Arg Met Tyr Arg Trp Gln Ile Ser Ser
                145              150              155

ttt gaa gaa cag gat gct cac gaa tta ttc cat gtc att acc tcg tca      588
Phe Glu Glu Gln Asp Ala His Glu Leu Phe His Val Ile Thr Ser Ser
                160              165              170

ttg gaa gat gag cga gac cgc cag cct cgg gtc aca cat ttg ttt gat      636
Leu Glu Asp Glu Arg Asp Arg Gln Pro Arg Val Thr His Leu Phe Asp
                175              180              185

gtg cat tcc ctg gag cag cag tca gaa ata act ccc aaa caa att acc      684
Val His Ser Leu Glu Gln Gln Ser Glu Ile Thr Pro Lys Gln Ile Thr

```



190	195	200	
tgc cgc aca aga ggg tca cct cac ccc aca tcc aat cac tgg aag tct			732
Cys Arg Thr Arg Gly Ser Pro His Pro Thr Ser Asn His Trp Lys Ser			
205	210	215	220
caa cat cct ttt cat gga aga ctc act agt aat atg gtc tgc aaa cac			780
Gln His Pro Phe His Gly Arg Leu Thr Ser Asn Met Val Cys Lys His			
	225	230	235
tgt gaa cac cag agt cct gtt cga ttt gat acc ttt gat agc ctt tca			828
Cys Glu His Gln Ser Pro Val Arg Phe Asp Thr Phe Asp Ser Leu Ser			
	240	245	250
cta agt att cca gcc gcc aca tgg ggt cac cca ttg acc ctg gac cac			876
Leu Ser Ile Pro Ala Ala Thr Trp Gly His Pro Leu Thr Leu Asp His			
	255	260	265
tgc ctt cac cac ttc atc tca tca gaa tca gtg cgg gat gtt gtg tgt			924
Cys Leu His His Phe Ile Ser Ser Glu Ser Val Arg Asp Val Val Cys			
	270	275	280
gac aac tgt aca aag att gaa gcc aag gga acg ttg aac ggg gaa aag			972
Asp Asn Cys Thr Lys Ile Glu Ala Lys Gly Thr Leu Asn Gly Glu Lys			
285	290	295	300
gtg gaa cac cag agg acc act ttt gtt aaa cag tta aaa cta ggg aag			1020
Val Glu His Gln Arg Thr Thr Phe Val Lys Gln Leu Lys Leu Gly Lys			
	305	310	315
ctc cct cag tgt ctc tgc atc cac cta cag cgg ctg agc tgg tcc agc			1068
Leu Pro Gln Cys Leu Cys Ile His Leu Gln Arg Leu Ser Trp Ser Ser			
	320	325	330
cac ggc acg cct ctg aag cgg cat gag cac gtg cag ttc aat gag ttc			1116
His Gly Thr Pro Leu Lys Arg His Glu His Val Gln Phe Asn Glu Phe			
	335	340	345
ctg atg atg gac att tac aag tac cac ctc ctt gga cat aaa cct agt			1164
Leu Met Met Asp Ile Tyr Lys Tyr His Leu Leu Gly His Lys Pro Ser			
	350	355	360
caa cac aac cct aaa ctg aac aag aac cca ggg cct aca ctg gag ctg			1212
Gln His Asn Pro Lys Leu Asn Lys Asn Pro Gly Pro Thr Leu Glu Leu			
365	370	375	380
cag gat ggg ccg gga gcc cca cac cag ttc tga atcagcca ggggccccca			1263
Gln Asp Gly Pro Gly Ala Pro His Gln Phe *			
	385	390	
aaacacagat ttttatgaat ggcgcctgct ccccatcttt attgccaacg ctgtcagcgc			1323
cgatgccctt ccctctccca gttgttcccg actacagctc ctccacatac ctcttcgggc			1383
tgatgggcag ttgtcgtcca ccatgggaga catggcactc tgggacactt tggttcattta			1443
ccgacgggtcc ccaccttttt gccaggggaa cctctttttc aattagggcan tcagttggct			1503
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tccagcg			1570

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 <213> Homo sapiens

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 <222> (291) .. (1805)

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 acttggaat gtgaacgcaa gaagcaggct tgattttttt ttctccccc ttctctctct 180  
 ctctctctct ctctcttct ctctccctct ttctcctctc tcaccacac tcacgcacac 240  
 ctccaaaccg cacaccaga cgacacgca taccacagcg cccggcagtt atg tat 296  
 Met Tyr  
 1  
 tct ccg ctc tgt ctc acc cag gat gaa ttt cat cct ttc atc gaa gca 344  
 Ser Pro Leu Cys Leu Thr Gln Asp Glu Phe His Pro Phe Ile Glu Ala  
 5 10 15  
 ctt ctg ccc cac gtc cga gcc ttt gcc tac aca tgg ttc aac ctg cag 392  
 Leu Leu Pro His Val Arg Ala Phe Ala Tyr Thr Trp Phe Asn Leu Gln  
 20 25 30  
 gcc cga aaa cga aaa tac ttc aaa aaa cat gaa aag cgt atg tca aaa 440  
 Ala Arg Lys Arg Lys Tyr Phe Lys Lys His Glu Lys Arg Met Ser Lys  
 35 40 45 50  
 gaa gaa gag aga gcc gtg aag gat gaa ttg cta agt gaa aaa cca gag 488  
 Glu Glu Glu Arg Ala Val Lys Asp Glu Leu Leu Ser Glu Lys Pro Glu  
 55 60 65  
 gtc aag cag aag tgg gca tct cga ctt ctg gca aag ttg cgg aaa gat 536  
 Val Lys Gln Lys Trp Ala Ser Arg Leu Leu Ala Lys Leu Arg Lys Asp  
 70 75 80  
 atc cga ccc gaa tat cga gag gat ttt gtt ctt aca gtt aca ggg aaa 584  
 Ile Arg Pro Glu Tyr Arg Glu Asp Phe Val Leu Thr Val Thr Gly Lys  
 85 90 95  
 aaa cct cca tgt tgt gtt ctt tcc aac cca gac cag aaa ggc aag atg 632  
 Lys Pro Pro Cys Cys Val Leu Ser Asn Pro Asp Gln Lys Gly Lys Met  
 100 105 110  
 cga aga att gac tgc ctc cgc cag gca gat aaa gtc tgg agg ttg gac 680  
 Arg Arg Ile Asp Cys Leu Arg Gln Ala Asp Lys Val Trp Arg Leu Asp  
 115 120 125 130  
 ctt gtt atg gtg att ttg ttt aaa ggt att ccg ctg gaa agt act gat 728  
 Leu Val Met Val Ile Leu Phe Lys Gly Ile Pro Leu Glu Ser Thr Asp  
 135 140 145  
 ggc gag cgc ctt gta aag tcc cca caa tgc tct aat cca ggg ctc tgt 776  
 Gly Glu Arg Leu Val Lys Ser Pro Gln Cys Ser Asn Pro Gly Leu Cys  
 150 155 160  
 gtc caa ccc cat cac ata ggg gtt tct gtt aag gaa ctc gat tta tat 824

Val	Gln	Pro	His	His	Ile	Gly	Val	Ser	Val	Lys	Glu	Leu	Asp	Leu	Tyr		
		165					170					175					
ttg	gca	tac	ttt	gtg	cat	gca	gca	gat	tca	agt	caa	tct	gaa	agt	ccc	872	
Leu	Ala	Tyr	Phe	Val	His	Ala	Ala	Asp	Ser	Ser	Gln	Ser	Glu	Ser	Pro		
	180					185					190						
agc	cag	cca	agt	gac	gct	gac	att	aag	gac	cag	cca	gaa	aat	gga	cat	920	
Ser	Gln	Pro	Ser	Asp	Ala	Asp	Ile	Lys	Asp	Gln	Pro	Glu	Asn	Gly	His		
195					200					205					210		
ttg	ggc	ttc	cag	gac	agt	ttt	gtc	aca	tca	ggg	gtt	ttt	agt	gtc	act	968	
Leu	Gly	Phe	Gln	Asp	Ser	Phe	Val	Thr	Ser	Gly	Val	Phe	Ser	Val	Thr		
				215					220					225			
gag	cta	gta	aga	gtg	tca	cag	aca	cca	ata	gct	gca	gga	act	ggc	cca	1016	
Glu	Leu	Val	Arg	Val	Ser	Gln	Thr	Pro	Ile	Ala	Ala	Gly	Thr	Gly	Pro		
			230					235					240				
aat	ttt	tct	ctc	tca	gat	ttg	gaa	agt	tct	tca	tac	tac	agc	atg	agt	1064	
Asn	Phe	Ser	Leu	Ser	Asp	Leu	Glu	Ser	Ser	Ser	Tyr	Tyr	Ser	Met	Ser		
		245					250					255					
cca	gga	gca	atg	agg	agg	tct	tta	ccc	agc	aca	tcc	tct	acg	agc	tcc	1112	
Pro	Gly	Ala	Met	Arg	Arg	Ser	Leu	Pro	Ser	Thr	Ser	Ser	Thr	Ser	Ser		
	260					265					270						
aca	aag	cgc	ctc	aag	tct	gtg	gag	gat	gaa	atg	gac	agt	cct	ggg	gag	1160	
Thr	Lys	Arg	Leu	Lys	Ser	Val	Glu	Asp	Glu	Met	Asp	Ser	Pro	Gly	Glu		
275					280				285					290			
gag	cca	ttt	tat	aca	ggc	caa	ggg	cgc	tcc	cca	gga	agt	ggc	agt	cag	1208	
Glu	Pro	Phe	Tyr	Thr	Gly	Gln	Gly	Arg	Ser	Pro	Gly	Ser	Gly	Ser	Gln		
				295					300					305			
tca	agt	gga	tgg	cat	gaa	gtg	gag	cca	gga	atg	cca	tct	cca	acc	aca	1256	
Ser	Ser	Gly	Trp	His	Glu	Val	Glu	Pro	Gly	Met	Pro	Ser	Pro	Thr	Thr		
			310					315					320				
ctg	aag	aag	tcg	gag	aag	tct	ggg	ttc	agc	agc	ccc	tcc	cct	tca	cag	1304	
Leu	Lys	Lys	Ser	Glu	Lys	Ser	Gly	Phe	Ser	Ser	Pro	Ser	Pro	Ser	Gln		
		325					330					335					
acc	tcc	tcc	ctg	gga	acg	gcg	ttc	aca	cag	cat	cac	cga	cct	gtc	att	1352	
Thr	Ser	Ser	Leu	Gly	Thr	Ala	Phe	Thr	Gln	His	His	Arg	Pro	Val	Ile		
	340					345					350						
aca	gga	ccc	aga	gca	agt	cca	cat	gca	aca	cca	tcg	act	ctt	cat	ttc	1400	
Thr	Gly	Pro	Arg	Ala	Ser	Pro	His	Ala	Thr	Pro	Ser	Thr	Leu	His	Phe		
355					360				365					370			
ccg	aca	tca	ccc	att	atc	cag	cag	cct	ggg	cct	tac	ttc	tca	cac	cca	1448	
Pro	Thr	Ser	Pro	Ile	Ile	Gln	Gln	Pro	Gly	Pro	Tyr	Phe	Ser	His	Pro		
				375					380					385			
gcc	atc	cgc	tat	cac	cct	cag	gag	acg	ctg	aaa	gaa	ttt	gtc	caa	ctt	1496	
Ala	Ile	Arg	Tyr	His	Pro	Gln	Glu	Thr	Leu	Lys	Glu	Phe	Val	Gln	Leu		
			390					395					400				
gtc	tgc	cct	gat	gct	ggg	cag	cag	gct	gga	cag	ccc	aat	ggg	agc	agc	1544	
Val	Cys	Pro	Asp	Ala	Gly	Gln	Gln	Ala	Gly	Gln	Pro	Asn	Gly	Ser	Ser		
		405				410						415					
caa	ggc	aag	gtg	cac	aac	cca	ttc	ctt	ccc	acc	cca	atg	ttg	cca	ccg	1592	

Gln Gly Lys Val His Asn Pro Phe Leu Pro Thr Pro Met Leu Pro Pro  
 420 425 430

cca ccg cca cca ccg atg gcc agg cct gtg cct ctg ccg gtg cca gac 1640  
 Pro Pro Pro Pro Pro Met Ala Arg Pro Val Pro Leu Pro Val Pro Asp  
 435 440 445 450

aca aag cct cca acc acg tca aca gaa gga ggt gca gcc tcc ccc acg 1688  
 Thr Lys Pro Pro Thr Thr Ser Thr Glu Gly Gly Ala Ala Ser Pro Thr  
 455 460 465

tca cca acc tac tcg aca ccc agc acc tcc ccc gca aac cga ttc gtc 1736  
 Ser Pro Thr Tyr Ser Thr Pro Ser Thr Ser Pro Ala Asn Arg Phe Val  
 470 475 480

agt gtt gga cca cgg gat cca agc ttt gta aat atc cct caa cag aca 1784  
 Ser Val Gly Pro Arg Asp Pro Ser Phe Val Asn Ile Pro Gln Gln Thr  
 485 490 495

cag tcc tgg tac ctg gga taa aa gttgcagcgt cccaccatcc accagacaga 1837  
 Gln Ser Trp Tyr Leu Gly \*  
 500 505

ccacctgac ccttctcaac tctgtaacat ggacgcaacc tcaaccagc gcagttacaa 1897

cttcactatc agcggaaggg gagaaaaacc gattcaaate aacttgtaca tggaaacagc 1957

aagcattatg gtcaaacagc aaaggccata accttttggg attttttttt ttttaaaata 2017

ctttagggac tgttggtatt ctcatatggt gctggaaatg gttgggcttt ggaacatttg 2077

aagtgtttcc atgtagcgtg catttaaggt acgtggctag ggaggactac cctgctcact 2137

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ctggccacct gccatgccct cagccggctc caggacaccc ccgtgggcga ccccatggac 180

ttgaagatgg tggagtctac tggctgggtc ctggaggaag agccggctgc agactcagca 240

tttgggaccc aggtcttggc agtg atg aga ccc cca ctt tgg gag ccc cag 291  
 Met Arg Pro Pro Leu Trp Glu Pro Gln  
 1 5

ctg cag gca atg gag gag ccc ccg gtg cca gtc agc gtc ctc cac cgc 339  
 Leu Gln Ala Met Glu Glu Pro Pro Val Pro Val Ser Val Leu His Arg  
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Phe Pro Phe Ser Ser Ala Leu Gln Arg Met Ser Val Val Val Ala Trp	
30 35 40	
cca ggg gcc act cag ccc gag gcc tac gtc aaa ggc tcc ccg gag ctg	435
Pro Gly Ala Thr Gln Pro Glu Ala Tyr Val Lys Gly Ser Pro Glu Leu	
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Val Ala Gly Leu Cys Asn Pro Glu Thr Val Pro Thr Asp Phe Ala Gln	
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Met Leu Gln Ser Tyr Thr Ala Ala Gly Tyr Arg Val Val Ala Leu Ala	
75 80 85	
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Ser Lys Pro Leu Pro Thr Val Pro Ser Leu Glu Ala Ala Gln Gln Leu	
90 95 100 105	
acg agg gac act gtg gaa gga gac ctg agc ctc ctg ggg ctg ctg gtc	627
Thr Arg Asp Thr Val Glu Gly Asp Leu Ser Leu Leu Gly Leu Leu Val	
110 115 120	
atg agg aac cta ctg aag ccg cag aca acg cca gtt atc cag gct ctg	675
Met Arg Asn Leu Leu Lys Pro Gln Thr Thr Pro Val Ile Gln Ala Leu	
125 130 135	
cga agg acc cgc atc cgc gcc gtc atg gtg aca ggg gac aac ctg cag	723
Arg Arg Thr Arg Ile Arg Ala Val Met Val Thr Gly Asp Asn Leu Gln	
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Thr Ala Val Thr Val Ala Arg Gly Cys Gly Met Val Ala Pro Gln Glu	
155 160 165	
cat ctg atc atc gtc cac gcc acc cac cct gag cgg ggt cag cct gcc	819
His Leu Ile Ile Val His Ala Thr His Pro Glu Arg Gly Gln Pro Ala	
170 175 180 185	
tct ctc gag ttc ctg ccg atg gag tcc ccc aca gcc gtg aat ggc gtt	867
Ser Leu Glu Phe Leu Pro Met Glu Ser Pro Thr Ala Val Asn Gly Val	
190 195 200	
aag gat cct gac cag gct gca agc tac acc gtg gag cca gac ccc cga	915
Lys Asp Pro Asp Gln Ala Ala Ser Tyr Thr Val Glu Pro Asp Pro Arg	
205 210 215	
tcc agg cac ctg gcc ctc agc ggg ccc acc ttt ggt atc att gtg aag	963
Ser Arg His Leu Ala Leu Ser Gly Pro Thr Phe Gly Ile Ile Val Lys	
220 225 230	
cac ttc ccc aag ctg ctg ccc aag gtc ctg gtc cag ggc act gtc ttt	1011
His Phe Pro Lys Leu Leu Pro Lys Val Leu Val Gln Gly Thr Val Phe	
235 240 245	
gcc cgc atg gcc cct gag cag aag aca gag ctg gtg tgc gag cta cag	1059
Ala Arg Met Ala Pro Glu Gln Lys Thr Glu Leu Val Cys Glu Leu Gln	
250 255 260 265	
aag ctt cag tac tgc gtg ggc atg tgc gga gac ggt gcc aat gac tgt	1107
Lys Leu Gln Tyr Cys Val Gly Met Cys Gly Asp Gly Ala Asn Asp Cys	
270 275 280	

ggg gcc ctg aag gcg gct gat gtc ggc atc tcg ctg tcc cag gca gaa	1155
Gly Ala Leu Lys Ala Ala Asp Val Gly Ile Ser Leu Ser Gln Ala Glu	
285 290 295	
gcc tca gtg gtc tca ccc ttc acc tcg agc atg gcc agt att gag tgc	1203
Ala Ser Val Val Ser Pro Phe Thr Ser Ser Met Ala Ser Ile Glu Cys	
300 305 310	
gtg ccc atg gtc atc agg gag ggg cgc tgt tcc ctt gac act tcg ttc	1251
Val Pro Met Val Ile Arg Glu Gly Arg Cys Ser Leu Asp Thr Ser Phe	
315 320 325	
agc gtc ttc aag tac atg gct ctg tac agc ctg acc cag ttc atc tcc	1299
Ser Val Phe Lys Tyr Met Ala Leu Tyr Ser Leu Thr Gln Phe Ile Ser	
330 335 340 345	
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Val Leu Ile Leu Tyr Thr Ile Asn Thr Asn Leu Gly Asp Leu Gln Phe	
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ctg gcc atc gac ctg gtc atc acc acc aca gtg gca gtg ctc atg agc	1395
Leu Ala Ile Asp Leu Val Ile Thr Thr Thr Val Ala Val Leu Met Ser	
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Arg Thr Gly Pro Ala Leu Val Leu Gly Arg Val Arg Pro Pro Gly Ala	
380 385 390	
ctg ctc agc gtg ccc gtg ctc agc agc ctg ctg ctg cag atg gtc ctg	1491
Leu Leu Ser Val Pro Val Leu Ser Ser Leu Leu Leu Gln Met Val Leu	
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Val Thr Gly Val Gln Leu Gly Gly Tyr Phe Leu Thr Leu Ala Gln Pro	
410 415 420 425	
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Trp Phe Val Pro Leu Asn Arg Thr Val Ala Ala Pro Asp Asn Leu Pro	
430 435 440	
aac tac gag aac acc gtg gtc ttc tct ctg tcc agc ttc cag tac ctc	1635
Asn Tyr Glu Asn Thr Val Val Phe Ser Leu Ser Ser Phe Gln Tyr Leu	
445 450 455	
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Ile Leu Ala Ala Ala Val Ser Lys Gly Ala Pro Phe Arg Arg Pro Leu	
460 465 470	
tac acc aat gag cgt gct aga cca gtg cct ccc cgc ctg cct gcg ccg	1731
Tyr Thr Asn Glu Arg Ala Arg Pro Val Pro Pro Arg Leu Pro Ala Pro	
475 480 485	
cct ccg gcc caa gcg ggc ctc caa gaa gcg ctt caa gca gct gga acg	1779
Pro Pro Ala Gln Ala Gly Leu Gln Glu Ala Leu Gln Ala Ala Gly Thr	
490 495 500 505	
aga gct ggc cga gca gcc ctg gcc gcc gct gcc cgc cgg ccc cct gag	1827
Arg Ala Gly Arg Ala Ala Leu Ala Ala Ala Ala Arg Arg Pro Pro Glu	
510 515 520	
gta gtg cag gcc cac ggg cac ccc aga cac tgg aac tcc ctg cct ctg	1875
Val Val Gln Ala His Gly His Pro Arg His Trp Asn Ser Leu Pro Leu	
525 530 535	



```

agc cac caa ctg gac ccc tct cca gca aca cca ccg cca cca cct ccc 1923
Ser His Gln Leu Asp Pro Ser Pro Ala Thr Pro Pro Pro Pro Pro
      540                545                550

aca tcc ctg agg ttg gcg act gtc tac act cct ccc ccg aga cca ccc 1971
Thr Ser Leu Arg Leu Ala Thr Val Tyr Thr Pro Pro Pro Arg Pro Pro
      555                560                565

cca ccc tgg gga agc gtt gac tac tgt ccc cta cct tgg acc atc ccg 2019
Pro Pro Trp Gly Ser Val Asp Tyr Cys Pro Leu Pro Trp Thr Ile Pro
      570                575                580                585

cgt agg ggt ggc agc ccc cag ctg ccc tca gtg ctg ctg tca gtg tag 2067
Arg Arg Gly Gly Ser Pro Gln Leu Pro Ser Val Leu Leu Ser Val *
      590                595                600

caaataaagt catgatattt tcctggcaaa aaaaaaaaaa 2106

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<210> 446
<211> 1555
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (808)..(966)

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<220>
<221> misc_feature
<222> (1)..(1555)
<223> n = a,t,c or g

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<400> 446
ggtaacgcgc ccgcagaatt ccgcgtcgac gatattcgtg ggggagggcc ccacagaggc 60
gctgcaagaa atccagatcc caggcgacac ctgctgcctt gcctgctgcc cccgcaaaat 120
ccctgcatct ggagccaccc acctggagga actcatcggg ctctctctgt agacgggaaa 180
aaacaaacgc accacaaacc gacaatcaaa gccatggcgg atgcggggcc gccaccagtt 240
catctccctg gagccaggcg gctccaggcc tctctcacct ttcttggtgt gaacgcaggc 300
ttgcaatgtt ctgagcccac ctgtcctcgg gctagtccca ttttcaaaag ttctgagtac 360
gcaggtgaga agacaccccc acaaaacccc aaaactagcc ttaggctgtt tttccccaac 420
acaacgcacc tccacacccc acaccgccag cagcccacct gggtagccaa agtgagctgc 480
caggggggtc cgaggaccct gcctggtgcc ttccagctca taaggagagg ccaagagcca 540
tggggaggaa gccacacggc ccagcgtca gggcttgta tccaagagtg agagaagtgg 600
ggagagaggt gacggagggt ggagtgggtg gtggcgtcna aataggctag ccagagagag 660
aggtgcttgt gggattctgc tggctggagc caggaggtaa gtgtgaacag ggaggccaaa 720
gatgaaagtt atctgaaaga gcccgtagcc cctataaaca cggcagagga atgtcttaag 780
agccaccaac agtaattccc tttccgg atg tta aca ggt tat ttg tat ctt 831
Met Leu Thr Gly Tyr Leu Tyr Leu

```

1

5

```

atg tgg cgt cgt aaa gca ttc tgg agt ggc aca caa cgt cat ccc ctt      879
Met Trp Arg Arg Lys Ala Phe Trp Ser Gly Thr Gln Arg His Pro Leu
   10                15                20

ccc ggt ggt ctg aag agg agg agg aga cca ggg agg ggt cct tgg cca      927
Pro Gly Gly Leu Lys Arg Arg Arg Arg Pro Gly Arg Gly Pro Trp Pro
   25                30                35                40

gcc cct ggc ggc caa ggg gtg ggt cct tct gct cta tag aaggcaggaa      976
Ala Pro Gly Gly Gln Gly Val Gly Pro Ser Ala Leu *
           45                50

gcccgccagc taaccgcccg ggtcagggggg agcaggcctg atctctccca agcctgtgac 1036
cgaggtcctg cctgatgtcc aaggggcccc tgtgccagta ccccaacttc ccacgcccc 1096
cagccttcct cacctccaga atcagccgcc caggtgcagc actatctcct ttctttttct 1156
tggaagccgt ctcaggggcc tgagtgcagg gacctgaccgt ccccgctacc gcctgctgcc 1216
atgcgaccag atggctgacc cggcccggct tctcagggcc cagaccagcc tggcctcgtg 1276
cccacctgct tcgctcccaa cctcaccacc aggcaagggt ttccagaaaa ccgagacacg 1336
caaacaccca ccaccacgac aacaacacaa accaaagtgc actgcgaacc gccctttggc 1396
ctccttcttg taggtgcctt gaaacttcaa tgttgagatg aatgtgatta actacttggt 1456
cctattttct gtttgtctat tttcatagaa aatgtccaag tccacttgcc ttgttctttc 1516
ttgaaataaa tagaaagatt taactttaaa aaaaaaaaaa 1555

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<210> 447  
 <211> 2205  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(2205)

<400> 447

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atg cac gaa tct gtc cac gtg ggt ttc ctg tcc ata cca tcc aag gag      48
Met His Glu Ser Val His Val Gly Phe Leu Ser Ile Pro Ser Lys Glu
   1                5                10                15

aaa ggc ctt ggc ctc ctc cag ctg ggt ctg ctc ctt cct ttg aac ccc      96
Lys Gly Leu Gly Leu Leu Gln Leu Gly Leu Leu Leu Pro Leu Asn Pro
           20                25                30

atc ggt acc tat gcc cac acc ttt cag agc ttt cct gat cag tgt caa      144
Ile Gly Thr Tyr Ala His Thr Phe Gln Ser Phe Pro Asp Gln Cys Gln
           35                40                45

cat gct gct ctt cct ctt aca aaa tgt acc atc aat aca gcc cag gca      192
His Ala Ala Leu Pro Leu Thr Lys Cys Thr Ile Asn Thr Ala Gln Ala
           50                55                60

cat ggc tcc cac aaa gct agc cac tta tat agt atg ggt cac atc aaa      240

```

His	Gly	Ser	His	Lys	Ala	Ser	His	Leu	Tyr	Ser	Met	Gly	His	Ile	Lys	
65					70					75					80	
aat	gac	tcc	agc	aca	atc	att	cat	aca	gac	ttc	tct	cac	act	aaa	cct	288
Asn	Asp	Ser	Ser	Thr	Ile	Ile	His	Thr	Asp	Phe	Ser	His	Thr	Lys	Pro	
				85					90					95		
tta	aac	aag	caa	ggc	tca	gta	gct	aca	gaa	ctc	tcc	atc	atc	atc	atc	336
Leu	Asn	Lys	Gln	Gly	Ser	Val	Ala	Thr	Glu	Leu	Ser	Ile	Ile	Ile	Ile	
			100					105					110			
atc	atc	atc	tgg	ttg	ctt	ttg	gca	agg	ttc	agt	agc	tac	aga	act	ctc	384
Ile	Ile	Ile	Trp	Leu	Leu	Leu	Ala	Arg	Phe	Ser	Ser	Tyr	Arg	Thr	Leu	
			115				120					125				
ctt	cat	cat	cat	cat	cat	ctg	gtt	gct	ttt	ggc	aag	caa	ggc	tca	gta	432
Leu	His	His	His	His	His	Leu	Val	Ala	Phe	Gly	Lys	Gln	Gly	Ser	Val	
			130				135				140					
gct	aca	gaa	ctc	tcc	tcc	tcc	tcc	tcc	tcc	tcc	tca	tca	tca	tca	tca	480
Ala	Thr	Glu	Leu	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	
145					150					155					160	
tct	ggc	tgc	ttt	cag	caa	ggc	tca	gta	gct	aca	gaa	ctc	tcc	atc	atc	528
Ser	Gly	Cys	Phe	Gln	Gln	Gly	Ser	Val	Ala	Thr	Glu	Leu	Ser	Ile	Ile	
				165					170					175		
atc	atc	atc	atc	atc	atc	atc	atc	atc	atc	atc	atc	tgg	ttg	ctt	ttg	576
Ile	Ile	Ile	Ile	Ile	Ile	Ile	Ile	Ile	Ile	Ile	Ile	Trp	Leu	Leu	Leu	
				180					185					190		
agg	ttc	agt	agc	tac	aga	act	ctc	ctc	ctc	ctc	ctc	ctc	ctc	ctc	ctc	624
Arg	Phe	Ser	Ser	Tyr	Arg	Thr	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
			195				200						205			
ctc	ctc	atc	atc	atc	atc	atc	atc	tgg	ttg	ctt	tta	gca	agg	ttc	agt	672
Leu	Leu	Ile	Ile	Ile	Ile	Ile	Ile	Trp	Leu	Leu	Leu	Ala	Arg	Phe	Ser	
			210				215					220				
agc	tac	aga	act	ctc	ctc	ctc	ctc	ctc	ctc	ctc	ctc	atc	atc	atc	atc	720
Ser	Tyr	Arg	Thr	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Ile	Ile	Ile	Ile	
225					230					235					240	
atc	tgg	ttg	ctt	tca	gca	agg	ttc	agt	agc	tac	aga	act	ctc	ctt	cat	768
Ile	Trp	Leu	Leu	Ser	Ala	Arg	Phe	Ser	Ser	Tyr	Arg	Thr	Leu	Leu	His	
				245					250					255		
cat	cat	caa	cat	cat	cat	ctg	gtt	gct	ttt	ggc	aag	caa	ggc	tca	gta	816
His	His	Gln	His	His	His	Leu	Val	Ala	Phe	Gly	Lys	Gln	Gly	Ser	Val	
			260					265					270			
gct	aca	gaa	ctc	tcc	tcc	tcc	tcc	tcc	tcc	tcc	tca	tca	tca	tca	tca	864
Ala	Thr	Glu	Leu	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	
			275					280					285			
tct	ggc	tgc	ttt	cag	caa	ggc	tca	gta	gct	aca	gaa	ctc	tcc	atc	atc	912
Ser	Gly	Cys	Phe	Gln	Gln	Gly	Ser	Val	Ala	Thr	Glu	Leu	Ser	Ile	Ile	
			290				295					300				
atc	atc	atc	atc	atc	atc	atc	atc	atc	atc	atc	tgg	ttg	ctt	ttg	gca	960
Ile	Ile	Ile	Ile	Ile	Ile	Ile	Ile	Ile	Ile	Ile	Trp	Leu	Leu	Leu	Ala	
305					310					315					320	
agg	ttc	agt	agc	tac	aga	act	ctc	ctt	cat	cat	cat	cat	cat	cat	cat	1008

Arg	Phe	Ser	Ser	Tyr	Arg	Thr	Leu	Leu	His	His	His	His	His	His	His	
				325					330					335		
ctg	gtt	gct	ttt	ggc	aag	caa	ggt	tca	gta	gct	aca	gaa	ctc	tcc	atc	1056
Leu	Val	Ala	Phe	Gly	Lys	Gln	Gly	Ser	Val	Ala	Thr	Glu	Leu	Ser	Ile	
			340					345					350			
atc	atc	atc	atc	atc	atc	atc	atc	atc	atc	atc	atc	tgg	ttg	ctt	ttg	1104
Ile	Ile	Ile	Ile	Ile	Ile	Ile	Ile	Ile	Ile	Ile	Ile	Trp	Leu	Leu	Leu	
			355					360					365			
gca	agg	ttc	agt	agc	tac	aga	act	ctc	ctt	cat	cat	cat	cat	cat	cat	1152
Ala	Arg	Phe	Ser	Ser	Tyr	Arg	Thr	Leu	Leu	His	His	His	His	His	His	
	370					375					380					
cat	ctg	gtt	gct	ttt	ggc	aag	gcc	ctg	gca	aga	att	att	tgg	ctt	tac	1200
His	Leu	Val	Ala	Phe	Gly	Lys	Ala	Leu	Ala	Arg	Ile	Ile	Trp	Leu	Tyr	
385					390					395					400	
cga	aac	acc	tat	tcc	ata	ggt	aac	caa	ttc	cag	tca	aaa	atg	cca	gag	1248
Arg	Asn	Thr	Tyr	Ser	Ile	Gly	Asn	Gln	Phe	Gln	Ser	Lys	Met	Pro	Glu	
				405				410						415		
tat	tac	tcc	tca	acc	caa	tgc	cct	atc	tcc	tta	gtg	gat	tat	aaa	ctt	1296
Tyr	Tyr	Ser	Ser	Thr	Gln	Cys	Pro	Ile	Ser	Leu	Val	Asp	Tyr	Lys	Leu	
			420					425						430		
act	acg	aca	acc	tgt	ctt	ctt	tgg	atc	caa	tcc	ccg	ccc	aag	tct	gag	1344
Thr	Thr	Thr	Thr	Cys	Leu	Leu	Trp	Ile	Gln	Ser	Pro	Pro	Lys	Ser	Glu	
			435				440					445				
tct	tct	ctc	cca	ggc	tac	aag	ccc	cca	agt	cct	ggc	agc	tct	atg	ctt	1392
Ser	Ser	Leu	Pro	Gly	Tyr	Lys	Pro	Pro	Ser	Pro	Gly	Ser	Ser	Met	Leu	
	450					455					460					
gac	agc	tcg	ctg	acc	tcc	acc	tca	tca	gac	cat	tgg	gtc	gcc	ctt	ctc	1440
Asp	Ser	Ser	Leu	Thr	Ser	Thr	Ser	Ser	Asp	His	Trp	Val	Ala	Leu	Leu	
465					470					475					480	
gcc	gtc	ctc	cag	cct	tct	tcc	cgc	tca	gac	act	cat	cca	ctg	tcc	ggg	1488
Ala	Val	Leu	Gln	Pro	Ser	Ser	Arg	Ser	Asp	Thr	His	Pro	Leu	Ser	Gly	
				485				490						495		
gag	cct	cga	ccc	ctc	cta	tac	ccc	ctc	ccc	gat	ccc	gca	gtc	ccc	ttc	1536
Glu	Pro	Arg	Pro	Leu	Leu	Tyr	Pro	Leu	Pro	Asp	Pro	Ala	Val	Pro	Phe	
			500					505					510			
tgg	acc	ttg	cgg	acc	cct	ctc	agc	ccc	cgt	acc	ccc	tac	cgc	ctc	ttc	1584
Trp	Thr	Leu	Arg	Thr	Pro	Leu	Ser	Pro	Arg	Thr	Pro	Tyr	Arg	Leu	Phe	
			515				520					525				
ctc	ctc	cac	tcc	cac	aac	tcc	gcc	cga	gct	cca	ctg	cgc	ctg	tgc	ggc	1632
Leu	Leu	His	Ser	His	Asn	Ser	Ala	Arg	Ala	Pro	Leu	Arg	Leu	Cys	Gly	
			530			535					540					
caa	cga	ggc	cgc	gcg	cag	gcg	atc	ggg	gca	gaa	gag	ctt	ccg	gtt	cct	1680
Gln	Arg	Gly	Arg	Ala	Gln	Ala	Ile	Gly	Ala	Glu	Glu	Leu	Pro	Val	Pro	
545					550				555						560	
gct	gtc	aat	aag	acg	tgg	acc	tgc	gag	ccg	ggg	caa	aag	ggc	ttc	cgg	1728
Ala	Val	Asn	Lys	Thr	Trp	Thr	Cys	Glu	Pro	Gly	Gln	Lys	Gly	Phe	Arg	
				565				570						575		
tct	gcg	gga	aac	tgg	agg	cta	gcg	gtg	ggc	gtg	gac	cgt	cga	ggt	gac	1776

Ser	Ala	Gly	Asn	Trp	Arg	Leu	Ala	Val	Gly	Val	Asp	Arg	Arg	Gly	Asp		
			580					585						590			
tgg	cgg	ttg	tcg	gat	ctg	ctg	ttg	ttt	gct	gac	cag	gca	gcc	gta	ggt	1824	
Trp	Arg	Leu	Ser	Asp	Leu	Leu	Leu	Phe	Ala	Asp	Gln	Ala	Ala	Val	Gly		
		595					600					605					
aat	gac	gga	tgc	cca	gac	cct	gtg	ggc	gga	gta	aag	gaa	tca	tgc	act	1872	
Asn	Asp	Gly	Cys	Pro	Asp	Pro	Val	Gly	Gly	Val	Lys	Glu	Ser	Cys	Thr		
		610				615					620						
gat	aca	cgc	aca	ctc	acc	gag	ggg	cgc	gtc	cgt	ctg	cgt	gcc	cct	cat	1920	
Asp	Thr	Arg	Thr	Leu	Thr	Glu	Gly	Arg	Val	Arg	Leu	Arg	Ala	Pro	His		
		625			630				635						640		
ctc	gta	gcc	gaa	agg	agc	gcg	ttc	cgg	ggc	agg	cct	ccg	ggt	act	tcc	1968	
Leu	Val	Ala	Glu	Arg	Ser	Ala	Phe	Arg	Gly	Arg	Pro	Pro	Gly	Thr	Ser		
				645				650						655			
cgc	aga	gga	ccg	ggc	ttt	ata	ctc	ttt	gct	cct	ttt	cct	ccc	cta	aaa	2016	
Arg	Arg	Gly	Pro	Gly	Phe	Ile	Leu	Phe	Ala	Pro	Phe	Pro	Pro	Leu	Lys		
			660					665					670				
gct	gtg	ctt	gac	ttc	ttg	gtg	tac	atg	gat	aaa	ggc	tac	aat	gaa	gga	2064	
Ala	Val	Leu	Asp	Phe	Leu	Val	Tyr	Met	Asp	Lys	Gly	Tyr	Asn	Glu	Gly		
		675					680					685					
aac	att	tta	gaa	ata	ctc	gcc	tac	ctg	gta	gtc	cac	aga	tct	tta	gat	2112	
Asn	Ile	Leu	Glu	Ile	Leu	Ala	Tyr	Leu	Val	Val	His	Arg	Ser	Leu	Asp		
		690				695					700						
ttc	att	ggc	cag	caa	aat	ctc	aaa	gga	aga	gaa	aga	gag	aac	aag	aga	2160	
Phe	Ile	Gly	Gln	Gln	Asn	Leu	Lys	Gly	Arg	Glu	Arg	Glu	Asn	Lys	Arg		
		705			710				715						720		
gac	cat	cat	atg	gaa	gac	aaa	ttt	gat	gcc	atc	act	tca	aaa	tga		2205	
Asp	His	His	Met	Glu	Asp	Lys	Phe	Asp	Ala	Ile	Thr	Ser	Lys	*			
				725				730						735			

&lt;210&gt; 448

&lt;211&gt; 1832

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (131) .. (1513)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (1832)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 448

tttgacctac cgggtccggaa ttcccgggtc gacccacgcg tccgcccaca tgggcccagc 60

aagctnnnnc cttccctttg ccagcttggg gcccgagcct gtccccgggtg gctgccagga 120

gcctgaggag atg agc tgg ccg cca tcg ggg gag att gcc agc cca cca 169  
Met Ser Trp Pro Pro Ser Gly Glu Ile Ala Ser Pro Pro

1	5	10	
gag ctg cca agc agc cca cct cct ggg ctt ccc gaa gtg gcc cca gat Glu Leu Pro Ser Ser Pro Pro Pro Gly Leu Pro Glu Val Ala Pro Asp 15 20 25			217
gca acc tcc act ggc ctc cct gat acc ccc gca gct cca gaa acc agc Ala Thr Ser Thr Gly Leu Pro Asp Thr Pro Ala Ala Pro Glu Thr Ser 30 35 40 45			265
acc aac tac cca gtg gag tgc acc gag ggg tct gca ggc ccc cag tct Thr Asn Tyr Pro Val Glu Cys Thr Glu Gly Ser Ala Gly Pro Gln Ser 50 55 60			313
ctc ccc ttg cct att ctg gag ccg gtc aaa aac ccc tgc tct gtc aaa Leu Pro Leu Pro Ile Leu Glu Pro Val Lys Asn Pro Cys Ser Val Lys 65 70 75			361
gac cag acg cca ctc caa ctt tct gta gaa gat acc acc tct cca aat Asp Gln Thr Pro Leu Gln Leu Ser Val Glu Asp Thr Thr Ser Pro Asn 80 85 90			409
acc aag ccg tgc cca cct act ccc acc acc cca gaa aca tcc cct cct Thr Lys Pro Cys Pro Pro Thr Pro Thr Thr Pro Glu Thr Ser Pro Pro 95 100 105			457
cct cct cct cct cct cct tca tct act cct tgt tca gct cac ctg acc Pro Pro Pro Pro Pro Pro Ser Ser Thr Pro Cys Ser Ala His Leu Thr 110 115 120 125			505
ccc tcc tcc ctg ttc cct tcc tcc ctg gaa tca tca tcg gaa cag aaa Pro Ser Ser Leu Phe Pro Ser Ser Leu Glu Ser Ser Ser Glu Gln Lys 130 135 140			553
ttc tat aac ttt gtg atc ctc cac gcc agg gca gac gaa cac atc gcc Phe Tyr Asn Phe Val Ile Leu His Ala Arg Ala Asp Glu His Ile Ala 145 150 155			601
ctg cgg gtt cgg gag aag ctg gag gcc ctt ggc gtg ccc gac ggg gcc Leu Arg Val Arg Glu Lys Leu Glu Ala Leu Gly Val Pro Asp Gly Ala 160 165 170			649
acc ttc tgc gag gat ttc cag gtg ccg ggg cgc ggg gag ctg agc tgc Thr Phe Cys Glu Asp Phe Gln Val Pro Gly Arg Gly Glu Leu Ser Cys 175 180 185			697
ctg cag gac gcc ata gac cac tca gct ttc atc atc cta ctt ctc acc Leu Gln Asp Ala Ile Asp His Ser Ala Phe Ile Ile Leu Leu Leu Thr 190 195 200 205			745
tcc aac ttc gac tgt cgc ctg agc ctg cac cag gtg aac caa gcc atg Ser Asn Phe Asp Cys Arg Leu Ser Leu His Gln Val Asn Gln Ala Met 210 215 220			793
atg agc aac ctc acg cga cag ggg tcg cca gac tgt gtc atc ccc ttc Met Ser Asn Leu Thr Arg Gln Gly Ser Pro Asp Cys Val Ile Pro Phe 225 230 235			841
ctg ccc ctg gag agc tcc ccg gcc cgg ctc agc tcc gac acg gcc agc Leu Pro Leu Glu Ser Ser Pro Ala Arg Leu Ser Ser Asp Thr Ala Ser 240 245 250			889
ctg ctc tcc ggg ctg gtg cgg ctg gac gaa cac tcc cag atc ttc gcc Leu Leu Ser Gly Leu Val Arg Leu Asp Glu His Ser Gln Ile Phe Ala			937



255	260	265	
agg aag gtg gcc aac acc ttc aag ccc cac agg ctt cag gcc cga aag			985
Arg Lys Val Ala Asn Thr Phe Lys Pro His Arg Leu Gln Ala Arg Lys			
270	275	280	285
gcc atg tgg agg aag gaa cag gac acc cga gcc ctg cgg gaa cag agc			1033
Ala Met Trp Arg Lys Glu Gln Asp Thr Arg Ala Leu Arg Glu Gln Ser			
	290	295	300
caa cac ctg gat ggt gag cgg atg cag gcg gcg gca ctg aac gca gcc			1081
Gln His Leu Asp Gly Glu Arg Met Gln Ala Ala Ala Leu Asn Ala Ala			
	305	310	315
tac tca gcc tac ctc cag agc tac ttg tcc tac cag gca cag atg gag			1129
Tyr Ser Ala Tyr Leu Gln Ser Tyr Leu Ser Tyr Gln Ala Gln Met Glu			
	320	325	330
cag ctc cag gtg gct ttt ggg agc cac atg tca ttt ggg act ggg gcg			1177
Gln Leu Gln Val Ala Phe Gly Ser His Met Ser Phe Gly Thr Gly Ala			
	335	340	345
ccc tat ggg gct cga atg ccc ttt ggg ggc cag gtg ccc ctg gga gcc			1225
Pro Tyr Gly Ala Arg Met Pro Phe Gly Gly Gln Val Pro Leu Gly Ala			
	350	355	360
ccg cca ccc ttt ccc act tgg ccg ggg tgc ccg cag ccg cca ccc ctg			1273
Pro Pro Pro Phe Pro Thr Trp Pro Gly Cys Pro Gln Pro Pro Pro Leu			
	370	375	380
cac gca tgg cag gct ggc acc ccc cca ccg ccc tcc cca cag cca gca			1321
His Ala Trp Gln Ala Gly Thr Pro Pro Pro Pro Ser Pro Gln Pro Ala			
	385	390	395
gcc ttt cca cag tca ctg ccc ttc ccg cag tcc cca gcc ttc cct acg			1369
Ala Phe Pro Gln Ser Leu Pro Phe Pro Gln Ser Pro Ala Phe Pro Thr			
	400	405	410
gcc tca ccc gca ccc cct cag agc cca ggg ctg caa ccc ctc att atc			1417
Ala Ser Pro Ala Pro Pro Gln Ser Pro Gly Leu Gln Pro Leu Ile Ile			
	415	420	425
cac cac gca cag atg gta cag ctg ggg ctg aac aac cac atg tgg aac			1465
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Gln Arg Gly Ser Gln Ala Pro Glu Asp Lys Thr Gln Glu Ala Glu *			
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ggctttcagg gtggtcagaa ctggatacgg tgttttacaat tccaatctct ctattttctgg			1753
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attaagaagg aaatatctcc attgttcatt ggc atg gaa aaa tgt tca gtg gga	174
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Gly Leu Glu Leu Thr Glu Gln Thr Pro Ala Leu Leu Gly Asn Met Ala	
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Cys Pro Leu Val Ser Arg Ser Arg Asn Ser Pro Val Glu Asp Asp Asp	
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Asp Asp Asp Asp Val Val Phe Ile Glu Ser Ile Gln Pro Pro Ser Ile	
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Ser Ala Pro Ala Ile Ala Asp Gln Arg Asn Phe Ile Phe Ala Ser Ser	
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aaa aat gaa aag cct caa gga aat tat tct gta att cct cct tct tca	462
Lys Asn Glu Lys Pro Gln Gly Asn Tyr Ser Val Ile Pro Pro Ser Ser	
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Arg Asp Leu Ala Ser Gln Lys Gly Asn Ile Ser Glu Thr Ile Val Ile	
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gat gat gaa gag gac ata gaa aca aat gga gga gca gag aaa aag tct	558
Asp Asp Glu Glu Asp Ile Glu Thr Asn Gly Gly Ala Glu Lys Lys Ser	
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Ser Cys Phe Ile Glu Trp Gly Leu Pro Gly Thr Lys Asn Lys Thr Asn	
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Asp Leu Asp Phe Ser Thr Ser Ser Leu Ser Arg Ser Lys Thr Lys Thr	
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Gly Val Arg Pro Phe Asn Pro Gly Arg Met Asn Val Ala Gly Asp Leu	
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Ser	Gln	Ser	Ala	Ser	Phe	Pro	Ser	Asn	Gln	Lys	Gln	Pro	Gly	Val	Asp	
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Ser	Leu	Ser	Pro	Val	Ala	Leu	Leu	Arg	Lys	Gln	Asn	Phe	Gln	Pro	Thr	
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Lys	Lys	Pro	Leu	Gln	Lys	Gly	Gln	Thr	Ala	Tyr	Gln	Arg	Lys	Gly	Ser	
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Arg	Thr	Gln	Asn	Thr	Arg	Ser	Ile	Ile	Cys	Lys	Lys	Asp	Ala	Ser	Thr	
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Lys	Lys	Ala	Asn	Val	Ile	Leu	Pro	Val	Glu	Ser	Ser	Lys	Ser	Phe	Gln	
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Glu	Phe	Tyr	Ser	Thr	Ser	Cys	Leu	Ser	Pro	Cys	Glu	Asn	Asn	Trp	Asn	
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ctt	aaa	aaa	gga	gtt	ttt	aat	aag	tca	aga	tgt	aca	att	tgt	agt	aaa	1182
Leu	Lys	Lys	Gly	Val	Phe	Asn	Lys	Ser	Arg	Cys	Thr	Ile	Cys	Ser	Lys	
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Leu	Ala	Glu	Val	Trp	Ile	Phe	Ile	Pro	Lys	Leu	Leu	Phe	Arg	Leu	Thr	
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Val	Ile	Ile	Leu	Thr	Phe	Lys	Cys	Tyr	Tyr	Val	Leu	Phe	His	Leu	His	
360				365					370					375		
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attaagaagg aaatatctcc attgttcatt ggc atg gaa aaa tgt tca gtg gga 174  
Met Glu Lys Cys Ser Val Gly  
1 5

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Gly Leu Glu Leu Thr Glu Gln Thr Pro Ala Leu Leu Gly Asn Met Ala  
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Met Ala Thr Ser Leu Met Asp Ile Gly Asp Ser Phe Gly His Pro Ala  
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Cys Pro Leu Val Ser Arg Ser Arg Asn Ser Pro Val Glu Asp Asp Asp  
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gat gat gat gat gtt gtg ttt att gaa tct ata caa cct cct tca att 366  
Asp Asp Asp Asp Val Val Phe Ile Glu Ser Ile Gln Pro Pro Ser Ile  
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Ser Ala Pro Ala Ile Ala Asp Gln Arg Asn Phe Ile Phe Ala Ser Ser  
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Lys Asn Glu Lys Pro Gln Gly Asn Tyr Ser Val Ile Pro Pro Ser Ser  
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Arg Asp Leu Ala Ser Gln Lys Gly Asn Ile Ser Glu Thr Ile Val Ile  
105 110 115

gat gat gaa gag gac ata gaa aca aat gga gga gca gag aaa aag tct 558  
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120 125 130 135

tcc tgt ttt atc gaa tgg gga ctt cct gga act aaa aac aaa acc aac 606  
Ser Cys Phe Ile Glu Trp Gly Leu Pro Gly Thr Lys Asn Lys Thr Asn  
140 145 150

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Phe Gln Asn Gly Glu Phe Ala Thr His His Ser Pro Asp Asp Ala Ser  
185 190 195

aca aag aag gct aat gtc att ctt cca gta gaa tca agc aaa tcc ttc 798  
Thr Lys Lys Ala Asn Val Ile Leu Pro Val Glu Ser Ser Lys Ser Phe  
200 205 210 215

caa gaa ttt tat agg aca tct tgt ttg tct ccc tgt gaa aac aac tgg 846  
Gln Glu Phe Tyr Arg Thr Ser Cys Leu Ser Pro Cys Glu Asn Asn Trp

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Asn Leu Lys Lys Gly Val Phe Asn Lys Ser Arg Cys Thr Ile Cys Ser				
	235	240	245	
aaa tta gca gag gtc tgg att ttt ata cct aag ttg ttg ttt agg cta				942
Lys Leu Ala Glu Val Trp Ile Phe Ile Pro Lys Leu Leu Phe Arg Leu				
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aca gtg ata att tta act ttt aag tgc tat tat gga ctc ttt cat cta				990
Thr Val Ile Ile Leu Thr Phe Lys Cys Tyr Tyr Gly Leu Phe His Leu				
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His Asn Ala Arg Val Leu Asp Val *				
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Tyr His Pro Phe Leu Pro His Arg Ala Pro Asp Phe Ala Met Ser Ala	
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Val Leu Gly His Gln Pro Pro Phe Phe Pro Ala Leu Thr Leu Pro Pro	
35 40 45	
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Asn Gly Ala Ala Ala Leu Ser Leu Pro Gly Ala Leu Ala Lys Pro Ile	
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Met Asp Gln Leu Val Gly Ala Ala Glu Thr Gly Ile Pro Phe Ser Ser	
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Leu Gly Pro Gln Ala His Leu Arg Pro Leu Lys Thr Met Glu Pro Glu	
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Glu Glu Val Glu Asp Asp Pro Lys Val His Leu Glu Ala Lys Glu Leu	
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Gly	Arg	Arg	Met	Phe	Pro	Pro	Phe	Lys	Val	Arg	Cys	Ser	Gly	Leu	Asp		
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aaa	aaa	gcc	aaa	tac	att	tta	ttg	atg	gac	att	ata	gct	gct	gat	gac	480	
Lys	Lys	Ala	Lys	Tyr	Ile	Leu	Leu	Met	Asp	Ile	Ile	Ala	Ala	Asp	Asp		
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tgt	cgt	tat	aaa	ttt	cac	aat	tct	cgg	tgg	atg	gtg	gct	ggg	aag	gcc	528	
Cys	Arg	Tyr	Lys	Phe	His	Asn	Ser	Arg	Trp	Met	Val	Ala	Gly	Lys	Ala		
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gac	ccc	gaa	atg	cca	aag	agg	atg	tac	att	cac	ccg	gac	agc	ccc	gct	576	
Asp	Pro	Glu	Met	Pro	Lys	Arg	Met	Tyr	Ile	His	Pro	Asp	Ser	Pro	Ala		
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Thr	Gly	Glu	Gln	Trp	Met	Ser	Lys	Val	Val	Thr	Phe	His	Lys	Leu	Lys		
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Leu	Thr	Asn	Asn	Ile	Ser	Asp	Lys	His	Gly	Phe	Thr	Ile	Leu	Asn	Ser		
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Met	His	Lys	Tyr	Gln	Pro	Arg	Phe	His	Ile	Val	Arg	Ala	Asn	Asp	Ile		
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Leu	Lys	Leu	Pro	Tyr	Ser	Thr	Phe	Arg	Thr	Tyr	Leu	Phe	Pro	Glu	Thr		
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gaa	ttc	atc	gct	gtg	act	gca	tac	cag	aat	gat	aag	ata	acc	cag	tta	816	
Glu	Phe	Ile	Ala	Val	Thr	Ala	Tyr	Gln	Asn	Asp	Lys	Ile	Thr	Gln	Leu		
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Lys	Ile	Asp	Asn	Asn	Pro	Phe	Ala	Lys	Gly	Phe	Arg	Asp	Thr	Gly	Asn		
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Gly	Arg	Arg	Glu	Lys	Arg	Lys	Gln	Leu	Thr	Leu	Gln	Ser	Met	Arg	Val		
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Phe	Asp	Glu	Arg	His	Lys	Lys	Glu	Asn	Gly	Thr	Ser	Asp	Glu	Ser	Ser		
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Ser	Glu	Gln	Ala	Ala	Phe	Asn	Cys	Phe	Ala	Gln	Ala	Ser	Ser	Pro	Ala		
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gcc	tcc	act	gta	ggg	aca	tgc	aac	ctc	aaa	gat	tta	tgt	ccc	agc	gag	1056	
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Gly	Glu	Ser	Asp	Ala	Glu	Ala	Glu	Ser	Lys	Glu	Glu	His	Gly	Pro	Glu		
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Arg Asp Lys Gly Ser Pro Ala Val Lys Ala His Leu Phe Ala Ala Glu	
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Arg Pro Arg Asp Ser Gly Arg Leu Asp Lys Ala Ser Pro Asp Ser Arg	
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His Ser Pro Ala Thr Ile Ser Ser Ser Thr Arg Gly Leu Gly Ala Glu	
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Glu Ala Arg Ala Leu Pro Gly Lys Glu Ala Phe Ala Pro Leu Thr Val	
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Gln Thr Asp Ala Ala Ala Ala His Leu Ala Gln Gly Pro Leu Pro Gly	
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Leu Gly Phe Ala Pro Gly Leu Ala Gly Gln Gln Phe Phe Asn Gly His	
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Ala Ser Thr Gly Val Ser Gly Leu Asp Ser Thr Ala Met Ala Ser Ala	
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Phe Gly Ser Leu Phe Pro Tyr Pro Tyr Thr Tyr Met Ala Ala Ala Ala	
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Ala Ala Ser Leu Arg Gln Pro Gln Leu Arg Cys Thr Ala Pro Leu Leu	
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Ser Pro *	
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1170

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cag tac atc acc agt aat ccc tgc ata cgc ttc gtc tcc att gat aat Gln Tyr Ile Thr Ser Asn Pro Cys Ile Arg Phe Val Ser Ile Asp Asn 215 220 225			1148
aag aag cgc aat ata gag tca tca gaa att ggg cct tcc ctc gtg att Lys Lys Arg Asn Ile Glu Ser Ser Glu Ile Gly Pro Ser Leu Val Ile 230 235 240			1196
cac acc act gtc cca ttt gga gtt aca tac ttg gaa cac agc att gag His Thr Thr Val Pro Phe Gly Val Thr Tyr Leu Glu His Ser Ile Glu 245 250 255 260			1244
gat gtg caa gag tta gtc ttc cag cag ctg gaa aac att ttg ccg ggt Asp Val Gln Glu Leu Val Phe Gln Gln Leu Glu Asn Ile Leu Pro Gly 265 270 275			1292
ttg cct cag cca att gct acc aaa tgc caa aaa tgg aga cat tca cag Leu Pro Gln Pro Ile Ala Thr Lys Cys Gln Lys Trp Arg His Ser Gln 280 285 290			1340
gtt aca aat gct gct gcc aac tgt cct ggc caa atg act ctg cat cac Val Thr Asn Ala Ala Ala Asn Cys Pro Gly Gln Met Thr Leu His His 295 300 305			1388
aaa cct ttc ctt gca tgt gga ggg gat gga ttt act cag tcc aac ttt Lys Pro Phe Leu Ala Cys Gly Gly Asp Gly Phe Thr Gln Ser Asn Phe 310 315 320			1436
gat ggc tgc atc act tct gcc cta tgt gtt ctg gaa gct tta aag aat Asp Gly Cys Ile Thr Ser Ala Leu Cys Val Leu Glu Ala Leu Lys Asn 325 330 335 340			1484
tat att tag tgcctat atccttattc tctacatgtg tattgggttt ttattttcac Tyr Ile *			1540
aattttctgt tattgattat tttgttttct attttgctaa gaaaaattac tggaaaattg			1600
ttcttcactt attatcattt ttcattgtgga gtataaaatc aattttgtaa ttttgatagt			1660
tacaacccat gctagaatgg aaattcctca caccttgcac cttccctact tttctgaatt			1720
gctatgacta ctccctgttg gaggaaaagt ggtacttaaa aaataacaaa cgactctctc			1780
aaaaaaatta cattaaatca caataacagt ttgtatgcca aaaacttgat tctccttatg			1840
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                                         Met Leu Ser Val Ala Ala
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cgc tgc ggc ccg ttc gcg ccc gtc ctg tgc gcc acc ccg gag cag cct      160
Arg Ser Gly Pro Phe Ala Pro Val Leu Ser Ala Thr Pro Glu Gln Pro
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gtg ttg gac ctg aag cgg ccc ttc ctc agc cgg gag tgc ctg agc ggc      208
Val Leu Asp Leu Lys Arg Pro Phe Leu Ser Arg Glu Ser Leu Ser Gly
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cag gcc gtg cgc cgg cct ttg gtc gcc tcc gtg ggc ctc aat gtc cct      256
Gln Ala Val Arg Arg Pro Leu Val Ala Ser Val Gly Leu Asn Val Pro
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gct tct gtt tgt tat tcc cac aca gac atc aag gtg cct gac ttc tct      304
Ala Ser Val Cys Tyr Ser His Thr Asp Ile Lys Val Pro Asp Phe Ser
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gaa tac cgc cgc ctt gaa gtt tta gat agt acg aag tct tca aga gaa      352
Glu Tyr Arg Arg Leu Glu Val Leu Asp Ser Thr Lys Ser Ser Arg Glu
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agc agc gag gct agg aaa ggt ttc tcc tat ttg gta act gga gta act      400
Ser Ser Glu Ala Arg Lys Gly Phe Ser Tyr Leu Val Thr Gly Val Thr
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Thr Val Gly Val Ala Tyr Ala Ala Lys Asn Ala Val Thr Gln Phe Val
              105              110              115

tcc agc atg agt gct tct gct gat gtg ttg gcc ctg gcg aaa atc gaa      496
Ser Ser Met Ser Ala Ser Ala Asp Val Leu Ala Leu Ala Lys Ile Glu
              120              125              130

atc aag tta tcc gat att cca gaa ggc aag aac atg gct ttc aaa tgg      544
Ile Lys Leu Ser Asp Ile Pro Glu Gly Lys Asn Met Ala Phe Lys Trp
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aga ggc aaa ccc ctg ttt gtg cgt cat aga acc cag aag gaa att gag      592
Arg Gly Lys Pro Leu Phe Val Arg His Arg Thr Gln Lys Glu Ile Glu
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cag gaa gct gca gtt gaa tta tca cag ttg agg gac cca cag cat gat      640
Gln Glu Ala Ala Val Glu Leu Ser Gln Leu Arg Asp Pro Gln His Asp
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cta gat cga gta aag aaa cct gaa tgg gtt atc ctg ata ggt gtt tgc      688
Leu Asp Arg Val Lys Lys Pro Glu Trp Val Ile Leu Ile Gly Val Cys
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act cat ctt ggc tgt gta ccc att gca aat gca gga gat ttt ggt ggt      736
Thr His Leu Gly Cys Val Pro Ile Ala Asn Ala Gly Asp Phe Gly Gly

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Tyr Tyr Cys Pro Cys His Gly Ser His Tyr Asp Ala Ser Gly Arg Ile			
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aga ttg ggt cct gct cct ctc aac ctt gaa gtc ccc acg tat gag ttc			832
Arg Leu Gly Pro Ala Pro Leu Asn Leu Glu Val Pro Thr Tyr Glu Phe			
	235	240	245
acc agt gac gat atg gtg att gtt ggt taa g agacttggac tcaagtcata			883
Thr Ser Asp Asp Met Val Ile Val Gly *			
	250	255	
ggcttctttc agtctttatg tcacctcagg agacttattt gagaggaagc cttctgtact			943
tgaagttgat ttgaaatatg taagaattga tgatgtattt gcaaacatta atgtgaaata			1003
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Trp Val Gly Arg Gln Arg Asp Ser Gly Val Leu Ser Arg Pro Cys Pro	
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tcg act gcg gcc ttg ccc gaa gcc ctt ttg tgc agc tcc gcg ccc gca	151
Ser Thr Ala Ala Leu Pro Glu Ala Leu Leu Cys Ser Ser Ala Pro Ala	
	20 25 30
gcc cga cgc ccc agc ttg tgc ggg gcc acg gga ggg tca tgc gcg gat	199
Ala Arg Arg Pro Ser Leu Cys Gly Ala Thr Gly Gly Ser Cys Ala Asp	
	35 40 45
ttc gac tcg ggt gtg gat ttc gtc cgt aga gag agc agc ggt ctg tgg	247
Phe Asp Ser Gly Val Asp Phe Val Arg Arg Glu Ser Ser Gly Leu Trp	
	50 55 60 65
ggc cca cag cct cca ctt tct cct gtt aaa aat tat act gag atg ttt	295
Gly Pro Gln Pro Pro Leu Ser Pro Val Lys Asn Tyr Thr Glu Met Phe	
	70 75 80
cag gac cca gtg gct ttt aag gat gtg gct gtg aac ttc acc cag gag	343
Gln Asp Pro Val Ala Phe Lys Asp Val Ala Val Asn Phe Thr Gln Glu	
	85 90 95
gag tgg gct ttg ctg gat att tcc cag aag aat ctc tac agg gaa gtg	391



Glu Trp Ala Leu Leu Asp Ile Ser Gln Lys Asn Leu Tyr Arg Glu Val	
100 105 110	
atg ctg gaa act ttc tgg aac ctg acc tct ata gga aaa aag tgg aaa	439
Met Leu Glu Thr Phe Trp Asn Leu Thr Ser Ile Gly Lys Lys Trp Lys	
115 120 125	
gac cag aac att gaa tat gag tac caa aac ccc agg aga aac ttc agg	487
Asp Gln Asn Ile Glu Tyr Glu Tyr Gln Asn Pro Arg Arg Asn Phe Arg	
130 135 140 145	
agt gtc aca gaa gag aaa gtc aat gaa att aaa gaa gac agt cat tgt	535
Ser Val Thr Glu Glu Lys Val Asn Glu Ile Lys Glu Asp Ser His Cys	
150 155 160	
gga gaa act ttt acc cca gtt cca gat gac agg ctg aac ttc cag aag	583
Gly Glu Thr Phe Thr Pro Val Pro Asp Asp Arg Leu Asn Phe Gln Lys	
165 170 175	
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Lys Lys Ala Ser Pro Glu Val Lys Ser Cys Asp Ser Phe Val Cys Glu	
180 185 190	
gtt ggc cta ggt aac tca tct tct aat atg aac atc aga ggt gac act	679
Val Gly Leu Gly Asn Ser Ser Ser Asn Met Asn Ile Arg Gly Asp Thr	
195 200 205	
gga cac aag gca tgt gaa tgt cag gaa tat gga cca aag cca tgg aag	727
Gly His Lys Ala Cys Glu Cys Gln Glu Tyr Gly Pro Lys Pro Trp Lys	
210 215 220 225	
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Ser Gln Gln Pro Lys Lys Ala Phe Arg Tyr His Pro Ser Leu Arg Thr	
230 235 240	
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Gln Glu Arg Asp His Thr Gly Lys Lys Pro Tyr Ala Cys Lys Glu Cys	
245 250 255	
gga aaa aac att att tac cat tca agc att caa aga cac atg gta gtg	871
Gly Lys Asn Ile Ile Tyr His Ser Ser Ile Gln Arg His Met Val Val	
260 265 270	
cac agt ggg gat gga cct tat aaa tgt aag ttt tgt ggg aaa gca ttc	919
His Ser Gly Asp Gly Pro Tyr Lys Cys Lys Phe Cys Gly Lys Ala Phe	
275 280 285	
cat tgt ctc agt tta tat ctt atc cat gaa aga act cac act gga gag	967
His Cys Leu Ser Leu Tyr Leu Ile His Glu Arg Thr His Thr Gly Glu	
290 295 300 305	
aaa ccg tat gaa tgt aaa caa tgt ggt aaa tct ttt agt tat tct gct	1015
Lys Pro Tyr Glu Cys Lys Gln Cys Gly Lys Ser Phe Ser Tyr Ser Ala	
310 315 320	
acc cat cga ata cat gaa aga act cac att gga gaa aag cct tat gaa	1063
Thr His Arg Ile His Glu Arg Thr His Ile Gly Glu Lys Pro Tyr Glu	
325 330 335	
tgt cag gaa tgt ggg aaa gca ttc cat agt ccc aga tcc tgt cac aga	1111
Cys Gln Glu Cys Gly Lys Ala Phe His Ser Pro Arg Ser Cys His Arg	
340 345 350	
cat gaa agg agt cac atg gga gag aag gct tat caa tgt aag gaa tgt	1159

His	Glu	Arg	Ser	His	Met	Gly	Glu	Lys	Ala	Tyr	Gln	Cys	Lys	Glu	Cys		
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Gly	Lys	Ala	Phe	Met	Cys	Pro	Arg	Tyr	Val	Arg	Arg	His	Glu	Arg	Thr		
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Ser	Ser	Leu	Thr	Ser	Phe	Gln	Thr	His	Ile	Arg	Met	His	Ser	Gly	Glu		
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Arg	Pro	Tyr	Glu	Cys	Lys	Thr	Cys	Gly	Lys	Gly	Phe	Tyr	Ser	Ala	Lys		
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Ser	Phe	Gln	Arg	His	Glu	Lys	Thr	His	Ser	Gly	Glu	Lys	Pro	Tyr	Lys		
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tgc	aag	caa	tgt	ggc	aaa	gcc	ttc	act	cgt	tcc	ggc	tcc	ttt	cga	tat	1447	
Cys	Lys	Gln	Cys	Gly	Lys	Ala	Phe	Thr	Arg	Ser	Gly	Ser	Phe	Arg	Tyr		
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His	Glu	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Gln	Cys		
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Gly	Lys	Ala	Phe	Arg	Ser	Ala	Pro	Asn	Leu	Gln	Ser	His	Gly	Arg	Thr		
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cac	act	gga	gag	aaa	ccg	tat	caa	tgt	aag	gaa	tgt	ggg	aaa	gct	ttc	1591	
His	Thr	Gly	Glu	Lys	Pro	Tyr	Gln	Cys	Lys	Glu	Cys	Gly	Lys	Ala	Phe		
		500					505					510					
aga	tct	gcc	tca	caa	ctt	cga	atc	cat	cgt	agg	att	cac	act	gga	gag	1639	
Arg	Ser	Ala	Ser	Gln	Leu	Arg	Ile	His	Arg	Arg	Ile	His	Thr	Gly	Glu		
	515					520					525						
aaa	ccc	tat	gaa	tgt	aag	aaa	tgt	ggg	aaa	gcc	ttc	aga	tat	gtc	cag	1687	
Lys	Pro	Tyr	Glu	Cys	Lys	Lys	Cys	Gly	Lys	Ala	Phe	Arg	Tyr	Val	Gln		
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aac	ttt	cga	ttt	cat	gaa	agg	aca	cac	aat	gga	gag	aaa	ccc	tat	gaa	1735	
Asn	Phe	Arg	Phe	His	Glu	Arg	Thr	His	Asn	Gly	Glu	Lys	Pro	Tyr	Glu		
				550					555					560			
tgt	aaa	gaa	tgc	aga	aaa	gca	ttc	agc	ttg	cct	act	tcc	ttt	cat	aga	1783	
Cys	Lys	Glu	Cys	Arg	Lys	Ala	Phe	Ser	Leu	Pro	Thr	Ser	Phe	His	Arg		
			565					570						575			
cat	gaa	aag	aca	ttg	gaa	gga	aac	cct	atg	aag	gca	agc	aat	gtg	gca	1831	
His	Glu	Lys	Thr	Leu	Glu	Gly	Asn	Pro	Met	Lys	Ala	Ser	Asn	Val	Ala		
		580				585						590					
aag	ctt	tca	ctt	ctt	cca	gtt	ctt	ttc	aat	atc	atg	aaa	gaa	ttc	aca	1879	
Lys	Leu	Ser	Leu	Leu	Pro	Val	Leu	Phe	Asn	Ile	Met	Lys	Glu	Phe	Thr		
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Gly	Ser	Leu	Leu	Pro	Val	Lys	Ile	Ile	Glu	Thr	Asp	Phe	Glu	Lys	Ala	
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Val	Phe	Leu	Ala	Thr	Cys	Phe	Asn	Ala	Leu	Leu	Pro	Ala	Val	Arg	Glu	
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aag	ctc	cag	aag	gtc	ctg	agc	ctc	ggc	cac	atc	agc	acc	gac	tac	ccg	546

Lys	Leu	Gln	Lys	Val	Leu	Ser	Leu	Gly	His	Ile	Ser	Thr	Asp	Tyr	Pro	
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Leu	Ala	Glu	Thr	Ile	Leu	Leu	Leu	Gly	Phe	Phe	Met	Thr	Val	Phe	Leu	
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Glu	Gln	Leu	Ile	Leu	Thr	Phe	Arg	Lys	Glu	Lys	Pro	Ser	Phe	Ile	Asp	
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Leu	Glu	Thr	Phe	Asn	Ala	Gly	Ser	Asp	Val	Gly	Ser	Asp	Ser	Glu	Tyr	
100					105					110					115	
gag	agc	ccc	ttc	atg	ggg	ggc	gcg	cgg	ggc	cac	gcg	ctg	tac	gtg	gag	738
Glu	Ser	Pro	Phe	Met	Gly	Gly	Ala	Arg	Gly	His	Ala	Leu	Tyr	Val	Glu	
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Pro	His	Gly	His	Gly	Pro	Ser	Leu	Ser	Val	Gln	Gly	Leu	Ser	Arg	Ala	
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Ser	Pro	Val	Arg	Leu	Leu	Ser	Leu	Ala	Phe	Ala	Leu	Ser	Ala	His	Ser	
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Val	Phe	Glu	Gly	Leu	Ala	Leu	Gly	Leu	Gln	Glu	Glu	Gly	Glu	Lys	Val	
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Val	Ser	Leu	Phe	Val	Gly	Val	Ala	Val	His	Glu	Thr	Leu	Val	Ala	Val	
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Ser	Val	Leu	Leu	Gln	Gly	Leu	Ala	Gly	Gly	Thr	Phe	Leu	Phe	Ile	Thr	
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Phe	Leu	Glu	Ile	Leu	Ala	Lys	Glu	Leu	Glu	Glu	Lys	Ser	Asp	Arg	Leu	
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ctc	aag	gtc	ctc	ttc	ctg	gtg	ctg	ggc	tac	acc	gtc	ctg	gcc	ggg	atg	1218
Leu	Lys	Val	Leu	Phe	Leu	Val	Leu	Gly	Tyr	Thr	Val	Leu	Ala	Gly	Met	
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gtc	ttc	ctc	aag	tgg	tga	gcggcc	ttgccattgt	ccctgccgcc	ggagcccgcc							1272
Val	Phe	Leu	Lys	Trp	*											
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 Gln Phe Pro His Leu Glu Ser Arg Asn Asp Asn Arg Thr Cys His Trp  
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 Cys Asp Thr Glu Ile His Ile Val Asn Ala Thr Ile Ser Asp Thr Asp  
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 Cys Met Lys Ser Ala Met Val Val Ala Leu Ser Lys Arg Ser Gln Glu  
 45 50 55 60

gcg gag gct gct ttt ctg agt gtt tac aag caa tta att gaa gca cca 241  
 Ala Glu Ala Ala Phe Leu Ser Val Tyr Lys Gln Leu Ile Glu Ala Pro  
 65 70 75

gcc ctg tgg gaa ctc aag ctc aag tcc agg cct gcc ctt gga gac tct 289  
 Ala Leu Trp Glu Leu Lys Leu Lys Ser Arg Pro Ala Leu Gly Asp Ser  
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cgg gtt cag caa gga caa cat gac cca aag aca gac aac cag aat aca 337  
 Arg Val Gln Gln Gly Gln His Asp Pro Lys Thr Asp Asn Gln Asn Thr  
 95 100 105

caa cag aaa gca ggc ttc aag gaa gga tgg ctg gca gag gcc tca gag 385  
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 125 130 135 140

gcg gca cgc agc cta gac gac aga ctg cag ccc ccc agc ttt gac ccc 481  
 Ala Ala Arg Ser Leu Asp Asp Arg Leu Gln Pro Pro Ser Phe Asp Pro  
 145 150 155

agt ggg cag ccc cgg cga gac ctc cac act tcg tgg aag agg aac ccc 529  
 Ser Gly Gln Pro Arg Arg Asp Leu His Thr Ser Trp Lys Arg Asn Pro  
 160 165 170

gag ctc ctc agc ccc aaa gcg cta aag gct acg cag gca gag ctg cta Glu Leu Leu Ser Pro Lys Ala Leu Lys Ala Thr Gln Ala Glu Leu Leu 175 180 185	577
gag ctg cgg cgg aag tac gac gag gag gca gca tcc aag gca gat gaa Glu Leu Arg Arg Lys Tyr Asp Glu Glu Ala Ala Ser Lys Ala Asp Glu 190 195 200	625
gtc ggc ctg atc atg acc aac ctg gag aaa gct aat cag cga gct gag Val Gly Leu Ile Met Thr Asn Leu Glu Lys Ala Asn Gln Arg Ala Glu 205 210 215 220	673
gct gcc cag cgg gag gtg gaa agt ctc cgg gaa cag ctg gcc tct gtc Ala Ala Gln Arg Glu Val Glu Ser Leu Arg Glu Gln Leu Ala Ser Val 225 230 235	721
aac agc tcc atc cgc ctg gct tgc tgc tct ccc cag ggg ccc agt ggg Asn Ser Ser Ile Arg Leu Ala Cys Cys Ser Pro Gln Gly Pro Ser Gly 240 245 250	769
gat aag gtg aac ttc act ctg tgc tgc ggc cct cgg ctg gag gcc gcg Asp Lys Val Asn Phe Thr Leu Cys Ser Gly Pro Arg Leu Glu Ala Ala 255 260 265	817
ctg gcc tcc aag gac agg gag atc ctg cgg ctg ctg aag gac gtg cag Leu Ala Ser Lys Asp Arg Glu Ile Leu Arg Leu Leu Lys Asp Val Gln 270 275 280	865
cac ctc cag agc tca ctg cag gag ctg gag gag gca tcc gcc aac cag His Leu Gln Ser Ser Leu Gln Glu Leu Glu Glu Ala Ser Ala Asn Gln 285 290 295 300	913
atc gcc gac ctg gag cgg cag ctc acg gcc aag tcc gag gcc ata gaa Ile Ala Asp Leu Glu Arg Gln Leu Thr Ala Lys Ser Glu Ala Ile Glu 305 310 315	961
aag ctg gaa gag aag ctc cag gcc cag tct gac tat gag gaa att aaa Lys Leu Glu Glu Lys Leu Gln Ala Gln Ser Asp Tyr Glu Glu Ile Lys 320 325 330	1009
acg gag ctg agc atc ctg aaa gcc atg aag ctg gcc tcc agc acc tgc Thr Glu Leu Ser Ile Leu Lys Ala Met Lys Leu Ala Ser Ser Thr Cys 335 340 345	1057
agc ctc ccc cag ggc atg gcc aag cct gaa gac tca ctg ctt att gca Ser Leu Pro Gln Gly Met Ala Lys Pro Glu Asp Ser Leu Leu Ile Ala 350 355 360	1105
aag gag gcc ttc ttc ccc acg cag aaa ttc ctt ctg gag aag ccc agc Lys Glu Ala Phe Phe Pro Thr Gln Lys Phe Leu Leu Glu Lys Pro Ser 365 370 375 380	1153
ctc ctg gcc agc cct gag gaa gac cca tca gag gac gat tcc atc aag Leu Leu Ala Ser Pro Glu Glu Asp Pro Ser Glu Asp Asp Ser Ile Lys 385 390 395	1201
gat tca ctg ggc acg gag cag tcc tac ccc tcc cct cag cag ctc cca Asp Ser Leu Gly Thr Glu Gln Ser Tyr Pro Ser Pro Gln Gln Leu Pro 400 405 410	1249
cct cca cca ggg cca gaa gac ccc ctg tct ccc agc ccc ggg cag ccc Pro Pro Pro Gly Pro Glu Asp Pro Leu Ser Pro Ser Pro Gly Gln Pro 415 420 425	1297



ctg ctg ggc ccc agc ttg ggg cct gac ggc act cgg act ttc tcg ctg Leu Leu Gly Pro Ser Leu Gly Pro Asp Gly Thr Arg Thr Phe Ser Leu 430 435 440	1345
tcc ccc ttc ccc agc ctg gca tca ggg gag aga ctg atg atg ccc cca Ser Pro Phe Pro Ser Leu Ala Ser Gly Glu Arg Leu Met Met Pro Pro 445 450 455 460	1393
gcc gcc ttc aag gga gag gcg ggc ggc ctg ctg gtg ttc ccc cca gcc Ala Ala Phe Lys Gly Glu Ala Gly Gly Leu Leu Val Phe Pro Pro Ala 465 470 475	1441
ttc tat ggc gcc aag ccc ccc aca gcc cct gcc acc ccg gcc cct ggc Phe Tyr Gly Ala Lys Pro Pro Thr Ala Pro Ala Thr Pro Ala Pro Gly 480 485 490	1489
cct gag cca ctg ggc ggt cct gag ccc gcg gat ggt ggt ggg ggc gga Pro Glu Pro Leu Gly Gly Pro Glu Pro Ala Asp Gly Gly Gly Gly Gly 495 500 505	1537
gcg gcg ggg ccc ggg gca gag gag gag cag ctg gac acg gca gag atc Ala Ala Gly Pro Gly Ala Glu Glu Glu Gln Leu Asp Thr Ala Glu Ile 510 515 520	1585
gcc ttc cag gtg aag gag cag ctg ctg aaa cac aac atc ggg cag cgg Ala Phe Gln Val Lys Glu Gln Leu Leu Lys His Asn Ile Gly Gln Arg 525 530 535 540	1633
gtg ttt ggg cat tac gtg ctg ggg ctg tcg cag ggc tcg gtc agc gag Val Phe Gly His Tyr Val Leu Gly Leu Ser Gln Gly Ser Val Ser Glu 545 550 555	1681
atc cta gcc cgg ccc aag ccc tgg cgc aag ctc acg gtg aag ggc aag Ile Leu Ala Arg Pro Lys Pro Trp Arg Lys Leu Thr Val Lys Gly Lys 560 565 570	1729
gag ccc ttc atc aag atg aag cag ttc ctg tcg gat gag cag aat gta Glu Pro Phe Ile Lys Met Lys Gln Phe Leu Ser Asp Glu Gln Asn Val 575 580 585	1777
ctg gcg ctc agg acc atc caa gtg cgg cag cga ggc agc atc acc ccg Leu Ala Leu Arg Thr Ile Gln Val Arg Gln Arg Gly Ser Ile Thr Pro 590 595 600	1825
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cta gag cag gcc aag aag gag atc gag tcg cag aag ggc ggc gag ccc Leu Glu Gln Ala Lys Lys Glu Ile Glu Ser Gln Lys Gly Gly Glu Pro 625 630 635	1921
aag acc tcg gtg gcc ccg ctg agc atc gcc aac ggc acg acc ccc gcc Lys Thr Ser Val Ala Pro Leu Ser Ile Ala Asn Gly Thr Thr Pro Ala 640 645 650	1969
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agg ggc cgc tcg gtg ccc ccc tcg ccc ccg gag cgg cca tca ctg gcc	2113
Arg Gly Arg Ser Val Pro Pro Ser Pro Pro Glu Arg Pro Ser Leu Ala	
685 690 695 700	
acc gcg agc cag aac ggg gcc ccg gcc ttg gtg aag cag gag gag ggc	2161
Thr Ala Ser Gln Asn Gly Ala Pro Ala Leu Val Lys Gln Glu Glu Gly	
705 710 715	
agc ggg ggc ccc gcg cag gcg ccg ctc ccg gtc ctg tcc ccc gcc gcc	2209
Ser Gly Gly Pro Ala Gln Ala Pro Leu Pro Val Leu Ser Pro Ala Ala	
720 725 730	
ttc gtg cag agc atc atc cgc aag gtc aag tcc gag atc ggc gac gcc	2257
Phe Val Gln Ser Ile Ile Arg Lys Val Lys Ser Glu Ile Gly Asp Ala	
735 740 745	
ggc tac ttc gac cac cac tgg gcc tcc gac cgc ggc ctg ctc agc cgc	2305
Gly Tyr Phe Asp His His Trp Ala Ser Asp Arg Gly Leu Leu Ser Arg	
750 755 760	
ccc tac gcc tcc gtg tcg ccc tcg ctg tcc tcc tcc tcc tcc tct ggc	2353
Pro Tyr Ala Ser Val Ser Pro Ser Leu Ser Ser Ser Ser Ser Gly	
765 770 775 780	
tac tct ggc cag ccc aac ggc cgc gcc tgg ccc cgc ggg gac gag gcc	2401
Tyr Ser Gly Gln Pro Asn Gly Arg Ala Trp Pro Arg Gly Asp Glu Ala	
785 790 795	
cct gtg ccc ccc gag gac gag gcg gcg gca ggg gcg gag gac gaa ccc	2449
Pro Val Pro Pro Glu Asp Glu Ala Ala Gly Ala Glu Asp Glu Pro	
800 805 810	
ccc agg acg ggc gag ctc aag gct gag ggc gcg acg gcc gag gcg ggc	2497
Pro Arg Thr Gly Glu Leu Lys Ala Glu Gly Ala Thr Ala Glu Ala Gly	
815 820 825	
gcg cgg ctg ccc tac tac ccg gcc tac gtg ccg cgc acc ctg aag ccc	2545
Ala Arg Leu Pro Tyr Tyr Pro Ala Tyr Val Pro Arg Thr Leu Lys Pro	
830 835 840	
acc gtg ccg ccg ctg acc ccc gag cag tac gag ctg tac atg tac cgt	2593
Thr Val Pro Pro Leu Thr Pro Glu Gln Tyr Glu Leu Tyr Met Tyr Arg	
845 850 855 860	
gag gta gac acg ctg gag ctc acc cgc cag gtc aag gag aag ctg gcc	2641
Glu Val Asp Thr Leu Glu Leu Thr Arg Gln Val Lys Glu Lys Leu Ala	
865 870 875	
aag aac ggc atc tgc cag agg atc ttc ggg gag aag gtg ctg ggc ctg	2689
Lys Asn Gly Ile Cys Gln Arg Ile Phe Gly Glu Lys Val Leu Gly Leu	
880 885 890	
tca cag ggc agc gtg agc gac atg ctg tcc ccg ccg aag cca tgg agc	2737
Ser Gln Gly Ser Val Ser Asp Met Leu Ser Arg Pro Lys Pro Trp Ser	
895 900 905	
aag ctg acg cag aag ggg ccg gag ccc ttc atc cgc atg cag ctg tgg	2785
Lys Leu Thr Gln Lys Gly Arg Glu Pro Phe Ile Arg Met Gln Leu Trp	
910 915 920	
ctc tct gac cag ctc ggc cag gca gtg ggc cag cag cct ggt gcc tcc	2833
Leu Ser Asp Gln Leu Gly Gln Ala Val Gly Gln Gln Pro Gly Ala Ser	
925 930 935 940	

cag gcc agt ccc aca gaa cca agg tcc tca cca tcc cca ccc ccc agc	2881
Gln Ala Ser Pro Thr Glu Pro Arg Ser Ser Pro Ser Pro Pro Pro Ser	
945 950 955	
ccc aca gag cct gag aag agc tcc cag gag ccg ttg agc ctg tcc ctg	2929
Pro Thr Glu Pro Glu Lys Ser Ser Gln Glu Pro Leu Ser Leu Ser Leu	
960 965 970	
gag agc agc aag gag aac cag cag cca gag ggc cgc tcc agc tcc tcg	2977
Glu Ser Ser Lys Glu Asn Gln Gln Pro Glu Gly Arg Ser Ser Ser Ser	
975 980 985	
ttg agc ggg aag atg tac tca ggc agc cag gcc cca ggg ggc atc cag	3025
Leu Ser Gly Lys Met Tyr Ser Gly Ser Gln Ala Pro Gly Gly Ile Gln	
990 995 1000	
gag atc gtg gcc atg tcc ccc gag ctg gac acg tac tcc atc acc aag	3073
Glu Ile Val Ala Met Ser Pro Glu Leu Asp Thr Tyr Ser Ile Thr Lys	
1005 1010 1015 1020	
agg gtg aag gag gtc ctc aca gac aac aat cta ggg cag cgg ctg ttt	3121
Arg Val Lys Glu Val Leu Thr Asp Asn Asn Leu Gly Gln Arg Leu Phe	
1025 1030 1035	
ggg gaa agc atc ctg ggt ctg aca cag ggc tcc gtg tct gac ctg ctg	3169
Gly Glu Ser Ile Leu Gly Leu Thr Gln Gly Ser Val Ser Asp Leu Leu	
1040 1045 1050	
tcc cgg ccc aaa ccc tgg cac aag ctg agc ctg aag ggg cgg gag cct	3217
Ser Arg Pro Lys Pro Trp His Lys Leu Ser Leu Lys Gly Arg Glu Pro	
1055 1060 1065	
ttt gtc cgc atg cag ctg tgg ctc aat gac ccc cat aac gtg gag aag	3265
Phe Val Arg Met Gln Leu Trp Leu Asn Asp Pro His Asn Val Glu Lys	
1070 1075 1080	
ctg agg gat atg aag aag ctg gag aag aaa gcc tac ctg aaa cgt cgc	3313
Leu Arg Asp Met Lys Lys Leu Glu Lys Lys Ala Tyr Leu Lys Arg Arg	
1085 1090 1095 1100	
tat ggc ctc atc agc acc ggc tca gac agt gag tcc ccg gcc acc cgc	3361
Tyr Gly Leu Ile Ser Thr Gly Ser Asp Ser Glu Ser Pro Ala Thr Arg	
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tca gag tgc ccc agc ccc tgc ctg cag ccc cag gac ctg agc ctc ctg	3409
Ser Glu Cys Pro Ser Pro Cys Leu Gln Pro Gln Asp Leu Ser Leu Leu	
1120 1125 1130	
cag atc aag aag ccc cgg gtg gtg ctg gca ccc gag gag aag gag gca	3457
Gln Ile Lys Lys Pro Arg Val Val Leu Ala Pro Glu Glu Lys Glu Ala	
1135 1140 1145	
ctg cgg aag gcc tat cag ctg gaa ccc tac ccc tcg cag cag acc atc	3505
Leu Arg Lys Ala Tyr Gln Leu Glu Pro Tyr Pro Ser Gln Gln Thr Ile	
1150 1155 1160	
gag ctc ctc tcc ttc cag ctc aac ctc aag acc aac acc gtc atc aac	3553
Glu Leu Leu Ser Phe Gln Leu Asn Leu Lys Thr Asn Thr Val Ile Asn	
1165 1170 1175 1180	
tgg ttc cac aac tac agg tcc cgg atg cgc cgg gag atg ttg gtg gag	3601
Trp Phe His Asn Tyr Arg Ser Arg Met Arg Arg Glu Met Leu Val Glu	
1185 1190 1195	

ggg acc cag gat gag cca gac ctt gat cca agc ggg ggt cct gga atc Gly Thr Gln Asp Glu Pro Asp Leu Asp Pro Ser Gly Gly Pro Gly Ile 1200 1205 1210	3649
cta ccg cca ggc cac tcc cac cca gac ccc acc ccg cag agc cct gac Leu Pro Pro Gly His Ser His Pro Asp Pro Thr Pro Gln Ser Pro Asp 1215 1220 1225	3697
tct gag act gag gac cag aag cca acc gtg aag gaa ctg gag ctt cag Ser Glu Thr Glu Asp Gln Lys Pro Thr Val Lys Glu Leu Glu Leu Gln 1230 1235 1240	3745
gag ggc cct gag gag aac agc aca ccc ctg acc acc cag gac aag gcc Glu Gly Pro Glu Glu Asn Ser Thr Pro Leu Thr Thr Gln Asp Lys Ala 1245 1250 1255 1260	3793
caa gtg agg atc aag cag gaa cag atg gag gag gac gct gag gaa gag Gln Val Arg Ile Lys Gln Glu Gln Met Glu Glu Asp Ala Glu Glu Glu 1265 1270 1275	3841
gca ggc agc cag ccc cag gac tca ggg gag ctg gac aaa ggc caa ggt Ala Gly Ser Gln Pro Gln Asp Ser Gly Glu Leu Asp Lys Gly Gln Gly 1280 1285 1290	3889
ccc ccc aaa gag gag cat ccc gac cct ccg ggt aat gat gga ctc cca Pro Pro Lys Glu Glu His Pro Asp Pro Pro Gly Asn Asp Gly Leu Pro 1295 1300 1305	3937
aaa gtg gct ccc ggg ccc ctc ctt cca ggt gga tcc acc cca gac tgt Lys Val Ala Pro Gly Pro Leu Leu Pro Gly Gly Ser Thr Pro Asp Cys 1310 1315 1320	3985
ccc tca ctt cat ccc caa cag gag agt gag gcc ggg gag cga ctt cac Pro Ser Leu His Pro Gln Gln Glu Ser Glu Ala Gly Glu Arg Leu His 1325 1330 1335 1340	4033
ccg gac cct tta agt ttt aag tca gcc tca gag tcc tca cgc tgc agc Pro Asp Pro Leu Ser Phe Lys Ser Ala Ser Glu Ser Ser Arg Cys Ser 1345 1350 1355	4081
ctg gag gtg tca ctg aac tcg ccc tcg gcc gcc tcc tca cca ggc ctc Leu Glu Val Ser Leu Asn Ser Pro Ser Ala Ala Ser Ser Pro Gly Leu 1360 1365 1370	4129
atg atg tct gtg tca cct gtc ccc tcc tcc tca gct ccc atc tcc cca Met Met Ser Val Ser Pro Val Pro Ser Ser Ser Ala Pro Ile Ser Pro 1375 1380 1385	4177
tcc cca cct ggc gcc ccc cct gcc aaa gtg ccg agt gcc agc ccc act Ser Pro Pro Gly Ala Pro Pro Ala Lys Val Pro Ser Ala Ser Pro Thr 1390 1395 1400	4225
gct gac atg gct gga gcc ttg cac ccc agt gcc aag gtg aac ccc aac Ala Asp Met Ala Gly Ala Leu His Pro Ser Ala Lys Val Asn Pro Asn 1405 1410 1415 1420	4273
ttg cag cgg cgg cat gag aag atg gcc aat ctg aac aac atc att tac Leu Gln Arg Arg His Glu Lys Met Ala Asn Leu Asn Asn Ile Ile Tyr 1425 1430 1435	4321
cga cta gag cgg gct gcc aat cgg gag gag gcc ctg gag tgg gag ttc Arg Leu Glu Arg Ala Ala Asn Arg Glu Glu Ala Leu Glu Trp Glu Phe 1440 1445 1450	4369

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tattttgaca ataggaaaca gtgaccattt tcagagtaat caaatctgga acaaatgaaa 6229  
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<210> 457
<211> 1461
<212> DNA
<213> Homo sapiens
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<221> CDS
<222> (262) .. (1323)
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1185



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aca aaa gca ttc agc ggt aaa cac aca ctt gtt cag cag cag aga acc Thr Lys Ala Phe Ser Gly Lys His Thr Leu Val Gln Gln Gln Arg Thr 140 145 150	723
ctc act aca gaa aga tgt tac ata tgc agt gaa tgt ggg aaa tcc ttt Leu Thr Thr Glu Arg Cys Tyr Ile Cys Ser Glu Cys Gly Lys Ser Phe 155 160 165 170	771
agc aaa agc tac agt ctc aat gac cat tgg aga ctt cac act gga gaa Ser Lys Ser Tyr Ser Leu Asn Asp His Trp Arg Leu His Thr Gly Glu 175 180 185	819
aag cct tat gaa tgt cga gag tgt ggg aag tcc ttt agg caa agc tct Lys Pro Tyr Glu Cys Arg Glu Cys Gly Lys Ser Phe Arg Gln Ser Ser 190 195 200	867
agt ctc att caa cac cgg aga ggt cac act gca gta cga cct cat gag Ser Leu Ile Gln His Arg Arg Gly His Thr Ala Val Arg Pro His Glu 205 210 215	915
ggg gat gaa tgt gga aaa tta ttt agc aac ccg tct aac ctc att aaa Gly Asp Glu Cys Gly Lys Leu Phe Ser Asn Pro Ser Asn Leu Ile Lys 220 225 230	963
cat cgg aga gtt cac act ggg gaa agg cca tat gag tgc agc gaa tgt His Arg Arg Val His Thr Gly Glu Arg Pro Tyr Glu Cys Ser Glu Cys 235 240 245 250	1011
ggg aaa tcc ttt aac caa agg tct gca ctc ctt caa cat cgg gga ggt Gly Lys Ser Phe Asn Gln Arg Ser Ala Leu Leu Gln His Arg Gly Gly 255 260 265	1059
cac act ggg gag agg cct tat gag tgc agt gaa tgt ggg aag ttt ttt His Thr Gly Glu Arg Pro Tyr Glu Cys Ser Glu Cys Gly Lys Phe Phe 270 275 280	1107
ccc tac agc tcc agt ctc cga aaa cac cag aga gtt cac act gga tca Pro Tyr Ser Ser Ser Leu Arg Lys His Gln Arg Val His Thr Gly Ser 285 290 295	1155
aga ccc tat gag tgc agt gaa tgt ggg aaa tcc ttt act caa aat tcc Arg Pro Tyr Glu Cys Ser Glu Cys Gly Lys Ser Phe Thr Gln Asn Ser 300 305 310	1203
ggc ctc att aag cac agg agg gtt cac act ggg gag aag cct tat gag Gly Leu Ile Lys His Arg Arg Val His Thr Gly Glu Lys Pro Tyr Glu 315 320 325 330	1251
tgc acg gaa tgt ggg aaa tcc ttt agc cat aac tcc agc ctt att aaa Cys Thr Glu Cys Gly Lys Ser Phe Ser His Asn Ser Ser Leu Ile Lys 335 340 345	1299
cat cag aga att cat agt cga taa aaggcattatg agtggcaaatt gtggaaaatc His Gln Arg Ile His Ser Arg *	1353
tgtagcacc ctggagaaag tccttgagta cacagtgaat gtcagaaagc ttcagctgaa	1413
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<220>
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<222> (206)..(1009)
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1187

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170                      175                      180                      185

gtg gcc tcc tcc tcc agg cat gga ggt ctg tcc act act ggg ctt ctg      808
Val Ala Ser Ser Ser Arg His Gly Gly Leu Ser Thr Thr Gly Leu Leu
                      190                      195                      200

ggc tat ttg ccc ctg att tgc tcc ctg gta cgg gct ctt gtt aac agg      856
Gly Tyr Leu Pro Leu Ile Cys Ser Leu Val Arg Ala Leu Val Asn Arg
                      205                      210                      215

cag gca agg ggt gcg ggg acc agg caa ggg ctt caa agg gta cag tac      904
Gln Ala Arg Gly Ala Gly Thr Arg Gln Gly Leu Gln Arg Val Gln Tyr
                      220                      225                      230

caa atc ttc caa act cag cac ttg tgc cct ggg gtc tcc aaa ctg tct      952
Gln Ile Phe Gln Thr Gln His Leu Cys Pro Gly Val Ser Lys Leu Ser
                      235                      240                      245

tct gcc cta gga ttt att cat act gtt aaa tta cca gtt tat gca aat      1000
Ser Ala Leu Gly Phe Ile His Thr Val Lys Leu Pro Val Tyr Ala Asn
250                      255                      260                      265

gat atg taa ataaagctca atttttttgaa aaaaaa      1035
Asp Met *
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<213> Homo sapiens
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<220>
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<222> (49)..(756)
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                                   1

gct ctg ctc ctc ctg acc ctc ctc act cac tct gca gtg tca gtg gtc      105
Ala Leu Leu Leu Leu Thr Leu Leu Thr His Ser Ala Val Ser Val Val
                    5                      10                      15

cag gca ggg ctg act cag cca ccc tcg gtg tcc aag ggc ttg aga cag      153
Gln Ala Gly Leu Thr Gln Pro Pro Ser Val Ser Lys Gly Leu Arg Gln
20                      25                      30                      35

acc gcc aca ctc acc tgc act ggg aac agc aac aat gtt ggc gac caa      201
Thr Ala Thr Leu Thr Cys Thr Gly Asn Ser Asn Asn Val Gly Asp Gln
                      40                      45                      50

gga gca tct tgg ctg cag cag cac cag ggc cac cct ccc aaa ctc ctc      249
Gly Ala Ser Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
                      55                      60                      65

tcc tac agg aat aac aac cgg ccc tca ggg atc tca gag aga tta tct      297
Ser Tyr Arg Asn Asn Asn Arg Pro Ser Gly Ile Ser Glu Arg Leu Ser
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70	75	80	
gca tcc agg tca gga aac aca gcc tcc ctg acc att act gga ctc cag			345
Ala Ser Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln			
85	90	95	
cct gag gac gag gct gac tat tac tgc tca gca tgg gac agc agc ctc			393
Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Ser Ser Leu			
100	105	110	115
agt gct tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag			441
Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln			
	120	125	130
ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct gag gag			489
Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu			
	135	140	145
ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac ttc tac			537
Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr			
	150	155	160
ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc agc ccc gtc aag			585
Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys			
	165	170	175
gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac aag tac			633
Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr			
180	185	190	195
gcg gcc agc agc tac ctg agc ctg acg cct gag cag tgg aag tcc cac			681
Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His			
	200	205	210
aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg gag aag			729
Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys			
	215	220	225
aca gtg gcc cct aca gaa tgt tca tag gttct caaccctcac cccaccacg			781
Thr Val Ala Pro Thr Glu Cys Ser *			
	230	235	
ggagactaga gctgcaggat cccaggggag ggggtctctcc tcccacccca aggcataag			841
cccttctccc tgcactcaat aaaccctcaa taaatattct cattgtcaat caaaaaaaaa			901
aaaaa			906

<210> 460  
<211> 1941  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (203)..(1588)

<400> 460	
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cttgcgctgg ggtgccacac ttaggctgag ctgcaggttt tcgcacagtc gcgagttaac	120

1190

1191



1192

135	140	145	150	
gat gaa agc ttt ggg gca gtg aag aag aaa ttc tgt acc ttt cga gaa				715
Asp Glu Ser Phe Gly Ala Val Lys Lys Lys Phe Cys Thr Phe Arg Glu				
	155	160	165	
gat tat gat gac att tcc aat cag ata gac ttc atc atc tgc ctg ggg				763
Asp Tyr Asp Asp Ile Ser Asn Gln Ile Asp Phe Ile Ile Cys Leu Gly				
	170	175	180	
gga gac ggg acg ctg ctg tac gct tcc tcg ctt ttc cag gga acg cag				811
Gly Asp Gly Thr Leu Leu Tyr Ala Ser Ser Leu Phe Gln Gly Thr Gln				
	185	190	195	
ctg ttg ttc tcc gga gtc ggc tga aggtcagggt ggtgaaggag ctccggggga				865
Leu Leu Phe Ser Gly Val Gly *				
	200	205		
agaagacggc cgtgcacaat gggctgggtg agaaaggctc gcaggctgca ggccctggaca				925
tggatgtcgg gaagcaggcc atgcagtacc aggtcctgaa tgagggtggtg attgacagag				985
gccccctctc ctacctgtcc aatgtggatg tctacctgga cggacacctc atcaccacgg				1045
tgcagggcga cggagtgatc gtgtccaccc cgacgggcag cacggcgtat gcggccgcaa				1105
gctta				1110

<210> 462  
 <211> 3344  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (602)..(2251)

<400> 462	
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ctggcatttc atcaaccaga ggaaaaaaaa aataagacat cataaaggga gagaagcccc	120
ttatgggtct ttcaactctc gtatatattt aaatgcaatt ggagccccgc agggaatacc	180
agatcaattt aaagcttgaa atcaaatagt tacaggactg aagtcaatat tttggtagat	240
gacagtcaat aaaaatgtaa attagatata ctacatctat tacaaccaac agcaacgagc	300
ttttcatgag ttaaaaagaa aaactcatgt cggccccagc cctgggggcta cctgacctga	360
caaaactctt tacactccat gtgtcaaaaa gagaaaaaat ggcagttgga gttttaacct	420
agactgtggg gccctggcca aggccagtgg cctatctctc aaaacaacta gatgggtttc	480
caaaggctgg ccactatgtc taaggaccct ggcagcaaca gccctgttag cacaagaagc	540
agataaacta acccttgggc aaaacctgaa tataaaggcc ccccatgctg tggtaacttt	600
g atg act acc gaa gga cat cat tgg cta aca aat gct aga tta acc	646
Met Thr Thr Glu Gly His His Trp Leu Thr Asn Ala Arg Leu Thr	
1 5 10 15	

aag tac caa agc ttg cca tgt gaa aat ccc cac ata act att gaa gtc Lys Tyr Gln Ser Leu Pro Cys Glu Asn Pro His Ile Thr Ile Glu Val	694
20 25 30	
tgt aac acc cta aat ccc acc acc ctg ctc cca gta tca gag agc ccg Cys Asn Thr Leu Asn Pro Thr Thr Leu Leu Pro Val Ser Glu Ser Pro	742
35 40 45	
ggc gag cat aac tgt gta gag gtg ttg gac tca gtc tat tct agc aga Gly Glu His Asn Cys Val Glu Val Leu Asp Ser Val Tyr Ser Ser Arg	790
50 55 60	
cct gac ctt cgg gac cag cca tgg gca tca tca gta gac tgg gag tta Pro Asp Leu Arg Asp Gln Pro Trp Ala Ser Ser Val Asp Trp Glu Leu	838
65 70 75	
tac atg gac ggg agc agc ttc atc aac tca caa gga gaa aga tgt gca Tyr Met Asp Gly Ser Ser Phe Ile Asn Ser Gln Gly Glu Arg Cys Ala	886
80 85 90 95	
gga tat gcg gtg gta act ttg gat gct gtc att aaa gcc aaa ctg tgg Gly Tyr Ala Val Val Thr Leu Asp Ala Val Ile Lys Ala Lys Leu Trp	934
100 105 110	
cta cag ggc act tca gcc cag aag gct gag ctc att gct tta act cgg Leu Gln Gly Thr Ser Ala Gln Lys Ala Glu Leu Ile Ala Leu Thr Arg	982
115 120 125	
gct gta gaa ctc agt gaa ggg caa gag tca ctt gaa gaa ttg tta ggc Ala Val Glu Leu Ser Glu Gly Gln Glu Ser Leu Glu Glu Leu Leu Gly	1030
130 135 140	
cgg tac ttc tac gtc tca cac ttg cca gcc ttt gcc aaa gca gta gca Arg Tyr Phe Tyr Val Ser His Leu Pro Ala Phe Ala Lys Ala Val Ala	1078
145 150 155	
caa ctg tgc att aca tgc cga cag cac aat gcg agg caa agc ccc act Gln Leu Cys Ile Thr Cys Arg Gln His Asn Ala Arg Gln Ser Pro Thr	1126
160 165 170 175	
gtt tcg ccc cac ata caa gct tat gga gca gct cct ttt gag gat ctt Val Ser Pro His Ile Gln Ala Tyr Gly Ala Ala Pro Phe Glu Asp Leu	1174
180 185 190	
cag gtg gat ttc aca gaa atg cca aaa tgt gga ggt aac aag tat ttg Gln Val Asp Phe Thr Glu Met Pro Lys Cys Gly Gly Asn Lys Tyr Leu	1222
195 200 205	
ctg gtt ctt acg tgt act tac tct ggg tgg gtg gag gct tat cca aca Leu Val Leu Thr Cys Thr Tyr Ser Gly Trp Val Glu Ala Tyr Pro Thr	1270
210 215 220	
cga act gaa aag gcc tac gaa gta acc cgt gtg ctt ctc cga gat ctt Arg Thr Glu Lys Ala Tyr Glu Val Thr Arg Val Leu Leu Arg Asp Leu	1318
225 230 235	
att cct agg ttt gga ctg ccc tta cga att ggc tca cat aac ggg ccg Ile Pro Arg Phe Gly Leu Pro Leu Arg Ile Gly Ser His Asn Gly Pro	1366
240 245 250 255	
gtg ttt gtg gct gac ttg gac tgt gtg gaa atc aat gtg gat act ggt Val Phe Val Ala Asp Leu Asp Cys Val Glu Ile Asn Val Asp Thr Gly	1414
260 265 270	

gtc att tgg gcc act tgg ata aaa aat gaa aag gat cca gtg cag ctt Val Ile Trp Ala Thr Trp Ile Lys Asn Glu Lys Asp Pro Val Gln Leu 275 280 285	1462
cag aaa gga aaa agt ggc cct tcc tgt act aag gga caa tgt aac ccc Gln Lys Gly Lys Ser Gly Pro Ser Cys Thr Lys Gly Gln Cys Asn Pro 290 295 300	1510
tta gag cta gta ata acc aat ccc ctt gat cct cgc tgg aaa aaa ggg Leu Glu Leu Val Ile Thr Asn Pro Leu Asp Pro Arg Trp Lys Lys Gly 305 310 315	1558
gag cgt gtg acc tta gga atc aat ggg gct gga ctg aat ccc cga gta Glu Arg Val Thr Leu Gly Ile Asn Gly Ala Gly Leu Asn Pro Arg Val 320 325 330 335	1606
aat atc ttg gtt cga gga gaa gtt tac aaa tgc tct ctt gag cca gtg Asn Ile Leu Val Arg Gly Glu Val Tyr Lys Cys Ser Leu Glu Pro Val 340 345 350	1654
ttt caa act ttc tat gat gaa cta aat gtg cca ata aca gaa ttt cca Phe Gln Thr Phe Tyr Asp Glu Leu Asn Val Pro Ile Thr Glu Phe Pro 355 360 365	1702
gga aaa aca aga aat ttg ttt ttg caa tta gcc gag cat gta gcc cag Gly Lys Thr Arg Asn Leu Phe Leu Gln Leu Ala Glu His Val Ala Gln 370 375 380	1750
tct ctc act gtc act tca tgt tat gta tgt gga gga act gta ata gca Ser Leu Thr Val Thr Ser Cys Tyr Val Cys Gly Gly Thr Val Ile Ala 385 390 395	1798
gat caa tgg cca tgg gaa gcc cga gaa tta gta cct aca gac cca gtt Asp Gln Trp Pro Trp Glu Ala Arg Glu Leu Val Pro Thr Asp Pro Val 400 405 410 415	1846
cct gat gaa ttc cca gct caa aag aat cac cct gat aat ttc tgg gtc Pro Asp Glu Phe Pro Ala Gln Lys Asn His Pro Asp Asn Phe Trp Val 420 425 430	1894
cta aaa gcc tca atc att aga caa tac tat ata gca aga gtg gag aag Leu Lys Ala Ser Ile Ile Arg Gln Tyr Tyr Ile Ala Arg Val Glu Lys 435 440 445	1942
gac ttc acc ctt cct gta gga aga cta cat ggt gga gtt caa acc aca Asp Phe Thr Leu Pro Val Gly Arg Leu His Gly Gly Val Gln Thr Thr 450 455 460	1990
cag aga aaa atc cat tca gta aat ttc caa agt tgc aga ccg ttt agg Gln Arg Lys Ile His Ser Val Asn Phe Gln Ser Cys Arg Pro Phe Arg 465 470 475	2038
ccc acc cag aat ccc acc ggg act gga cag ccc cca ctg ggc tat act Pro Thr Gln Asn Pro Thr Gly Thr Gly Gln Pro Pro Leu Gly Tyr Thr 480 485 490 495	2086
gga tat gtg gac ata gag cct aca cta agc tgc ctg aca agt agt tgt Gly Tyr Val Asp Ile Glu Pro Thr Leu Ser Cys Leu Thr Ser Ser Cys 500 505 510	2134
gtt att ggc act att aaa cca tct ttc ttc cta ctg tcc ata aaa aca Val Ile Gly Thr Ile Lys Pro Ser Phe Phe Leu Leu Ser Ile Lys Thr 515 520 525	2182

gga gaa ctc ctg ggc ttc cct gtc tat gct tcc cgt gaa aag cat agc 2230  
 Gly Glu Leu Leu Gly Phe Pro Val Tyr Ala Ser Arg Glu Lys His Ser  
 530 535 540  
 tat aag aaa ttg aaa caa tga ta aatggccccc tgagagaatc atacagtatt 2283  
 Tyr Lys Lys Leu Lys Gln \*  
 545 550  
 atgggcctgc tacttaggca caagatggct cgtggggata ccggatcccc atttatatga 2343  
 tcaaccgaat catacgggta caagctgtct taaaaataat cactgcaacc ggcagagcct 2403  
 tgactattct ggcccagcaa gaaactcaga tgagaaatgc tatctatcaa aatagattag 2463  
 ctctcgacta cttgctagca gctgaaggag aggtctgtag gaaatttaac cttactaatt 2523  
 gctgcctaca catagataac caagggcaag tagttgaaga catagttaga gatatgacaa 2583  
 aagtggcaca tgtgcccgtg caagtgtggc atggatttga tcctggggcc atgttttagaa 2643  
 aatgggtccc agcgctagga ggatttaaaa ctcttataat aagaggtata atagtaatag 2703  
 gaacctactt actgctccct cgtttgctac ctgtacttct tcaaatagata aaaagcttca 2763  
 tcgctacctt agtgtaccaa aatgcatcat cacaggtgta ctatataaat cactattgat 2823  
 ctgtctagca cgaagacatg ggtagtaaac atgaaacaac tcctgctatt gagtgagagt 2883  
 ctcaaagtgg gggaataagg gaggagacca cccctcatat tgtcttatgc ccaatttctg 2943  
 cctccaaaga aagaaaaagt aaaaactaaa aggcagaaat gaaatccaca agcagacagc 3003  
 ccgggcgcca caccctggga ctggtagttg aaaatcaatc ccggacctaa tcggttatgt 3063  
 tatctataga ttacagacat tgtatagaaa agcattgtga aaatctcatt cctgttttgt 3123  
 tccaatctaa ttactggtgc gtgcagcccc cagtcacgta cccacgtacc tcctgcttgc 3183  
 tcaatcgatc acgaccctct cagcacacc cccttagact tgtgagtcct taaaaggac 3243  
 aggaattgct cactcggggc gggggctcgg ctcttgagac aggagtcttg ctgcactgcc 3303  
 ggctaataa accccttctt tctttaaaaa aaaaaaaaaa a 3344

<210> 463  
 <211> 673  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (240) .. (575)

<400> 463  
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 tgccctcagt tgcatgttca ctgggcatct tcccttcgac ccctttgccc acgtggtgac 120  
 cgctggggag ctgtgagagt gtgaggggca cgttccagcc gtctggactc tttctctcct 180

actgagacgc agcctatagg tccgcaggcc agtcctccca ggaactgaaa tagtgaaat 239  
 atg agt tgg cga gga aga tca aca tat agg cct agg cca aga aga agt 287  
 Met Ser Trp Arg Gly Arg Ser Thr Tyr Arg Pro Arg Pro Arg Arg Ser  
 1 5 10 15  
  
 tta cag cct cct gag ctg att ggg gct atg ctt gaa ccc act gat gaa 335  
 Leu Gln Pro Pro Glu Leu Ile Gly Ala Met Leu Glu Pro Thr Asp Glu  
 20 25 30  
  
 gag cct aaa gaa gag aaa cca ccc act aaa agt cgg aat cct aca cct 383  
 Glu Pro Lys Glu Glu Lys Pro Pro Thr Lys Ser Arg Asn Pro Thr Pro  
 35 40 45  
  
 gat cag aag aga gaa gat gat cag ggt gca gct gag att caa gtg cct 431  
 Asp Gln Lys Arg Glu Asp Asp Gln Gly Ala Ala Glu Ile Gln Val Pro  
 50 55 60  
  
 gac ctg gaa gcc gat ctc cag gag cta tgt cag aca aag act ggg gat 479  
 Asp Leu Glu Ala Asp Leu Gln Glu Leu Cys Gln Thr Lys Thr Gly Asp  
 65 70 75 80  
  
 gga tgt gaa ggt ggt act gat gtc aag ggg aag att cta cca aaa gca 527  
 Gly Cys Glu Gly Gly Thr Asp Val Lys Gly Lys Ile Leu Pro Lys Ala  
 85 90 95  
  
 gag cac ttt aaa atg cca gaa gca ggt gaa ggg aaa tca cag gtt taa 575  
 Glu His Phe Lys Met Pro Glu Ala Gly Glu Gly Lys Ser Gln Val \*  
 100 105 110  
  
 aggaagataa gctgaaacaa cacaaactgt ttttatatta gatattttac tttaaaatat 635  
  
 cttaataaag ttttaagctt ttctccaaaa aaaaaaaa 673

<210> 464  
 <211> 987  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (733)..(909)

<220>  
 <221> misc\_feature  
 <222> (1)..(987)  
 <223> n = a,t,c or g

<400> 464  
 gatccaaatt tanagctatc aacataaggt tgaccctact aaaggaata agcttgccgc 60  
 cgcatagggt tttttttttt ttttttacia agaatcaact ttattgaaca ttcagggtca 120  
 ggttctcttc ttgctcttgc ctgtgacctt ggctgggtgtg aggactggag ctgctgcctg 180  
 gtacagggtg gaggagatct tgttgatgta gtacagacca accatggaga agatgaagca 240  
 ggtgggtgaca cagactcggg ggatgaggcc agatgcaaag agagccaaca ggaggcacag 300  
 gagaatctca gggaagatct ttgcttgga tcttttgccc aagacaagat tttccaaatt 360  
 attgaaggca gtgagcgaga acacgaagag accctaacca agcaggccgc cttggatggt 420



gagccactcg gtggaggcca gctgacggct gtacatctgc atcccagcaa agagcagcag 480  
 ggacaggagg gaggagagcg ccagcgaggt gcccgtaccc accactggag gggatgggag 540  
 aagggacgga gagtcaggct ccgccctccc tccggcaagc tacgggcaga tcagccggtc 600  
 cggaagctcg gtgggcccgc cccctccaag aactcccggg actgcagcca cagccccaa 660  
 ctccccacac cgcgcggcaa cccctacgta ttccccagcc ccggacaccc cgaaccctcc 720  
 cgtccgggtg aa atg ccc gct ccc ggt gga acc cag gac acg tca gct 768  
 Met Pro Ala Pro Gly Gly Thr Gln Asp Thr Ser Ala  
 1 5 10  
 ctg tcg gga gag gac gag gaa agc ttg tcc acc caa acc ccg acc ccc 816  
 Leu Ser Gly Glu Asp Glu Glu Ser Leu Ser Thr Gln Thr Pro Thr Pro  
 15 20 25  
 tct agg act tcc tgg gga ccc cac cgg tcc tgt tac cca tca tgc ccc 864  
 Ser Arg Thr Ser Trp Gly Pro His Arg Ser Cys Tyr Pro Ser Cys Pro  
 30 35 40  
 gcc cgt gag tcc aac cgg cgc ctc tgg cca aga aag gcg agc tga acc 912  
 Ala Arg Glu Ser Asn Arg Arg Leu Trp Pro Arg Lys Ala Ser \*  
 45 50 55  
 ggggtgcgggt agctatgcgc atgcgtcagc gacgaaatcg tcgacccggg aattccggac 972  
 cggtacctca ggcgt 987

<210> 465  
 <211> 1618  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (255) .. (809)

<400> 465  
 ttccactgg aggtgggctt tattactgtc gccatgatgt gaaaagagga agacagcacc 60  
 cattcccacg cctcctagac actgtgcacc aacaactgtc tgctgggggtt agcacggagc 120  
 tgtccccacc cccaggggtca gagcaccac aggtgccgag ctggcccagg agacccccac 180  
 gctgctgacg ctgtttgcct tgtgtctgca caggcctcta ctaaactctc ccacacaatt 240  
 agtgtcttaa atat atg tac acg tat ata ttt tgt ccc aac tgt gtc agt 290  
 Met Tyr Thr Tyr Ile Phe Cys Pro Asn Cys Val Ser  
 1 5 10  
 tat aaa atg aaa act gac cac ttc tcc tta cgt tat ctt cac agt agc 338  
 Tyr Lys Met Lys Thr Asp His Phe Ser Leu Arg Tyr Leu His Ser Ser  
 15 20 25  
 tgt gca gaa gac aac aaa tcc agt gtt gat agc tca ggg cag gct gcc 386  
 Cys Ala Glu Asp Asn Lys Ser Ser Val Asp Ser Ser Gly Gln Ala Ala  
 30 35 40

cac ccc agc aaa ggg aag ttc ttc ccc cat ggg acc cac tgg ggg acc	434
His Pro Ser Lys Gly Lys Phe Phe Pro His Gly Thr His Trp Gly Thr	
45 50 55 60	
cag tgc cgc ggc cac atc tcc gtg ctt ggg tgg cag tgt agc tgc cca	482
Gln Cys Arg Gly His Ile Ser Val Leu Gly Trp Gln Cys Ser Cys Pro	
65 70 75	
tct acg ggg tgc cgg gtt ggc ttg ggc ctt gcc atg tgc cag acg cat	530
Ser Thr Gly Cys Arg Val Gly Leu Gly Leu Ala Met Cys Gln Thr His	
80 85 90	
gca tac ata cac aca cac aca cac aca cac aca cac acc cca ccc gat	578
Ala Tyr Ile His Thr His Thr His Thr His Thr His Thr Pro Pro Asp	
95 100 105	
tat gga gca cat cac acc gat ccc ttg cag agg tgg ggg ctg ggg ccc	626
Tyr Gly Ala His His Thr Asp Pro Leu Gln Arg Trp Gly Leu Gly Pro	
110 115 120	
agg aca atc aga agc agg gcc cct ccc cca gct gtc tcg aga cca aag	674
Arg Thr Ile Arg Ser Arg Ala Pro Pro Pro Ala Val Ser Arg Pro Lys	
125 130 135 140	
cca tcc agg gcc tct gag ccc tgg ggc atc acc cag aag cgc tgg gct	722
Pro Ser Arg Ala Ser Glu Pro Trp Gly Ile Thr Gln Lys Arg Trp Ala	
145 150 155	
ccc agg ctg gca ccc agc aca cca gga gcc cag ggc gcg tgg gag atg	770
Pro Arg Leu Ala Pro Ser Thr Pro Gly Ala Gln Gly Ala Trp Glu Met	
160 165 170	
cgc cag gga cgg tct ttc act cca gac cag gct gac taa taaatatgac	819
Arg Gln Gly Arg Ser Phe Thr Pro Asp Gln Ala Asp *	
175 180 185	
atccagtgtt gtcaggagat gagaaaataa cgtagacttg gctggactct gttgtcaagg	879
ccattcccag tcacagagga aacatcccag gtggtctcca ggcgtccagg tggtcttgca	939
cctgccgacc cccagaggcc agtgagggtc tggcagcaag atgtgctcca ttaggcaggc	999
aaagcagggc gacctgaacc aacgacatgt gtggggggtg tgggtctccac attctattca	1059
tgttcgagga gcgtcagtct cccaaggctg cggatggagg cccctagggt gctgcgactc	1119
ccactcctca cctgccccta accctgccgc catggccact ttcacccatg cctcgccgtg	1179
gggaaaggaa ggcccgcaaa ccctgcccct ggccggacagg gcagcccttg cctctgctca	1239
gtcagtgcac ggaaatgccc acagctccag ggagaccccc tagcaggcag agtgaccgtc	1299
aaggtaaggc ccacggtggc ccagcagcag cacacagctc agcggccccag accccaccct	1359
gggggatgcc cagaggcttc ctagacctgc actcaggcag acaagcatgt ggctgggcgg	1419
ccaccagcag acatctggcc gcctcaggag gctcttcctg gctctaaaga gaatccagtt	1479
ccaaattccc actttctctg ctcaaagtta cagtgtggtc ataattgcac gctctcatgg	1539
accacgtcc caccgagtg acaatgatgc cacagccact cagcttctag ctggctctac	1599
tccgaattcc accagactg	1618

<210> 466  
 <211> 4258  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (50)..(3259)

<400> 466  
 agaaggctct gtctactgca gcatcaatag agaacagtat gcaggcctt atg cca 55  
 Met Pro  
 1

act cag act gat gtc aag tta aaa ttc aag cca tta tct aaa aaa gtt 103  
 Thr Gln Thr Asp Val Lys Leu Lys Phe Lys Pro Leu Ser Lys Lys Val  
 5 10 15

gta tct gcc gct ctt cag ttt tca tta tct tgc att ttt ctg agg gaa 151  
 Val Ser Ala Ala Leu Gln Phe Ser Leu Ser Cys Ile Phe Leu Arg Glu  
 20 25 30

gga aaa gcc aca gat gaa gac atg caa agt ttg gct agt ttg atg agt 199  
 Gly Lys Ala Thr Asp Glu Asp Met Gln Ser Leu Ala Ser Leu Met Ser  
 35 40 45 50

atg aag cag gct gac att ggc aat tta gat gac ttc gaa gaa gat aat 247  
 Met Lys Gln Ala Asp Ile Gly Asn Leu Asp Asp Phe Glu Glu Asp Asn  
 55 60 65

gaa gat gat gat gag aac aga gtg aac caa gaa gaa aag gca gct aaa 295  
 Glu Asp Asp Asp Glu Asn Arg Val Asn Gln Glu Glu Lys Ala Ala Lys  
 70 75 80

att aca gag ctt atc aac aaa ctt aac ttt ttg gat gaa gca gaa aag 343  
 Ile Thr Glu Leu Ile Asn Lys Leu Asn Phe Leu Asp Glu Ala Glu Lys  
 85 90 95

gac ttg gcc acc gtg aat tca aat cca ttt gat gat cct gat gct gca 391  
 Asp Leu Ala Thr Val Asn Ser Asn Pro Phe Asp Asp Pro Asp Ala Ala  
 100 105 110

gaa tta aat cca ttt gga gat cct gac tca gaa gaa cct atc act gaa 439  
 Glu Leu Asn Pro Phe Gly Asp Pro Asp Ser Glu Glu Pro Ile Thr Glu  
 115 120 125 130

aca gct tca cct aga aaa aca gaa gac tct ttt tat aat aac agc tat 487  
 Thr Ala Ser Pro Arg Lys Thr Glu Asp Ser Phe Tyr Asn Asn Ser Tyr  
 135 140 145

aat ccc ttt aaa gag gtg cag act cca cag tat ttg aac cca ttc gat 535  
 Asn Pro Phe Lys Glu Val Gln Thr Pro Gln Tyr Leu Asn Pro Phe Asp  
 150 155 160

gag cca gaa gca ttt gtg acc ata aag gat tct cct ccc cag tct aca 583  
 Glu Pro Glu Ala Phe Val Thr Ile Lys Asp Ser Pro Pro Gln Ser Thr  
 165 170 175

aaa aga aaa aat ata aga cct gtg gat atg agc aag tac ctc tat gct 631  
 Lys Arg Lys Asn Ile Arg Pro Val Asp Met Ser Lys Tyr Leu Tyr Ala  
 180 185 190

gat agt tct aaa act gaa gaa gaa gaa ttg gat gaa tca aat cct ttt Asp Ser Ser Lys Thr Glu Glu Glu Glu Leu Asp Glu Ser Asn Pro Phe 195 200 205 210	679
tat gaa cct aaa tca act cct cct cca aat aat ttg gta aat cct gtt Tyr Glu Pro Lys Ser Thr Pro Pro Pro Asn Asn Leu Val Asn Pro Val 215 220 225	727
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ctccctcctt tccaaataat atacagaact ccaaaatagc ttcatttaag gatttttttg      3361

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ttggtattgg aggtgttcaa gaaactgttc gaaaaagaac aaaaacactt ccctcgttat      3481

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gtaaggataa tggagttcct ctctctgtct ttcttcagag gatggtcctt taacatagcc      3781

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aatattttct tctttagcat agcactgtca ttttttgatg aaatgggttat gtttatttat      4081

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Arg Arg Thr Ala Leu Ile Leu Gly Ser Gly Leu Leu Ser Phe Val Ala
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Phe Trp Asn Ser Val Thr Trp His Leu Gln Arg Phe Trp Gly Ala Ser
          20                      25                      30

ggc tac ttt tgg caa gcc cag tgg gag agg ctg ctg act aca ttt gaa      200
Gly Tyr Phe Trp Gln Ala Gln Trp Glu Arg Leu Leu Thr Thr Phe Glu
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ggg aag gag tgg atc ctc ttc ttt ata ggt gcc atc caa gtg cct tgt      248
Gly Lys Glu Trp Ile Leu Phe Phe Ile Gly Ala Ile Gln Val Pro Cys
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ctc ttc ttc tgg agc ttc aat ggg ctt cta ttg gtg gtt gac aca aca      296
Leu Phe Phe Trp Ser Phe Asn Gly Leu Leu Leu Val Val Asp Thr Thr
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gga aaa cct aac ttc atc tct cgc tac cga att cag gtc ggc aag aat      344
Gly Lys Pro Asn Phe Ile Ser Arg Tyr Arg Ile Gln Val Gly Lys Asn
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gaa cct gtg gat cct gtg aaa ctg cac cag tgc atg ata tct ttc ccc      392
Glu Pro Val Asp Pro Val Lys Leu His Gln Cys Met Ile Ser Phe Pro
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atg gtg gtc ttc ctc tat ccc ttc ctc aaa tgg tgg aga gac ccc tgc      440
Met Val Val Phe Leu Tyr Pro Phe Leu Lys Trp Trp Arg Asp Pro Cys
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cgc cgt gag cta ccc acc ttc cac tgg ttc ctc ctg gag ctg gcc atc      488
Arg Arg Glu Leu Pro Thr Phe His Trp Phe Leu Leu Glu Leu Ala Ile
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ttc acg ctg atc gag gaa gtc ttg ttc tac tat tca cac cgg ctc ctt      536
Phe Thr Leu Ile Glu Glu Val Leu Phe Tyr Tyr Ser His Arg Leu Leu
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cac cac cca aca ttc tac aag aaa atc cac aag aaa cac cat gag tgg      584
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tcc cac ttg tcc tcc atc acc atg tgg ttt tcc ttg gcc ctc atc atc      728
Ser His Leu Ser Ser Ile Thr Met Trp Phe Ser Leu Ala Leu Ile Ile
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acc acc atc tcc cac tgt ggc tac cac ctt ccc ttc ctg cct tcg cct      776

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1211

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gca gtt agc tct gag gga gca ttg ttc tgt tct gtg ggt gat gat aaa Ala Val Ser Ser Glu Gly Ala Leu Phe Cys Ser Val Gly Asp Asp Lys 60 65 70	544
gca atg aag gtg ttt gat gta gtg aac ttt gac atg atc aac atg ctg Ala Met Lys Val Phe Asp Val Val Asn Phe Asp Met Ile Asn Met Leu 75 80 85 90	592
aaa ctt ggc tat ttt cct gga cag tgt gag tgg atc tat tgc cca ggg Lys Leu Gly Tyr Phe Pro Gly Gln Cys Glu Trp Ile Tyr Cys Pro Gly 95 100 105	640
gat gca att tct tca gtt gct gct tcc gaa aag agt aca gga aaa att Asp Ala Ile Ser Ser Val Ala Ala Ser Glu Lys Ser Thr Gly Lys Ile 110 115 120	688
ttc att tat gat ggc cga gga gat aac cag cca ctt cat att ttt gac Phe Ile Tyr Asp Gly Arg Gly Asp Asn Gln Pro Leu His Ile Phe Asp 125 130 135	736
aaa ctc cat aca tca cct ctt act cag ata cgg cta aac cca gtt tac Lys Leu His Thr Ser Pro Leu Thr Gln Ile Arg Leu Asn Pro Val Tyr 140 145 150	784
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cgt gag ttg gag aag gtt gat gct gta aga tta att aat ata gtt ttt Arg Glu Leu Glu Lys Val Asp Ala Val Arg Leu Ile Asn Ile Val Phe 270 275 280	1168

gat gaa act gga cac ttc gtg ctg tat gga aca atg ctg ggc att aaa	1216
Asp Glu Thr Gly His Phe Val Leu Tyr Gly Thr Met Leu Gly Ile Lys	
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Val Ile Asn Val Glu Thr Asn Arg Cys Val Arg Ile Leu Gly Lys Gln	
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Glu Asn Ile Arg Val Met Gln Leu Ala Leu Phe Gln Gly Ile Ala Lys	
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Lys His Arg Ala Ala Thr Thr Ile Glu Met Lys Ala Ser Glu Asn Pro	
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Val Leu Gln Asn Ile Gln Ala Asp Pro Thr Ile Val Cys Thr Ser Phe	
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Lys Lys Asn Arg Phe Tyr Met Phe Thr Lys Arg Glu Pro Glu Asp Thr	
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Lys Ser Ala Asp Ser Asp Arg Asp Val Phe Asn Glu Lys Pro Ser Lys	
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Asp Ser Ala Ile Ile His Thr Ser Met Gly Asp Ile His Thr Lys Leu	
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Phe Pro Val Glu Cys Pro Lys Thr Val Glu Asn Phe Cys Val His Ser	
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Ser Ile Trp Gly Gly Glu Phe Glu Asp Glu Phe His Ser Thr Leu Arg	
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His Asp Arg Pro Tyr Thr Leu Ser Met Ala Asn Ala Gly Ser Asn Thr	
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Asn Gly Ser Gln Phe Phe Ile Thr Val Val Pro Thr Pro Trp Leu Asp	
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 555 560 565

taatgtactt gcaaataaaaa atacaatatt aaacagatta ttttacatta ggaagcttag 2094

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 Met Ala Ala Ser Arg Lys Pro Pro Arg Val Arg Val  
 1 5 10

aat cac cag gat ttt caa ctg aga aat tta aga ata att gaa cct aac 159  
 Asn His Gln Asp Phe Gln Leu Arg Asn Leu Arg Ile Ile Glu Pro Asn  
 15 20 25

gag gtg aca cac tca gga gac aca ggt gtg gaa aca gac ggc aga atg 207  
 Glu Val Thr His Ser Gly Asp Thr Gly Val Glu Thr Asp Gly Arg Met  
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cct cca aag gtg act tca gag ctg ctt cgg cag ctg aga caa gcc atg 255  
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agg aac tct gag tat gtg acc gaa ccg atc cag gcc tac atc atc cca 303  
 Arg Asn Ser Glu Tyr Val Thr Glu Pro Ile Gln Ala Tyr Ile Ile Pro  
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tcg gga gat gct cat cag agt gag tat att gct cca tgt gac tgt cgg 351  
 Ser Gly Asp Ala His Gln Ser Glu Tyr Ile Ala Pro Cys Asp Cys Arg  
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cgg gct ttt gtc tct gga ttc gat ggc tct gcg ggc aca gcc atc atc 399  
 Arg Ala Phe Val Ser Gly Phe Asp Gly Ser Ala Gly Thr Ala Ile Ile  
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 Thr Glu Glu His Ala Ala Met Trp Thr Asp Gly Arg Tyr Phe Leu Gln

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cct tgc aag cct ctc ctc aca ctg ggc ctg gat tac aca ggc atc tcc Pro Cys Lys Pro Leu Leu Thr Leu Gly Leu Asp Tyr Thr Gly Ile Ser 205 210 215 220			735
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ata gac gcc ccc agt gtg aag gag cac ctg ctt ctt gac ttg ggt ctg Ile Asp Ala Pro Ser Val Lys Glu His Leu Leu Leu Asp Leu Gly Leu 285 290 295 300			975
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365	370	375	380	
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Ala Val Ala Leu Cys Glu Leu Phe Asn Trp Leu Glu Lys Glu Val Pro				
	385	390	395	
aaa ggt ggt gtg aca gag atc tca gct gct gac aaa gct gag gag ttt				1311
Lys Gly Gly Val Thr Glu Ile Ser Ala Ala Asp Lys Ala Glu Glu Phe				
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cgc agg caa cag gca gac ttt gtg gac ctg agc ttc cca aca att tcc				1359
Arg Arg Gln Gln Ala Asp Phe Val Asp Leu Ser Phe Pro Thr Ile Ser				
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agt acg gga ccc aac ggc gcc atc att cac tac gcg cca gtc cct gag				1407
Ser Thr Gly Pro Asn Gly Ala Ile Ile His Tyr Ala Pro Val Pro Glu				
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Thr Asn Arg Thr Leu Ser Leu Asp Glu Val Tyr Leu Ile Asp Ser Gly				
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gct caa tac aag gat ggc acc aca gat gtg acg cgg aca atg cat ttt				1503
Ala Gln Tyr Lys Asp Gly Thr Thr Asp Val Thr Arg Thr Met His Phe				
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Gly Thr Pro Thr Ala Tyr Glu Lys Glu Cys Phe Thr Tyr Val Leu Lys				
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Gly His Ile Ala Val Ser Ala Ala Val Phe Pro Thr Gly Thr Lys Gly				
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cac ctt ctt gac tcc ttt gcc cgt tca gct tta tgg gat tca ggc cta				1647
His Leu Leu Asp Ser Phe Ala Arg Ser Ala Leu Trp Asp Ser Gly Leu				
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gat tac ttg cac ggg act gga cat ggt gtt ggg tct ttt ttg aat gtc				1695
Asp Tyr Leu His Gly Thr Gly His Gly Val Gly Ser Phe Leu Asn Val				
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cat gag ggt cct tgc ggc atc agt tac aaa aca ttc tct gat gag ccc				1743
His Glu Gly Pro Cys Gly Ile Ser Tyr Lys Thr Phe Ser Asp Glu Pro				
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Leu Glu Ala Gly Met Ile Val Thr Asp Glu Pro Gly Tyr Tyr Glu Asp				
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Gly Ala Phe Gly Ile Arg Ile Glu Asn Val Val Leu Val Val Pro Val				
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cta aca ttg gtt cca att cag acc aaa atg ata gat gtg gat tct ctt				1935
Leu Thr Leu Val Pro Ile Gln Thr Lys Met Ile Asp Val Asp Ser Leu				
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Thr Asp Lys Glu Cys Asp Trp Leu Asn Asn Tyr His Leu Thr Cys Arg				

625

630

635

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 640 645 650

gag tgg ctc atc aga gag acg caa ccc atc tcc aaa cag cat taa taa 2079  
 Glu Trp Leu Ile Arg Glu Thr Gln Pro Ile Ser Lys Gln His \*  
 655 660 665

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 Met Pro Glu Asn Pro Ala  
 1 5

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 Thr Asp Lys Leu Gln Val Leu Gln Val Leu Asp Arg Leu Lys Met Lys  
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 Leu Gln Glu Lys Gly Asp Thr Ser Gln Asn Glu Lys Leu Ser Met Phe  
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 Tyr Glu Thr Leu Lys Ser Pro Leu Phe Asn Gln Ile Leu Thr Leu Gln  
 40 45 50

cag tcc atc aag caa ctg aag ggt caa ctc aac cat ata ccc tca gat 364  
 Gln Ser Ile Lys Gln Leu Lys Gly Gln Leu Asn His Ile Pro Ser Asp  
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 Cys Ser Ala Asn Phe Asp Phe Ser Arg Lys Gly Leu Leu Val Phe Thr  
 75 80 85

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 90 95 100

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Phe	Asn	Ser	Val	Ile	Gln	Gln	Met	Ala	Gln	Gly	Arg	Gln	Ile	Glu	Tyr	
		120				125					130					
ata	gat	ata	gaa	cgg	cct	tca	act	gga	ggc	ctt	gga	ttc	agt	gtg	gtg	604
Ile	Asp	Ile	Glu	Arg	Pro	Ser	Thr	Gly	Gly	Leu	Gly	Phe	Ser	Val	Val	
135					140					145					150	
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Ala	Leu	Arg	Ser	Gln	Asn	Leu	Gly	Lys	Val	Asp	Ile	Phe	Val	Lys	Asp	
				155					160					165		
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Val	Gln	Pro	Gly	Ser	Val	Ala	Asp	Arg	Asp	Gln	Arg	Leu	Lys	Glu	Asn	
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gat	caa	ata	ttg	gcc	att	aat	cac	acg	cca	ttg	gat	cag	aac	att	tcc	748
Asp	Gln	Ile	Leu	Ala	Ile	Asn	His	Thr	Pro	Leu	Asp	Gln	Asn	Ile	Ser	
		185					190					195				
cat	cag	caa	gca	att	gca	tta	tta	caa	caa	acc	act	gga	tct	ttg	aga	796
His	Gln	Gln	Ala	Ile	Ala	Leu	Leu	Gln	Gln	Thr	Thr	Gly	Ser	Leu	Arg	
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ctg	att	gtg	gcc	agg	gaa	cca	gtc	cac	aca	aaa	agc	agt	act	tct	agc	844
Leu	Ile	Val	Ala	Arg	Glu	Pro	Val	His	Thr	Lys	Ser	Ser	Thr	Ser	Ser	
215					220					225					230	
agc	cta	aat	gat	aca	act	ctg	cct	gaa	aca	gtt	tgt	tgg	ggc	cat	gtt	892
Ser	Leu	Asn	Asp	Thr	Thr	Leu	Pro	Glu	Thr	Val	Cys	Trp	Gly	His	Val	
				235					240					245		
gaa	gag	gtt	gag	ctc	att	aat	gat	ggc	tct	gga	cta	ggt	ttt	gga	ata	940
Glu	Glu	Val	Glu	Leu	Ile	Asn	Asp	Gly	Ser	Gly	Leu	Gly	Phe	Gly	Ile	
			250					255					260			
gtt	gga	gga	aaa	aca	agt	ggc	gtg	gtt	gtg	agg	act	ata	gtt	cct	gga	988
Val	Gly	Gly	Lys	Thr	Ser	Gly	Val	Val	Val	Arg	Thr	Ile	Val	Pro	Gly	
		265					270					275				
gga	tta	gca	gat	cga	gat	gga	aga	ctc	cag	aca	ggg	gac	cac	atc	ttg	1036
Gly	Leu	Ala	Asp	Arg	Asp	Gly	Arg	Leu	Gln	Thr	Gly	Asp	His	Ile	Leu	
		280				285						290				
aag	att	ggt	ggc	aca	aac	gtg	cag	gga	atg	acc	agt	gag	caa	gtt	gca	1084
Lys	Ile	Gly	Gly	Thr	Asn	Val	Gln	Gly	Met	Thr	Ser	Glu	Gln	Val	Ala	
295					300					305					310	
caa	gtt	cta	agg	aac	tgt	ggg	aat	tca	gtc	agg	atg	ctc	gtt	gct	aga	1132
Gln	Val	Leu	Arg	Asn	Cys	Gly	Asn	Ser	Val	Arg	Met	Leu	Val	Ala	Arg	
				315					320					325		
gat	cca	gct	ggt	gac	att	tca	gtc	acc	ccc	cct	gcc	cct	gca	gcc	tta	1180
Asp	Pro	Ala	Gly	Asp	Ile	Ser	Val	Thr	Pro	Pro	Ala	Pro	Ala	Ala	Leu	
			330					335					340			
cct	gtt	gcc	ctg	cct	act	gta	gcc	agc	aag	ggc	cct	ggt	tct	gac	agt	1228
Pro	Val	Ala	Leu	Pro	Thr	Val	Ala	Ser	Lys	Gly	Pro	Gly	Ser	Asp	Ser	
		345					350					355				
tct	ctt	ttt	gaa	act	tat	aat	gtt	gag	ctt	gtg	aga	aaa	gat	ggg	cag	1276

Ser	Leu	Phe	Glu	Thr	Tyr	Asn	Val	Glu	Leu	Val	Arg	Lys	Asp	Gly	Gln	
360						365					370					
agt	ctt	gga	att	aga	att	gtt	ggc	tat	gtt	gga	aca	tct	cat	aca	ggg	1324
Ser	Leu	Gly	Ile	Arg	Ile	Val	Gly	Tyr	Val	Gly	Thr	Ser	His	Thr	Gly	
375					380					385					390	
gaa	gct	tca	ggg	att	tat	gtg	aaa	agt	ata	ata	cct	ggc	agt	gct	gcg	1372
Glu	Ala	Ser	Gly	Ile	Tyr	Val	Lys	Ser	Ile	Ile	Pro	Gly	Ser	Ala	Ala	
				395					400					405		
tac	cac	aat	ggc	cac	att	caa	gtg	aat	gac	aaa	ata	gtt	gct	gtc	gat	1420
Tyr	His	Asn	Gly	His	Ile	Gln	Val	Asn	Asp	Lys	Ile	Val	Ala	Val	Asp	
			410					415					420			
ggc	gtg	aac	att	cag	ggg	ttt	gcc	aac	cat	gat	gtt	gtt	gaa	gta	tta	1468
Gly	Val	Asn	Ile	Gln	Gly	Phe	Ala	Asn	His	Asp	Val	Val	Glu	Val	Leu	
		425					430					435				
cga	aat	gca	ggg	cag	gtg	gta	cac	cta	acc	cta	gtt	cga	agg	aag	aca	1516
Arg	Asn	Ala	Gly	Gln	Val	Val	His	Leu	Thr	Leu	Val	Arg	Arg	Lys	Thr	
	440					445					450					
tcc	tca	tct	act	tct	cca	ctt	gaa	cca	cct	tca	gac	aga	gga	act	gtt	1564
Ser	Ser	Ser	Thr	Ser	Pro	Leu	Glu	Pro	Pro	Ser	Asp	Arg	Gly	Thr	Val	
455					460					465					470	
gta	gaa	cca	ctg	aaa	cca	cca	gct	ctc	ttt	cta	act	gga	gca	gtg	gaa	1612
Val	Glu	Pro	Leu	Lys	Pro	Pro	Ala	Leu	Phe	Leu	Thr	Gly	Ala	Val	Glu	
				475					480					485		
act	gaa	act	aat	gtg	gat	ggg	gaa	gat	gag	gaa	att	aaa	gaa	aga	att	1660
Thr	Glu	Thr	Asn	Val	Asp	Gly	Glu	Asp	Glu	Glu	Ile	Lys	Glu	Arg	Ile	
			490					495					500			
gat	act	tta	aaa	aat	gac	aac	ata	caa	gcc	tta	gaa	aaa	ttg	gaa	aaa	1708
Asp	Thr	Leu	Lys	Asn	Asp	Asn	Ile	Gln	Ala	Leu	Glu	Lys	Leu	Glu	Lys	
		505					510					515				
gtc	cca	gac	tct	cca	gaa	aat	gag	ctg	aaa	tcc	aga	tgg	gaa	aac	ctg	1756
Val	Pro	Asp	Ser	Pro	Glu	Asn	Glu	Leu	Lys	Ser	Arg	Trp	Glu	Asn	Leu	
	520					525					530					
ttg	ggg	cct	gat	tat	gaa	gta	atg	gtt	gct	act	ttg	gac	aca	cag	att	1804
Leu	Gly	Pro	Asp	Tyr	Glu	Val	Met	Val	Ala	Thr	Leu	Asp	Thr	Gln	Ile	
535					540					545					550	
gca	gat	gat	gct	gag	tta	cag	aaa	tat	tca	aag	ctg	ctg	cct	att	cac	1852
Ala	Asp	Asp	Ala	Glu	Leu	Gln	Lys	Tyr	Ser	Lys	Leu	Leu	Pro	Ile	His	
				555					560					565		
act	ctg	agg	ctt	ggg	gtg	gaa	gtg	gat	tcc	ttt	gat	ggg	cac	cat	tat	1900
Thr	Leu	Arg	Leu	Gly	Val	Glu	Val	Asp	Ser	Phe	Asp	Gly	His	His	Tyr	
			570					575					580			
att	tct	tca	att	gtt	tct	ggg	ggg	cct	gtt	gat	aca	ttg	ggg	ctc	cta	1948
Ile	Ser	Ser	Ile	Val	Ser	Gly	Gly	Pro	Val	Asp	Thr	Leu	Gly	Leu	Leu	
		585					590					595				
cag	cca	gaa	gat	gag	ctg	ctt	gag	gtc	aat	ggc	atg	cag	ctt	tat	gga	1996
Gln	Pro	Glu	Asp	Glu	Leu	Leu	Glu	Val	Asn	Gly	Met	Gln	Leu	Tyr	Gly	
	600					605				610						
aaa	tct	cgc	cga	gaa	gca	gtc	tcc	ttt	ctt	aaa	gaa	gtg	cca	ccc	cct	2044